

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 1, 2004, 11:56:15 ; Search time 63.2 Seconds
(without alignments)
71.531 Million cell updates/sec

Title: US-09-830-779-7

Perfect score: 92
Sequence: 1 RQIKWFEQRNRMKWK 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : A_Geneseq_29Jan04.*
1: Genesep1980s.*
2: Genesep1990s.*
3: Genesep2000s.*
4: Genesep2001s.*
5: Genesep2002s.*
6: Genesep2003s.*
7: Genesep2003bs.*
8: Genesep2004s.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	92	100.0	16	2 AAW45974	Aaw45974 Cysteine
2	92	100.0	16	2 AAW33407	Aaw33407 Peptide 4
3	92	100.0	16	2 AAW33410	Aaw33410 D-form pe
4	92	100.0	16	2 AAW82958	Aaw82958 Oestrogen
5	92	100.0	16	2 AAW56397	Aaw56397 Preferred
6	92	100.0	16	2 AAW71270	Aaw71270 Antennape
7	92	100.0	16	2 AAW71316	Aaw71316 Antennape
8	92	100.0	16	2 AAW30508	Aaw30508 Drosophil
9	92	100.0	16	2 AAW91046	Aaw91046 Internall
10	92	100.0	16	2 AAY52102	Aay52102 Peptide f
11	92	100.0	16	2 AAY00859	Aay00859 Peptide p
12	92	100.0	16	2 AAY13509	Aay13509 Signal se
13	92	100.0	16	3 AAY87920	Aay87920 Drosophil
14	92	100.0	16	3 AAB27060	Aab27060 Beta-Gate
15	92	100.0	16	3 AAY93667	Aay93667 Peptide w
16	92	100.0	16	3 AAY67966	Aay67966 Carboxyfl
17	92	100.0	16	3 AAY93551	Aay93551 Amino aci
18	92	100.0	16	3 AAY55818	Aay55818 Signal se
19	92	100.0	16	3 AAY71008	Aay71008 Drosophil
20	92	100.0	16	3 AAY51212	Aay51212 Antennape
21	92	100.0	16	3 AAY51167	Aay51167 Drosophil
22	92	100.0	16	3 AAB10343	Aab10343 Peptide A
23	92	100.0	16	3 AAB19251	Aab19251 Fragment
24	92	100.0	16	3 AAY93178	Aay93178 Protegrin
25	92	100.0	16	3 AAB35694	Aab35694 Peptide a

26	92	100.0	16	3 AAB22025	Aab22025 Membrane
27	92	100.0	16	3 AAB29423	Aab29423 ANTP pept
28	92	100.0	16	3 AAB03927	Aab03927 Internall
29	92	100.0	16	3 AAY33954	Aay33954 Peptide u
30	92	100.0	16	3 AAB29574	Aab29574 Antennape
31	92	100.0	16	3 ADE14785	Adel14785 Carrier m
32	92	100.0	16	3 ADE14761	Adel14761 Drosophil
33	92	100.0	16	4 AAB73091	Aab73091 Rheumatoi
34	92	100.0	16	4 AAB60004	Aab60004 Internall
35	92	100.0	16	4 AAB70753	Aab70753 Cell memb
36	92	100.0	16	4 AAE02974	Aae02974 Protein c
37	92	100.0	16	4 AAB06671	Aab06671 Antennape
38	92	100.0	16	4 AAU06064	Aau06064 Drosophil
39	92	100.0	16	4 AAB49914	Aab49914 HIF-1alph
40	92	100.0	16	4 AAB66996	Aab66996 Antennape
41	92	100.0	16	4 AAU00813	Aau00813 Fruit fly
42	92	100.0	16	4 AAE12205	Aae12205 Membrane
43	92	100.0	16	4 ABB78030	Abb78030 Peptide d
44	92	100.0	16	5 ABB78985	Abb78985 Cell pene
45	92	100.0	16	5 ABB78214	Abb78214 Amino aci
46	92	100.0	16	5 AAE15616	Aae15616 Drosophil
47	92	100.0	16	5 AAU15781	Aau15781 Antennape
48	92	100.0	16	5 AAU78345	Aau78345 Antennape
49	92	100.0	16	5 ABB68406	Abb68406 Transloca
50	92	100.0	16	5 ABB33153	Abb33153 Transduct
51	92	100.0	16	5 ABB53809	Abb53809 Penetrati
52	92	100.0	16	5 AAE35451	Aae35451 Drosophil
53	92	100.0	16	5 AAG75500	Ag75500 Fruit fly
54	92	100.0	16	5 ABB60447	Abb60447 Selective
55	92	100.0	16	5 ABB30763	Abb30763 B2F-1/CYC
56	92	100.0	16	5 AAU78912	Aau78912 Antennape
57	92	100.0	16	5 ABB81174	Abb81174 Antennape
58	92	100.0	16	5 AAU77234	Aau77234 Drosophil
59	92	100.0	16	5 ABB95801	Abb95801 Cell pene
60	92	100.0	16	5 ABB54754	Abb54754 Antennape
61	92	100.0	16	5 AAM47571	Aam47571 Penetrati
62	92	100.0	16	5 AAM48196	Aam48196 Drosophil
63	92	100.0	16	5 AAE23684	Aae23684 Fluoresce
64	92	100.0	16	5 ABB72298	Abb72298 ANTENNABE
65	92	100.0	16	6 ABB32768	Abb32768 DGI-3 spe
66	92	100.0	16	6 AAE35385	Aae35385 Antennape
67	92	100.0	16	6 AAG73390	Ag73390 Penetrati
68	92	100.0	16	6 ABB82532	Abb82532 Drosophil
69	92	100.0	16	6 ABB99502	Abb99502 Sequence
70	92	100.0	16	6 AAU19913	Aau19913 Antennape
71	92	100.0	16	6 ABB76121	Abb76121 Fruitfly
72	92	100.0	16	6 ABR56859	Ab56859 Antennape
73	92	100.0	16	6 ABU09581	Abu09581 Cell perm
74	92	100.0	16	6 ABB96963	Abb96963 Anti-infl
75	92	100.0	16	6 ABR84442	Ab84442 Penetrati
76	92	100.0	16	6 ABU07549	Abu07549 Fruitfly
77	92	100.0	16	6 AAE33891	Aae33891 Drosophil
78	92	100.0	16	6 AAE33889	Aae33889 Drosophil
79	92	100.0	16	6 AAU16665	Aau16665 Drosophil
80	92	100.0	16	6 ABR43125	Ab43125 Human mem
81	92	100.0	16	6 ABB70230	Abb70230 Membrane
82	92	100.0	16	6 ABB70225	Abb70225 Membrane
83	92	100.0	16	6 AAG79772	Ag79772 Penetrati
84	92	100.0	16	6 ABU09587	Abu09587 Antennape
85	92	100.0	16	6 ABR57028	Ab57028 Antennape
86	92	100.0	16	6 ABB82912	Abb82912 Antennape
87	92	100.0	16	6 ABB82912	Abb82912 Antennape
88	92	100.0	16	6 ABB82912	Abb82912 Antennape
89	92	100.0	16	6 ADA38246	Ada38246 Drosophil
90	92	100.0	16	7 ABB39031	Abb39031 Human tra
91	92	100.0	16	7 AAE38685	Aae38685 Antennape
92	92	100.0	16	7 AAE38689	Aae38689 D-penetra
93	92	100.0	16	7 ADC42900	Adc42900 D-penetra
94	92	100.0	16	7 ADC42896	Adc42896 Antennape
95	92	100.0	16	7 ADD28156	Add28156 Penetrati
96	92	100.0	16	7 ADE36650	Ade36650 Drosophil
97	92	100.0	16	7 ADE86319	Ade86319 Antennape
98	92	100.0	17	3 AAY83520	Aay83520 Peptide i

99 92 100.0 17 3 AAB13424 Synthetic
100 92 100.0 17 3 ADE14787 Carrier m

RESULT 2
AAW33407
ID AAW33407 standard; peptide; 16 AA.
XX
AC AAW33407;
XX
XX 27-AUG-2003 (revised)
DT 17-MAR-1998 (first entry)
XX
XX Peptide 43-58 of homeodomain Antp.
DE
XX homeodomain; transcription factor; Antennapedia; Antp; vector;
KW transfection; hydrophobic.
XX
OS Unidentified.
XX
XX WO9712912-A1.
FN
XX 10-APR-1997.
PD
XX
XX 04-OCT-1996; 96WO-FR001553.
PF
XX 05-OCT-1995; 95FR-00011714.
PR
XX (CNRS) CNRS CENT NAT RECH SCI.
PA
XX Chassaing G, Prochiantz A;
XX WPI; 1997-226166/20.
XX
XX New peptide(s) of high hydrophobic amino acid content - useful as vectors
PT for delivering peptides and nucleic acids to cells.
XX
XX Claim 1; Page 7; 35pp; French.

ALIGNMENTS

RESULT 1
AAW45974
ID AAW45974 standard; peptide; 16 AA.
XX
AC AAW45974;
XX
XX 01-JUL-1998 (first entry)
DT
XX Cysteine protease inhibiting peptide for preventing cell death.
DE
XX Neuronal cell death; neurodegenerative disorder; inhibition;
KW cysteine protease; cardiovascular; liver disease.
XX
OS Synthetic.
XX
XX Key Location/Qualifiers
FT Modified-site 1
FT /note= "N-3-nitro-2-pyridyl-sulphenyl-Arg"
XX
XX WO9735876-A1.
FN
XX
XX 02-OCT-1997.
PD
XX 04-MAR-1997; 97WO-US004158.
PF
XX 04-MAR-1996; 96US-00610220.
PR
XX (UYCO) UNIV COLUMBIA NEW YORK.
PA
XX
XX Troy CM;
PI
XX
XX WPI; 1997-489561/45.
DR
XX
XX New cysteine protease inhibiting peptide(s) for preventing cell death -
PT in cases of neurodegenerative, cardiovascular and liver diseases, and
PT their peptide mimetics, and general method for identifying enzyme
PT inhibiting peptides.
XX
XX Claim 8; Page 68; 112pp; English.

XX This sequence represents a specifically claimed peptide of the formula: V
CC -(AA1)n-Cys(V')-(AA2)m-V' (I), in which n and m = 0-5, totalling 2-5; if
CC n = 1, AA1 = Ala; if n = 2, (AA1)n = Gln-Ala; and if n = 3 or more, (AA1)n
CC = (X)p-Gln-Ala; X = any amino acid; p = 1-3, depending on value of n; if
CC m = 1, AA2 = Arg; if m = 2, (AA2)n = Arg-Gly; if m = 3 or more, (AA2)n =
CC Arg-Gly-(X)q; q = 1-3, depending on value of m; V, V', and V'', any or all
CC of which may be absent, = agent able to direct the compound to a specific
CC cell. The peptides are inhibitors of cysteine proteases, specifically
CC interleukin-1 beta converting enzyme (ICE). They inhibit death of cells,
CC particularly in humans, and can be used to treat neurodegenerative
CC diseases (e.g. ageing, Alzheimer's, Machado-Joseph, Parkinson's or
CC Huntington's diseases, multiple sclerosis, muscular dystrophy, stroke),
CC cardiovascular disease and liver disorders. The peptides should be more
CC specific than pseudosubstrate inhibitors
XX
XX Sequence 16 AA;

Query Match 100.0%; Score 92; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 8.6e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 RQIKWIFQNRRMKWK 16
DB 1 RQIKWIFQNRRMKWK 16

RESULT 3
AAW33410
ID AAW33410 standard; peptide; 16 AA.
XX
AC AAW33410;
XX
XX 17-MAR-1998 (first entry)
DT
XX D-form peptide 43-58 of homeodomain Antp.
DE
XX homeodomain; transcription factor; Antennapedia; Antp; vector;
KW

New peptides are provided which are 16 amino acids long and which are analogues of the peptide corresponding to residues 43-58 of the Antennapedia transcription factor homeodomain (AntpHD). The peptides contain 6-10 hydrophobic amino acids. They have the general formula: X1-X2-X3-X4-X5-Tyr-X6-X7-X8-X9-X10-X11-X12-X13-X14-X15-X16 or X16-X15-X14-X13-X12-X11-X10-X9-X8-X7-Trp-X5-X4-X3-X2-X1 in which X1-X5 and X7-X16 are any alpha-amino acids, provided that: (1) the peptide contains 6-10 hydrophobic amino acids; (2) X3 and X5 are not both Val; and (3) the natural Antp 43-58 sequence RQIKWIFQNRRMKWK (i.e. the present sequence) is excluded. Specific examples of these peptides are given in AAW33408 - AAW33416. The peptides are used as vectors for introducing into live cells compounds which affect cell function, esp. peptides and nucleic acids. They can cross cellular membranes and reach various cell compartments. They are as effective as helix 3 of a homeodomain peptide. (Updated on 27-AUG-2003 to correct OS field.)

Sequence 16 AA;
Query Match 100.0%; Score 92; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 8.6e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RQIKWIFQNRRMKWK 16
DB 1 RQIKWIFQNRRMKWK 16

KW transfection; hydrophobic.
XX OS
XX Synthetic.
XX Key
FH Location/Qualifiers
FT Misc-difference 1..16
FT /note= "all residues are D-form"
FT Modified-site 1
FT /note= "in determining the ability of this sequence to be
FT internalised in cells, a biotin-aminopentanoyl group was
FT attached to the N-terminal"
XX PA
XX WO9712912-A1.
XX PN
XX PD
XX 10-APR-1997.
XX PF
XX 04-OCT-1996; 96WO-FR001553.
XX PR
XX 05-OCT-1995; 95FR-00011714.
XX (CNRS) CNRS CENT NAT RECH SCI.
XX PA
XX Chassaing G, Prochiantz A;
XX WPI; 1997-226166/20.
XX DR
XX New peptide(s) of high hydrophobic amino acid content - useful as vectors
XX for delivering peptides and nucleic acids to cells.
XX PS
XX Disclosure; Page 7; 35pp; French.
XX CC
XX New peptides are provided which are 16 amino acids long and which are
XX analogues of the peptide corresponding to residues 43-58 of the
XX Antennapedia transcription factor homeodomain (AntpHD). The peptides
XX contain 6-10 hydrophobic amino acids. They have the general formula: X1-
XX X2-X3-X4-X5-Trp-X7-X8-X9-X10-X11-X12-X13-X14-X15-X16 or X16-X15-X14-X13-
XX X12-X11-X10-X9-X8-X7-Trp-X4-X3-X2-X1 in which X1-X5 and X7-X16 are any
XX alpha-amino acids, provided that: (1) the peptide contains 6-10
XX hydrophobic amino acids; (2) X3 and X5 are not both Val; and (3) the
XX natural Antp 43-58 sequence RQIKWQNRRMKWKK (see AAW33407) is excluded.
XX The present sequence (the D-form of the 43-58 peptide) is a specific
XX example of the new peptides. The peptides are used as vectors for
XX introducing into live cells compounds which affect cell function,
XX especially peptides and nucleic acids. They can cross cellular membranes
XX and reach various cell compartments. They are as effective as helix 3 of
XX a homeodomain peptide
XX SQ
XX Sequence 16 AA;
XX Query Match 100.0%; Score 92; DB 2; Length 16;
XX Best Local Similarity 100.0%; Pred. No. 8.6e-07;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 RQIKWQNRRMKWKK 16
XX Db 1 RQIKWQNRRMKWKK 16
XX RESULT 4
XX AAW82958
XX ID AAW82958 standard; peptide; 16 AA.
XX AC AAW82958;
XX DX
XX 04-FEB-1999 (first entry)
XX DE
XX Oestrogen receptor activity inhibiting peptide #14.
XX KW
XX Human; oestrogen receptor activity inhibitor; anti-oestrogen; diagnosis;
XX breast cancer; estrogen; tumour; phosphotyrosyl peptide;
XX malonyltyrosyl peptide; steroid receptor co-activator-1.
XX OS
XX Synthetic.
OS Homo sapiens.
XX PN WO9846250-A1.
XX PD 22-OCT-1998.
XX PF 14-APR-1998; 98WO-US007711.
XX PR 14-APR-1997; 97US-0043545P.
XX PA (REGC) UNIV CALIFORNIA.
XX PI Pietras RJ;
XX DR WPI; 1998-594522/50.
XX PF
XX New anti-oestrogen peptide compositions - comprise sequences based on
XX oestrogen receptor and steroid receptor co-activator-1 sequences, used
XX for treating cancers.
XX PS
XX Claim 59; Page 156; 182pp; English.
XX CC
XX The present invention describes a composition comprising an isolated
XX oestrogen receptor activity inhibiting (anti-oestrogen) peptide. The
XX peptides used in the composition comprise sequences of human oestrogen
XX receptor (OR) surrounding Tyr537 and steroid receptor co-activator-1 (SRC
XX -1). The peptide compositions, nucleic acids and vectors of the present
XX invention can reduce OR activity in a cell, reduced OR polypeptide
XX dimerisation in a cell and reduce the binding of SRC-1 polypeptide to an
XX OR polypeptide dimer in a cell. They can be used for killing cancer cells
XX and treating cancers, particularly breast cancer. The present sequence
XX represents a specifically claimed anti-oestrogen peptide
XX SQ
XX Sequence 16 AA;
XX Query Match 100.0%; Score 92; DB 2; Length 16;
XX Best Local Similarity 100.0%; Pred. No. 8.6e-07;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 RQIKWQNRRMKWKK 16
XX Db 1 RQIKWQNRRMKWKK 16
XX RESULT 5
XX AAW56397
XX ID AAW56397 standard; peptide; 16 AA.
XX AC AAW56397;
XX DX
XX 05-AUG-1998 (first entry)
XX DE
XX Preferred signal sequence of the invention.
XX KW
XX Signal peptide; nuclear localisation signal; NLS;
XX immunosuppressive activity; inhibition; nuclear translocation inhibitor;
XX nuclear translocation; treatment; immune disorder; autoimmune disease;
XX hypersensitivity; sepsis; prevention; septic shock; antiviral agent;
XX tumour growth suppressor.
XX OS
XX Unidentified.
XX PN WO9811907-A1.
XX PD 26-MAR-1998.
XX PF 15-SEP-1997; 97WO-US016217.
XX KW
XX 20-SEP-1996; 96US-0026978P.
XX PR 12-SEP-1997; 97US-00928958.
XX PA (BRIM) BRISTOL-MYERS SQUIBB CO.

PI Nadler SG, Cleaveland JS, Blake J, Haffar OK;

XX WPI; 1998-217028/19.

XX Nuclear translocation inhibitor polypeptides - comprising signal sequence
PT for delivery through the cytoplasmic membrane and at least 2 nuclear
PT localisation sequences.

XX Claim 5; Page 43; 69pp; English.

XX Peptides AAW56397-99 represent preferred signal sequences of the
CC invention. They are used to construct the nuclear translocation inhibitor
CC polypeptides of the invention. Nuclear translocation inhibitor
CC polypeptides comprise a signal sequence peptide capable of delivering the
CC polypeptide through the cytoplasmic membrane into a cell, and at least 2
CC nuclear localisation signals (NLSs). The polypeptides can be used to
CC inhibit nuclear translocation of a cellular protein. In addition, since
CC the nuclear translocation of certain cellular peptides is required for
CC the host organism to mount an immune response, the polypeptide inhibitors
CC are useful as immunosuppression agents. The polypeptides can therefore be
CC used for the treatment of immune disorders including autoimmune diseases.
CC The polypeptides can also be used for treating physical symptoms
CC manifested by responses to allergens which can initiate a state of
CC hypersensitivity, for the treatment of sepsis and in the prevention of
CC septic shock, antiviral agents, tumour growth suppressors, and for
CC transcriptionally modulating the expression of cellular genes

XX Sequence 16 AA;

Query Match 100.0%; Score 92; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 8.6e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ROIKIWFQNRMRKWK 16
Db 1 ROIKIWFQNRMRKWK 16

RESULT 5
AAW71270
ID AAW71270 standard; protein; 16 AA.

XX AAW71270;

XX 23-NOV-1998 (first entry)

XX Antennapedia peptide for directing antisense oligonucleotides to a cell.

XX Antisense oligonucleotide; inhibit; cell death; Nedd2; human Ich-1L gene;
XX neuronal cell death; treatment; aging; amyotrophic lateral sclerosis;
XX Alzheimer's disease; dentatorubral; pallidolysial atrophy;
XX Huntington's disease; Machado-Joseph disease; multiple sclerosis;
XX muscular dystrophy; Parkinson's disease; senility;
XX spinocerebellar ataxia type I; spinobulbar muscular atrophy; stroke;
XX trauma; antennapedia.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1
FT /note= "N-terminal protected with 3-nitro-2-pyridyl
FT sulphenyl group (NpYS)"

XX WO9838861-Al.

XX 11-SEP-1998.

XX 03-MAR-1998; 98WO-US004128.

XX 03-MAR-1997; 97US-00810540.

XX (UYCO) UNIV COLUMBIA NEW YORK.

XX

PI Troy CM, Shelanski ML;

XX WPI; 1998-506333/43.

XX Anti-sense oligonucleotide(s) to cysteine aspartase genes - used to
PT inhibit neurodegenerative disorder associated with e.g. ageing,
PT Alzheimer's, Huntington's or Parkinson's disease.

XX Claim 5; Page 39; 60pp; English.

XX AAW71270 and AAW71315-16 represent antennapedia peptides which are used
CC to, direct the antisense oligonucleotides (AAV54973-74) of the invention
CC to a cell. The antisense oligonucleotides are used to inhibit cell death
CC mediated by withdrawal of a trophic factor. AAV54973 inhibits the
CC expression of a Nedd2 rodent gene, while AAV54974 inhibits expression of
CC a human Ich-1L gene. The oligonucleotides are used to inhibit neuronal
CC cell death, especially for treatment of neuronal cell death caused by
CC e.g. aging, amyotrophic lateral sclerosis, Alzheimer's disease, Machado-
CC dentatorubral and pallidolysial atrophy, Huntington's disease, Parkinson's
CC Joseph disease, multiple sclerosis, muscular dystrophy, Parkinson's
CC disease, senility, spinocerebellar ataxia type I, spinobulbar muscular
CC atrophy, stroke or trauma

XX Sequence 16 AA;

Query Match 100.0%; Score 92; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 8.6e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ROIKIWFQNRMRKWK 16
Db 1 ROIKIWFQNRMRKWK 16

RESULT 7

AAW71316
ID AAW71316 standard; protein; 16 AA.

XX AAW71316;

XX 23-NOV-1998 (first entry)

XX Antennapedia peptide for directing antisense oligonucleotides to a cell.

XX Antisense oligonucleotide; inhibit; cell death; Nedd2; human Ich-1L gene;
XX neuronal cell death; treatment; aging; amyotrophic lateral sclerosis;
XX Alzheimer's disease; dentatorubral; pallidolysial atrophy;
XX Huntington's disease; Machado-Joseph disease; multiple sclerosis;
XX muscular dystrophy; Parkinson's disease; senility;
XX spinocerebellar ataxia type I; spinobulbar muscular atrophy; stroke;
XX trauma; antennapedia.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1
FT /note= "N-terminal protected with 3-nitro-2-pyridyl
FT sulphenyl group (NpYS)"

XX WO9838861-Al.

XX 11-SEP-1998.

XX 03-MAR-1998; 98WO-US004128.

XX 03-MAR-1997; 97US-00810540.

XX (UYCO) UNIV COLUMBIA NEW YORK.

XX Troy CM, Shelanski ML;

XX WPI; 1998-506333/43.

XX

PT Anti-sense oligonucleotide(s) to cysteine aspartase genes - used to
 PT inhibit neurodegenerative disorder associated with e.g. ageing,
 PT Alzheimer's, Huntington's or Parkinson's disease.
 XX
 PS Disclosure; Page 14; 60pp; English.
 CC
 CC AAW71270 and AAW71315-16 represent antennapedia peptides which are used
 CC to, direct the antisense oligonucleotides (AAV54973-74) of the invention
 CC to a cell. The antisense oligonucleotides are used to inhibit cell death
 CC mediated by withdrawal of a trophic factor. AAV54973 inhibits the
 CC expression of a Nedd2 rodent gene, while AAV54974 inhibits the
 CC expression of a human Ich-1L gene. The oligonucleotides are used to inhibit neuronal
 CC cell death, especially for treatment of neuronal cell death caused by
 CC e.g. aging, amyotrophic lateral sclerosis, Alzheimer's disease,
 CC denatorubral and pallidolysual atrophy, Huntington's disease, Machado-
 CC Joseph disease, multiple sclerosis, muscular dystrophy, Parkinson's
 CC disease, senility, spinocerebellar ataxia type I, spinobulbar muscular
 CC atrophy, stroke or trauma
 XX
 SQ Sequence 16 AA;

Query Match 100.0%; Score 92; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 8.6e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RQIKWQNRRMKWKK 16
 Db 1 RQIKWQNRRMKWKK 16

RESULT 8
 AAW30508
 ID AAW30508 standard; peptide; 16 AA.

AC AAW30508;

DT 26-OCT-1998 (first entry)

DE Drosophila membrane translocation sequence.

KW DP-1; transcription factor; antagonist; E2F protein; apoptosis;
 KW cell proliferation; cardiovascular cell; restenosis; tumour;
 KW surgical stent; therapy; membrane translocation; antennapedia protein.

XX Drosophila melanogaster.

OS WO9828334-A1.

PN 02-JUL-1998.

XX 22-DEC-1997; 97WO-GB003506.

XX 20-DEC-1996; 96GB-00026589.

XX (PROL-) PROLIFIX LTD.

XX La Thangue NB, Bandara LR;

XX WPI; 1998-377596/32.

XX Polypeptide fragments of the DP-1 transcription factor - used for
 XX inducing apoptosis, specifically in tumour and cardiovascular cells, e.g.
 XX for preventing re-stenosis.

PS Disclosure; Page 5; 55pp; English.

XX This polypeptide comprises a membrane translocation sequence derived from
 CC the Drosophila melanogaster antennapedia protein. Such membrane
 CC translocation sequences are useful in directing entry of a polypeptide
 CC into a cell. Polypeptides of the invention (see AAW30504-07) are derived
 CC from the DEF box region (see AAW30501) of transcription factor DP1. They
 CC act as antagonists of the heterodimerisation of a DP protein with an E2F
 CC protein, and can be used to induced apoptosis, specifically in tumour and

CC cardiovascular cells, e.g. for preventing restenosis. A claimed fusion
 CC protein comprises a DEF box peptide and the Drosophila antennapedia
 CC protein membrane translocation sequence
 XX
 SQ Sequence 16 AA;

Query Match 100.0%; Score 92; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 8.6e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RQIKWQNRRMKWKK 16
 Db 1 RQIKWQNRRMKWKK 16

RESULT 9
 AAW91046
 ID AAW91046 standard; peptide; 16 AA.

AC AAW91046;

DT 24-MAR-1999 (first entry)

DE Internalization sequence associated with cadherin modulating agents.

XX Alpha-catenin; beta-catenin; interaction; modulation; cell adhesion;
 KW cadherin-mediated function; demyelinating neurological disease;
 KW multiple sclerosis; drug delivery; cancer; angiogenesis; immune system;
 KW central nervous system; apoptosis induction; cadherin-expression cell;
 KW pregnancy prevention; vasopermeability; synaptic stability; diabetes;
 KW rheumatoid arthritis; allergic response; learning; antennapedia protein;
 KW antibody-mediated graft rejection; internalization sequence; memory.

OS Synthetic.

PN WO9845319-A2.

XX 15-OCT-1998.

XX 14-APR-1998; 98WO-CA000322.

XX 10-APR-1997; 97US-0043361P.

XX (UYMC-) UNIV MCGILL.

XX Blaschuk OW, Gour BJ;

XX WPI; 1999-024009/02.

XX New cadherin modulating agents - comprising peptides having a sequence HAV
 PT or analogues or antibodies, used for modulating cadherin-mediated
 PT functions.

XX Claim 16; Page 78; 106pp; English.

XX The present sequence represents antennapedia protein derived
 CC internalization sequence associated with cadherin modulating agents.
 CC These agents are used for modulating cadherin-mediated functions. They
 CC can be used for disrupting interaction between alpha-catenin and beta-
 CC catenin in a cell, inhibiting cell adhesion, e.g. between epithelial
 CC cells, endothelial cells, neural cells, tumour cells and lymphocytes, for
 CC treating a demyelinating neurological disease, e.g. multiple sclerosis,
 CC for reducing unwanted cellular adhesion in a mammal, for enhancing the
 CC delivery of a drug through the skin of a mammal, for enhancing the
 CC delivery of a drug to a tumour in a mammal, for treating cancer in a
 CC mammal, for inhibiting angiogenesis in a mammal, for enhancing drug
 CC delivery to the central nervous system of a mammal, for inducing
 CC apoptosis in a cadherin-expression cell, for modulating the immune system
 CC of a mammal, for preventing pregnancy in a mammal, for increasing
 CC vasopermeability in a mammal, or for inhibiting synaptic stability in a
 CC mammal. In particular they can be used for treating diabetes, rheumatoid
 CC arthritis, allergic responses, antibody-mediated graft rejection or for
 CC stimulating learning and memory

XX SQ - Sequence 16 AA;
 Query Match 100.0%; Score 92; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 8.6e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ROIKWIFQNRMRKWK 16
 DB 1 ROIKWIFQNRMRKWK 16

RESULT 10
 AAY52102
 ID 'AAY52102 standard; peptide; 16 AA.
 XX AC AAY52102;
 XX DT 28-JAN-2000 (first entry)
 XX PE Peptide from the third helix of antennapedia homeodomain protein.
 XX Rho binding region; Rho binding protein; ROCK II; ROCK I; Kinectin;
 KW ROCK/Kinectin homology domain; cell growth; assay; Skn 7; modulator;
 KW antifungal agent; antennapedia homeodomain protein; translocate.
 XX Drosophila melanogaster.
 OS WO9952941-A2.
 XX FN 21-OCT-1999.
 XX PD 09-APR-1999; 99WO-GB001096.
 XX PF 09-APR-1998; 98GB-00007848.
 XX PR (MEDI-) MEDICAL RES COUNCIL.
 XX PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY.
 XX PI Johnston LH, Treisman RH;
 XX WPI; 1999-620374/53.
 XX Assay for modulators of binding of Rho protein with its binding partners,
 PT potentially useful as antifungal agents.
 XX Disclosure; Page 16; 68pp; English.

XX This sequence is a peptide from the third helix of the Drosophila
 CC antennapedia protein that translocates across biological membranes. This
 CC sequence can be linked to the Rho binding region of the invention
 CC (AAY52100) to cause translocation across eukaryotic cell membranes. The
 CC Rho binding region is present in many Rho binding proteins, such as ROCK-
 CC I, ROCK-II and Kinectin and is also referred to as the ROCK/Kinectin
 CC homology domain. Rho-A is involved in many cellular processes including
 CC stress fibre formation, cell motility, cytokinesis and apoptosis. The Rho
 CC binding domain is used in the invention which relates to an assay for
 CC potential modulators of cell growth. The assay consists of a Skn7
 CC polypeptide, a beta2 polypeptide or a polypeptide consisting of a
 CC ROCK/kinectin homology domain, a Rho polypeptide which binds to the
 CC previous peptide and a test compound. The modulation of the binding of
 CC the two peptides caused by the test compound is measured. The method is
 CC used to identify modulators, particularly antagonists, of the interaction
 CC of Rho with its binding partners, e.g. to render pathogens sensitive to
 CC the host's defence system, particularly as antifungal agents. The
 CC ROCK/kinectin homology domain can be used to screen databases for other
 CC Rho-binding proteins

XX SQ Sequence 16 AA;
 Query Match 100.0%; Score 92; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 8.6e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ROIKWIFQNRMRKWK 16
 DB 1 ROIKWIFQNRMRKWK 16

RESULT 11
 AAY00859
 ID 'AAY00859 standard; peptide; 16 AA.
 XX AC AAY00859;
 XX DT 20-MAY-1999 (first entry)
 XX PE Peptide pAntp(43-56) used in membrane-permeable construct.
 XX Membrane-permeable construct; lipid membrane; membrane transport;
 KW oligonucleotide delivery; cancer therapy; signal transduction; inhibitor;
 KW gene therapy; transcription; translation; expression; replication.
 XX Synthetic.
 XX Key Location/Qualifiers
 FT Modified-site 16
 FT /note= "amidated"
 XX WO9905302-A1.
 XX PD 04-FEB-1999.
 XX PF 16-JUL-1998; 98WO-US014761.
 XX PR 24-JUL-1997; 97US-0053678P.
 XX PA (PEKE) PERKIN-ELMER CORP.
 XX PI Langel U, Bartfai T, Pooga M, Valkna A, Saar K, Hallbrink M;
 XX WPI; 1999-142952/12.
 XX New membrane-permeable constructs - comprise a peptide linked by a labile
 PT bond to a nucleic acid analogue capable of hybridising with an
 PT intracellular polynucleotide.
 XX Disclosure; Page 26; 60pp; English.

XX This sequence represents a peptide used in the construct of the
 CC invention. The construct is a membrane-permeable construct for transport
 CC across a lipid membrane, which comprises: (a) a nucleic acid analogue
 CC capable of hybridising with an intracellular polynucleotide (PN); (b) a
 CC peptide; and (c) a labile bond linking the nucleic acid analogue and the
 CC peptide. The membrane-permeable constructs can be used for delivery of
 CC oligonucleotides, nucleic acids and nucleic acid analogues into cells.
 CC They can be used for e.g. cancer therapy, signal transduction studies,
 CC identifying new intracellular drug targets or gene therapy. They can also
 CC be used for selectively inhibiting DNA transcription, RNA translation,
 CC RNA or DNA expression, DNA replication, or an DNA or RNA regulatory
 CC function of preselected DNA or RNA sequences in a living cell

XX SQ Sequence 16 AA;
 Query Match 100.0%; Score 92; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 8.6e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ROIKWIFQNRMRKWK 16
 DB 1 ROIKWIFQNRMRKWK 16

RESULT 12
 AAY13509
 ID 'AAY13509 standard; peptide; 16 AA.

XX AAY13509;
 AC 30-JUL-1999 (first entry)
 DT Signal sequence of antennapedia.
 DE
 XX Fusion protein; calpastatin; calpain; platelet aggregation; arthritis;
 KW hypoxia; erythrocyte sickling; sickle cell; HIV provirus; NF-kappaB;
 KW inflammation; asthma; immune response; restenosis; myocardial infarction;
 KW cancer; calpastat; antennapedia.
 XX
 OS Mammalia.
 XX
 XX WO9922756-A1.
 PN 14-MAY-1999.
 XX
 XX 04-NOV-1998; 98WO-US023526.
 PF
 XX 04-NOV-1997; 97US-00964302.
 PR
 XX (NEW-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.
 PA
 XX Potter DA, Skolnik PR;
 PI
 XX WPI; 1999-326923/27.
 DR
 XX Fusion protein of signal sequence and calpastatin.
 PT
 XX Disclosure; Page 5; 46pp; English.
 PS
 XX The invention features fusion proteins that contain a calpastatin peptide
 CC and a signal sequence capable of delivering the fusion protein into a
 CC eukaryotic cell. The fusion protein is used for the inhibition of calpain
 CC in a cell. The fusion proteins are specifically used: (a) to prevent
 CC aggregation and degradation of platelets (e.g. during storage); (b) to
 CC inhibit hypoxia-induced sickling of erythrocytes (during storage);
 CC facilitating subsequent transfusion of erythrocytes (during storage);
 CC sickle cell crises; and (c) to inhibit activation of human immune
 CC deficiency virus provirus in infected cells (or similarly for other
 CC viruses regulated by NF-kappaB). Other disclosed uses are: to treat or
 CC prevent inflammation (e.g. arthritis or asthma), unwanted immune
 CC responses (e.g. transplant rejection), restenosis (associated with
 CC angioplasty), cancer, subarachnoid hemorrhage, vasospasm, muscular
 CC dystrophy, cataracts and traumatic birth injury; to prevent spread of
 CC platelets on surfaces (e.g. when applied to the surface of stents,
 CC catheters etc.); to reduce coronary thrombosis in by-pass surgery and
 CC angioplasty; to treat myocardial infarction, or to prevent progression of
 CC infarction (myocardial or cerebral). The fusion protein has a reversible
 CC inhibitory effect and enters cells easily. It allows platelets to be
 CC stored cold with reduced change in shape
 XX
 XX Sequence 16 AA;
 SQ
 Query Match 100.0%; Score 92; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 8.6e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RQIKWFOQRNRMKWK 16
 DB 1 RQIKWFOQRNRMKWK 16
 RESULT 13
 AAY87920
 ID AAY87920 standard; peptide; 16 AA.
 XX
 AC AAY87920;
 XX
 XX 11-SEP-2000 (first entry)
 DT
 XX Drosophila sp. antennapedia protein fragment.
 DE

XX Rad51; cell proliferation; rad51TRI-131; rad51K-A134; immunosuppressive;
 KW cytostatic; antiinflammatory; antiproliferative; programmed cell death;
 KW treatment; autoimmune disorder; inflammation; cancer; graft rejection;
 KW proliferative disorder; hyperproliferative disorder; antennapedia.
 XX
 OS Drosophila sp.
 XX
 XX US6057104-A.
 PN 02-MAY-2000.
 XX
 XX 05-NOV-1997; 97US-00964614.
 PF
 XX 05-NOV-1996; 96US-00758280.
 PR
 XX (LEXI-) LEXICON GENETICS INC.
 PA
 XX Hasty P;
 PI
 XX WPI; 2000-349568/30.
 DR
 XX Mutant forms of mammalian Rad51 proteins and polypeptides that disrupt
 PT cell proliferation and promote programmed cell death, encoded by specific
 PT nucleotides.
 XX
 XX Disclosure; Col 31-32; 22pp; English.
 XX
 CC This invention describes novel truncated and altered forms of Rad51
 CC products encoded by rad51TRI-131 and rad51K-A134. The products of the
 CC invention have immunosuppressive, cytostatic, antiinflammatory and
 CC antiproliferative activity. Altered and mutant forms of Rad51 are useful
 CC for inhibiting cell proliferation and for promoting programmed cell
 CC death. Therapeutic agents, factors or compounds capable of disrupting the
 CC essential processes mediated by or associated with normal Rad51 or Rad52
 CC are useful for treating diseases like autoimmune disorders, inflammation,
 CC cancer, graft rejection and other proliferative and hyperproliferative
 CC disorders. This sequence represents a fragment of the Drosophila
 CC antennapedia protein which is described in the method of the invention
 XX
 XX Sequence 16 AA;
 SQ
 Query Match 100.0%; Score 92; DB 3; Length 16;
 Best Local Similarity 100.0%; Pred. No. 8.6e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RQIKWFOQRNRMKWK 16
 DB 1 RQIKWFOQRNRMKWK 16
 RESULT 14
 AAB27060
 ID AAB27060 standard; peptide; 16 AA.
 XX
 AC AAB27060;
 XX
 XX 15-FEB-2001 (first entry)
 DT
 XX Beta-catenin derived internalisation moiety SEQ ID NO: 47.
 DE
 XX Beta-catenin; cadherin-mediated intercellular adhesion;
 KW cell differentiation; modulating agent; hair loss; skin exfoliation;
 KW internalisation moiety; flanking sequence; transcription; hearing loss.
 XX
 OS Drosophila melanogaster.
 XX
 XX WO200053632-A1.
 PN
 XX 14-SEP-2000.
 PD
 XX 07-MAR-2000; 2000WO-CA000222.
 PF
 XX

PR 09-MAR-1999; 99US-00265107.
 XX (UYMC-) UNIV MCGILL.
 XX Blaschuk OW, Gour BU;
 XX WPI; 2000-594308/56.
 XX
 XX Stimulating beta-catenin mediated gene expression, cellular
 PT differentiation and hair growth, involves contacting cells with
 PT modulating agent capable of inhibiting interaction between alpha and beta
 PT catenin.
 XX
 XX Claim 8; Page 38; 77pp; English.
 XX
 XX The present invention is concerned with methods of modulating the amount
 CC of free beta-catenin in the cell, and methods of stimulating the
 CC expression of genes involved in cellular differentiation, the
 CC transcription of which is under the control of beta-catenin. The peptides
 CC given in AAB27053-B27088, AAB27284-B27300 and AAB27330-B27351 can be used
 CC as modulating agents which interrupt the interaction between alpha and
 CC beta catenin, causing increased levels of the latter and stimulating the
 CC activation of beta-catenin mediated transcription. This can be used to
 CC stimulate cell differentiation, which can then be used to promote hair
 CC growth and skin exfoliation. This latter is particularly useful in the
 CC improvement of photodamaged skin and to minimise wrinkles. The modulating
 CC peptide can also be used to reduce hearing loss resulting from inner ear
 CC disorders such as hyperacusis and tinnitus
 XX
 XX Sequence 16 AA;
 SQ
 Query Watch 100.0%; Score 92; DB 3; Length 16;
 Best Local Similarity 100.0%; Pred. No. 8.6e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RQIKWQNRKMKWK 16
 |||||
 Db 1 RQIKWQNRKMKWK 16
 |||||
 RESULT 15
 AAY93667
 ID AAY93667 standard; peptide; 16 AA.
 XX
 XX AAY93667;
 XX 25-SEP-2000 (first entry)
 XX Peptide which may be linked to anticancer agents.
 XX Anticancer agent; cancer cell; resistance; P-glycoprotein pump; cancer.
 XX Unidentified.
 XX WO200032237-A1.
 XX 08-JUN-2000.
 XX 26-NOV-1999; 99WO-FR002939.
 XX 30-NOV-1998; 98FR-00015073.
 XX (SYNT-) SYNT:EM SA.
 XX Tamsamani J, Kaczorek M, Colin De Verdier A;
 XX WPI; 2000-412166/35.
 XX New composition useful for cancer treatment and prevention, contains
 PT anticancer agent and peptide vector that transports agent into cells.
 XX Disclosure; Page 8; 34pp; French.
 XX

CC The specification describes a pharmaceutical composition, which comprises
 CC at least one anticancer agent associated with at least one peptide that
 CC can transport it into cancer cells and which inhibits development of
 CC resistance to the anticancer agent. By using the peptide as a vector for
 CC delivery of the anticancer agent, mechanisms that cause cancer cells to
 CC become resistant to the agent, particularly the P-glycoprotein pump, are
 CC avoided. Also, peptides are easily produced by chemical synthesis, can be
 CC coupled easily to the agent, cross mammalian cell membranes rapidly by a
 CC passive mechanism (no receptors required), and are non-toxic and non-
 CC lytic. The compositions are used to treat cancer. The present sequence
 CC represents a peptide which may be linked to the anticancer agents of the
 XX invention
 XX Sequence 16 AA;
 SQ
 Query Match 100.0%; Score 92; DB 3; Length 16;
 Best Local Similarity 100.0%; Pred. No. 8.6e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RQIKWQNRKMKWK 16
 |||||
 Db 1 RQIKWQNRKMKWK 16
 |||||
 RESULT 16
 AAY67966
 ID AAY67966 standard; peptide; 16 AA.
 XX
 XX AAY67966;
 XX 05-APR-2000 (first entry)
 XX Carboxyfluorescein cell permeant peptide #3.
 XX Kaposi syndrome; fibroblast growth factor; signal peptide; PNA;
 KW peptide nucleic acid; cell permeability; intracellular delivery;
 KW gene therapy; cancer.
 XX Unidentified.
 XX
 XX Key Location/Qualifiers
 FH Modified-site 1 /note= "labelled with carboxyfluorescein"
 FT
 XX WO9964449-A2.
 XX 16-DEC-1999.
 XX 10-JUN-1999; 99WO-GB001848.
 XX 10-JUN-1998; 98GB-00012376.
 XX 10-JUL-1998; 98GB-00014888.
 XX (UYBE-) UNIV QUEENS BELFAST.
 XX Nelson J, Harriott P, Wallace A;
 XX WPI; 2000-097517/08.
 XX New cell permeable signal peptides, useful for intracellular delivery of
 XX a molecule.
 XX Example 1; Page 29; 33pp; English.
 XX The present invention describes a cell permeable peptide comprising at
 CC least the hydrophobic core of a signal peptide (or analogue) containing
 CC at least 1 additional positively charged amino acid (or analogue). The
 CC peptides are useful for the intracellular delivery of molecules,
 CC especially peptide nucleic acids to in vivo targets. The peptides are
 CC useful in commercial drug-delivery systems, in e.g. gene therapy, cancer
 CC therapy and anti-infectious agent therapy. The peptides facilitate
 CC biochemical and molecular biological research. The modified peptides
 CC facilitate intracellular delivery of any cell-impermeable substances and

CC improve delivery into low permeability cells. Delivery into sub-
 CC compartments can be achieved by modifying the signal peptides. The
 CC present sequence represents a peptide used in the exemplification of the
 CC present invention

XX SQ Sequence 16 AA;

Query Match 100.0%; Score 92; DB 3; Length 16;
 Best Local Similarity 100.0%; Pred. No. 8.6e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWFOQRNMKWK 16
 |||||
 Db 1 RQIKWFOQRNMKWK 16

RESULT 17

AAV93551
 ID AAY93551 standard; peptide; 16 AA.

XX AC AAY93551;

XX DT 25-SEP-2000 (first entry)

XX DE Amino acid sequence of a synthetic protein transduction domain.

XX KW Protein transduction system; protein transduction domain;
 KW cytotoxic domain; pathogen infection; retroviral infection;
 KW plasmoidal infection; cancer; prostate cancer.

XX OS Synthetic.

XX PN WO200034308-A2.

XX PD 15-JUN-2000.

XX PF 10-DEC-1999; 99WO-US029289.

XX PR 10-DEC-1998; 98US-0111701P.

XX FA (UNIW) UNIV WASHINGTON.

XX FI Dowdy SF;

XX DR WPI; 2000-431269/37.

XX PT Protein transduction system for treating cancer and pathogenic infections
 PT has a fusion protein comprising a protein transduction domain covalently
 PT linked to a cytotoxic domain.

XX PS Example 10; Page 71; 127pp; English.

XX CC AAY93542-51 represent synthetic protein transduction domains, which are
 CC used in the protein transduction system of the invention. The
 CC specification describes a protein transduction system, which comprises a
 CC fusion protein. This fusion protein has a covalently linked protein
 CC transduction domain and cytotoxic domain. The system is useful for
 CC treating pathogen infection in mammals, infections such as those caused
 CC by CMV, HSV-1, KSHV, yellow fever virus, flavivirus or rhinovirus,
 CC retroviral infections such as HIV-1, HIV-2, HTLV-3 and/or LAV, plasmoidal
 CC infections associated with P.falciparum, P.vivax, P.ovale, P.malariae. It
 CC is also useful for treating cancer, especially prostate cancer

XX SQ Sequence 16 AA;

Query Match 100.0%; Score 92; DB 3; Length 16;
 Best Local Similarity 100.0%; Pred. No. 8.6e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWFOQRNMKWK 16
 |||||
 Db 1 RQIKWFOQRNMKWK 16

RESULT 18

AAV55818
 ID AAY55818 standard; peptide; 16 AA.

XX AC AAY55818;

XX DT 06-MAR-2000 (first entry)

XX DE Signal sequence for delivering polypeptide inhibitor.

XX KW Cellular protein; nuclear translocation; nuclear localization signal;
 KW immunosuppressant; immune response; viral infection; immune disorder;
 KW rheumatoid arthritis; multiple sclerosis; juvenile-onset diabetes; NLS;
 KW systemic lupus erythematosus; SLE; asthma; sepsis; tumor growth;
 KW fibroblast growth factor; signal sequence.

XX OS Synthetic.

XX PN WO9957138-A1.

XX PD 11-NOV-1999.

XX PF 26-APR-1999; 99WO-US008984.

XX PR 04-MAY-1998; 98US-00072429.

XX PA (BRIM) BRISTOL-MYERS SQUIBB CO.

XX FI Nadler SG;

XX DR WPI; 2000-062141/05.

XX PT Novel composition comprising a nuclear localization signal and an
 PT inhibitor of nuclear translocation, useful for preventing transplanted
 PT organ or tissue rejection.

XX PS Disclosure; Page 14; 68pp; English.

XX CC The invention provides a composition comprising an isolated polypeptide
 CC (I) (polypeptide inhibitor of a cellular protein nuclear translocation)
 CC which comprises a signal sequence peptide capable of delivering (I)
 CC through a cytoplasmic membrane into the cell; and a nuclear localization
 CC signal sequence (NLS) present along with an immunosuppressant. (I) or its
 CC derivatives provide useful tools for introducing an exogenous polypeptide
 CC comprising an NLS into an intact cell to inhibit nuclear translocation of
 CC a cellular protein, for studying the role of nuclear translocation in the
 CC regulation of cellular processes. See AAY55812 for detailed uses of (I)
 CC and compositions containing (I). The present sequence represents a signal
 CC sequence for delivering the (I) through the cytoplasmic membrane into the
 CC cell

XX SQ Sequence 16 AA;

Query Match 100.0%; Score 92; DB 3; Length 16;
 Best Local Similarity 100.0%; Pred. No. 8.6e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWFOQRNMKWK 16
 |||||
 Db 1 RQIKWFOQRNMKWK 16

RESULT 19

AAV71008
 ID AAY71008 standard; peptide; 16 AA.

XX AC AAY71008;

XX DT 29-AUG-2000 (first entry)

XX DE Drosophila antennapedia (ANT) transport peptide.

Fri Oct 1 16:13:10 2004

XX Phospholamban; PLB; sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a;
 KW cardiomyocyte; transport peptide; penetratin; cargo peptide; inhibitor;
 KW contractilin; cardiac contractility; cardiac disease; antennapedia; ANT;
 KW treatment; cardiant; heart failure; myocardial dysfunction; fruit fly.
 XX Drosophila sp.
 OS WO200025804-A2.
 XX 11-MAY-2000.
 XX 02-NOV-1999; 99WO-US025692.
 XX 02-NOV-1998; 98US-0106718P.
 PR 27-JUL-1999; 99US-0145883P.
 XX (REGC) UNIV CALIFORNIA.
 XX Chien K, Dillman W, Minamisawa S, He H, Hoshijima M, Meyer M;
 PI Scott C, Wang Y, Silverman GJ;
 XX WPI; 2000-365393/31.
 XX Treating cardiac diseases, e.g. heart failure or myocardial dysfunction
 PT comprises enhancing cardiac contractility by inhibiting interaction
 PT between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine
 PT triphosphatase.
 XX Example 4; Page 50; 56pp; English.
 XX The patent discloses a method for the treatment of heart failure, using
 CC small peptide complexes and recombinant proteins, that induces
 CC phospholamban (PLB) deficiency and inhibits the interaction between PLB
 CC and sarcoplasmic reticulum Ca 2+ ATPase (SERCA2a) within cardiomyocytes.
 CC The peptide complex comprises of transport peptide like penetratin and
 CC cargo peptide selected from mutant PLB, native PLB or antibody against
 CC PLB protein (contractilin). Penetratin-PLB peptide functions as a
 CC dominant negative inhibitor of PLB-SERCA2a interaction, enhances cardiac
 CC contractility and reduces blood pressure. This method is useful for the
 CC treatment of cardiac disease e.g. heart failure and myocardial
 CC dysfunction. The present amino acid sequence is the transport peptide
 CC composed of residues 43-58 of antennapedia (ANT), a drosophila
 CC transcription factor protein. This peptide can be used to transport
 CC therapeutic agents across a cell membrane into the cytoplasm and nucleus
 CC of cardiomyocytes
 XX Sequence 16 AA;
 SQ Query Match 100.0%; Score 92; DB 3; Length 16;
 Best Local Similarity 100.0%; Pred. No. 8.6e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ROIKIWFQNRKMKKK 16
 Db 1 ROIKIWFQNRKMKKK 16
 RESULT 20
 AAY51212
 ID AAY51212 standard; peptide; 16 AA.
 XX AAY51212;
 AC AAY51212;
 XX 04-APR-2000 (first entry)
 DT Antennapedia protein homeodomain peptide fragment 1.
 XX Antennapedia; homeodomain; fluorogenic; fluorescence; fluorophore;
 KW fluorescence resonance energy transfer; FRET; detection.
 XX Unidentified.
 OS EP969284-A1.
 XX

XX 05-JAN-2000.
 PD 01-JUL-1999; 99BP-00112544.
 PF 02-JUL-1998; 98DE-01029495.
 PR (PAYS/) PAYSAN J.
 XX (ANTZ/) ANTZ C.
 PA Paysan J, Antz C;
 PI WPI; 2000-099447/09.
 DR Fluorogenic conjugate for intracellular fluorescence labeling, especially
 XX for performing fluorescence resonance energy transfer assays in living
 PT cells.
 PT Claim 5; Page 5; 8pp; German.
 PS This invention describes a novel fluorogenic conjugate (vector) for
 XX fluorescence labeling of specific targets within cells which comprises a
 CC membrane translocation component, a targeting component and a
 CC fluorophore. A kit comprising two such conjugates, in which the
 CC fluorophores form a donor-acceptor pair for fluorescence resonance energy
 CC transfer (FRET), can be used to measure interactions between two
 CC substances, especially in living cells, when the targeting component of
 CC one of the conjugates targets one of the substances and the targeting
 CC component of the other conjugate targets the other substance. The
 CC conjugate or kit can be used to detect a target in a biologically
 CC functional cell. When the conjugate has a fluorophore capable of acting
 CC as a donor or acceptor for FRET with a fluorescent protein, it can be
 CC used to measure intracellular levels of a fusion protein of the
 CC fluorescent protein by FRET if the targeting component targets a sequence
 CC of the fusion protein, especially in a screening assay in which the gene
 CC encoding the fluorescent protein is linked to another coding sequence in
 CC an expression vector, the vector is used to transform a cell culture, the
 CC cell culture is incubated with the fluorogenic conjugate, and the cells
 CC are separated, preferably by means of a cell sorter or by FRET
 CC microscopy, especially where the fluorescent protein is green fluorescent
 CC protein (GFP) and the fluorophore is BODIPY, fluorescein, Oregon green,
 CC Rhodol green, rhodamine, Texas red, Cy2, Cy3, Cy5, Alexa, Marina blue,
 CC Pacific blue or AMCA. The cells are especially bacterial, yeast, insect,
 CC amphibian or mammalian cells. This sequence represents a fragment of the
 CC antennapedia homeodomain protein which is used to illustrate the method
 CC of the invention
 XX Sequence 16 AA;
 SQ Query Match 100.0%; Score 92; DB 3; Length 16;
 Best Local Similarity 100.0%; Pred. No. 8.6e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ROIKIWFQNRKMKKK 16
 Db 1 ROIKIWFQNRKMKKK 16
 RESULT 21
 AAY51167
 ID AAY51167 standard; protein; 16 AA.
 XX AAY51167;
 AC AAY51167;
 XX 31-MAR-2000 (first entry)
 DT Drosophila sp. derived peptide fragment.
 XX TAR protein; nuclear transport; cell adhesion; gene therapy.
 KW Drosophila sp.
 XX WO9966061-A1.
 PN

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OM protein - protein search, using sw model

Run on: October 1, 2004, 12:07:51 ; Search time 17 Seconds

(without alignments)
48.589 Million cell updates/sec

Title: US-09-830-779-7

Perfect score: 92

Sequence: 1 RQIKWIFQNRKMKKK 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 100 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/ptodata/2/iaa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PTUS.COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	92	100.0	16	2	US-08-928-958-7
2	92	100.0	16	2	US-08-810-540-3
3	92	100.0	16	2	US-08-810-540-6
4	92	100.0	16	2	US-09-072-429-7
5	92	100.0	16	3	US-08-964-302A-6
6	92	100.0	16	3	US-09-116-294-4
7	92	100.0	16	3	US-08-964-614A-4
8	92	100.0	16	3	US-08-849-486-1
9	92	100.0	16	3	US-08-849-486-4
10	92	100.0	16	3	US-09-208-966-54
11	92	100.0	16	3	US-09-308-935-8
12	92	100.0	16	3	US-09-441-416A-6
13	92	100.0	16	4	US-09-296-089-33
14	92	100.0	16	4	US-09-419-826-35
15	92	100.0	16	4	US-09-302-305C-10
16	92	100.0	16	4	US-09-346-847-1
17	92	100.0	16	4	US-09-346-847-25
18	92	100.0	16	4	US-09-057-363C-47
19	92	100.0	16	4	US-09-043-560B-3
20	92	100.0	16	4	US-09-648-400A-29
21	92	100.0	16	4	US-09-227-652B-4
22	92	100.0	16	4	US-09-780-070-38
23	92	100.0	16	4	US-08-610-220B-9
24	92	100.0	16	4	US-09-775-052A-54
25	92	100.0	16	4	US-09-155-165-22
26	92	100.0	16	4	US-09-792-480-29
27	92	100.0	16	4	US-09-551-976-33

28	92	100.0	16	4	US-09-265-107-47	Sequence 47, Appl
29	92	100.0	17	4	US-09-346-847-17	Sequence 17, Appl
30	92	100.0	17	4	US-09-346-847-20	Sequence 20, Appl
31	92	100.0	17	4	US-09-346-847-22	Sequence 22, Appl
32	92	100.0	17	4	US-09-346-847-27	Sequence 27, Appl
33	92	100.0	17	4	US-09-648-400A-30	Sequence 30, Appl
34	92	100.0	18	3	US-08-838-545-20	Sequence 20, Appl
35	92	100.0	18	3	US-09-349-532-20	Sequence 20, Appl
36	92	100.0	19	4	US-09-346-847-23	Sequence 23, Appl
37	92	100.0	19	4	US-09-658-517C-7	Sequence 7, Appl
38	92	100.0	20	4	US-09-346-847-16	Sequence 16, Appl
39	92	100.0	20	4	US-09-346-847-18	Sequence 18, Appl
40	92	100.0	20	4	US-09-346-847-30	Sequence 30, Appl
41	92	100.0	20	4	US-09-658-517C-8	Sequence 8, Appl
42	92	100.0	21	4	US-08-610-220B-11	Sequence 11, Appl
43	92	100.0	22	4	US-09-346-847-28	Sequence 28, Appl
44	92	100.0	22	4	US-09-057-363C-50	Sequence 50, Appl
45	92	100.0	22	4	US-08-610-220B-10	Sequence 10, Appl
46	92	100.0	22	4	US-09-155-165-5	Sequence 5, Appl
47	92	100.0	22	4	US-09-155-165-11	Sequence 11, Appl
48	92	100.0	22	4	US-09-265-107-50	Sequence 50, Appl
49	92	100.0	24	4	US-09-419-826-34	Sequence 34, Appl
50	92	100.0	24	4	US-09-428-082B-332	Sequence 332, Appl
51	92	100.0	27	3	US-09-051-934-51	Sequence 51, Appl
52	92	100.0	27	3	US-09-051-934-52	Sequence 52, Appl
53	92	100.0	27	4	US-09-040-725A-2	Sequence 2, Appl
54	92	100.0	34	4	US-09-347-504-79	Sequence 79, Appl
55	92	100.0	34	4	US-10-161-499-79	Sequence 79, Appl
56	92	100.0	36	4	US-09-428-082B-331	Sequence 331, Appl
57	92	100.0	61	2	US-08-202-044-3	Sequence 3, Appl
58	92	100.0	61	3	US-08-751-344B-3	Sequence 3, Appl
59	92	100.0	61	3	US-08-751-344B-6	Sequence 6, Appl
60	92	100.0	61	3	US-08-751-344B-9	Sequence 9, Appl
61	91	99.9	61	3	US-08-751-344B-7	Sequence 7, Appl
62	87	94.6	15	2	US-08-810-540-4	Sequence 4, Appl
63	87	94.6	16	4	US-09-732-480-30	Sequence 30, Appl
64	87	94.6	42	3	US-08-751-344B-4	Sequence 4, Appl
65	87	94.6	283	1	US-08-583-672-2	Sequence 2, Appl
66	87	94.6	283	2	US-08-202-044-2	Sequence 2, Appl
67	87	94.6	283	3	US-08-751-344B-2	Sequence 2, Appl
68	87	94.6	284	2	US-08-320-148B-2	Sequence 2, Appl
69	87	94.6	284	3	US-08-589-028-6	Sequence 6, Appl
70	87	94.6	284	3	US-08-784-582-6	Sequence 6, Appl
71	87	94.6	284	3	US-08-785-271-6	Sequence 6, Appl
72	87	94.6	284	3	US-09-031-898-2	Sequence 2, Appl
73	87	94.6	302	2	US-08-203-532F-4	Sequence 4, Appl
74	87	94.6	302	3	US-08-950-860-16	Sequence 16, Appl
75	87	94.6	302	3	US-09-072-455-4	Sequence 4, Appl
76	87	94.6	302	5	PCT-US95-01882A-4	Sequence 4, Appl
77	87	94.6	303	2	US-08-203-532F-2	Sequence 2, Appl
78	87	94.6	303	2	US-09-078-465-2	Sequence 2, Appl
79	87	94.6	303	5	PCT-US95-01882A-2	Sequence 2, Appl
80	86	93.5	16	3	US-08-849-486-5	Sequence 5, Appl
81	86	93.5	16	4	US-09-466-772-7	Sequence 7, Appl
82	86	93.5	16	4	US-09-466-772-3	Sequence 3, Appl
83	86	93.5	21	4	US-09-466-772-1	Sequence 1, Appl
84	86	93.5	22	4	US-09-466-772-2	Sequence 2, Appl
85	86	93.5	23	4	US-09-466-772-4	Sequence 4, Appl
86	83	90.2	16	3	US-08-849-486-8	Sequence 8, Appl
87	83	90.2	300	4	US-09-162-524-1	Sequence 1, Appl
88	83	90.2	349	4	US-09-162-524-3	Sequence 3, Appl
89	82	89.1	16	4	US-09-402-939-7	Sequence 7, Appl
90	80	87.0	16	3	US-08-849-486-7	Sequence 7, Appl
91	79	85.9	61	2	US-08-752-316C-30	Sequence 30, Appl
92	78	84.8	16	3	US-09-208-966-1	Sequence 1, Appl
93	78	84.8	16	4	US-09-775-052A-1	Sequence 1, Appl
94	78	84.8	342	4	US-09-165-847C-2	Sequence 2, Appl
95	77	83.7	60	3	US-08-751-344B-5	Sequence 5, Appl
96	76	82.6	367	4	US-09-009-816-2	Sequence 2, Appl
97	75	81.5	16	4	US-09-296-089-34	Sequence 34, Appl
98	75	81.5	16	4	US-09-336-033-3	Sequence 3, Appl
99	75	81.5	16	4	US-09-057-363C-48	Sequence 48, Appl
100	75	81.5	16	4	US-09-557-465D-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-08-928-958-7
; Sequence 7, Application US/08928958
; Patent No. 5877282
; GENERAL INFORMATION:
; APPLICANT: NADLER, STEVEN G.
; APPLICANT: CLEVELAND JEFFREY S.
; APPLICANT: BLAKE, JAMES
; APPLICANT: HAFKAR, OMAR K.
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF NUCLEAR PROTEIN
; TITLE OF INVENTION: TRANSLOCATION HAVING NUCLEAR LOCALIZATION SEQUENCES AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROBINS & ASSOCIATES
; STREET: 90 MIDDLEFIELD ROAD, SUITE 200
; CITY: MENLO PARK
; STATE: CA
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/928,958
; FILING DATE: 12-SEP-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/026978
; FILING DATE: 20-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: ROBINS, ROBERTA L.
; REGISTRATION NUMBER: 33,208
; REFERENCE/DOCKET NUMBER: 5998-0019
; TELEPHONE: (650) 325-7812
; TELEFAX: (650) 325-7823
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-928-958-7
Query Match 100.0%; Score 92; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RQIKWQNRRMKWKK 16
DB 1 RQIKWQNRRMKWKK 16
RESULT 2
US-08-810-540-3
; Sequence 3, Application US/08810540
; Patent No. 5929042
; GENERAL INFORMATION:
; APPLICANT: TROY, CAROL M.
; APPLICANT: SHELANSKI, MICHAEL L.
; TITLE OF INVENTION: ANTISENSE COMPOUNDS WHICH PREVENT CELL
; TITLE OF INVENTION: DEATH AND USES THEREOF
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOPER & DUNHAM, LLP
; STREET: 1185 AVENUE OF THE AMERICAS
; CITY: NEW YORK
; STATE: NY
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/810,540
; FILING DATE: 03-MAR-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: WHITE ESQ., JOHN P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51247
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0526

ADDRESSEE: COOPER & DUNHAM, LLP
STREET: 1185 AVENUE OF THE AMERICAS
CITY: NEW YORK
STATE: NY
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,540
FILING DATE: 03-MAR-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: WHITE ESQ., JOHN P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/51247
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0526
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-810-540-3
Query Match 100.0%; Score 92; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RQIKWQNRRMKWKK 16
DB 1 RQIKWQNRRMKWKK 16
RESULT 3
US-08-810-540-6
; Sequence 6, Application US/08810540
; Patent No. 5929042
; GENERAL INFORMATION:
; APPLICANT: TROY, CAROL M.
; APPLICANT: SHELANSKI, MICHAEL L.
; TITLE OF INVENTION: ANTISENSE COMPOUNDS WHICH PREVENT CELL
; TITLE OF INVENTION: DEATH AND USES THEREOF
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOPER & DUNHAM, LLP
; STREET: 1185 AVENUE OF THE AMERICAS
; CITY: NEW YORK
; STATE: NY
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/810,540
; FILING DATE: 03-MAR-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: WHITE ESQ., JOHN P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51247
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0526

INFORMATION FOR SEQ ID NO: 6;
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-810-540-6

Query Match 100.0%; Score 92; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWIFQNRRMKWK 16
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DB 1 RQIKWIFQNRRMKWK 16

RESULT 4

US-09-072-429-7
Sequence 7, Application US/09072429
Patent No. 5982415

GENERAL INFORMATION:
APPLICANT: Nadler, Steven G.
TITLE OF INVENTION: COMPOSITIONS COMPRISING A PEPTIDE
TITLE OF INVENTION: INHIBITOR OF NUCLEAR PROTEIN TRANSLOCATION AND AN
TITLE OF INVENTION: IMMUNOSUPPRESSANT AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESS: Bristol-Myers Squibb Company
STREET: P.O. Box 4000
CITY: Princeton
STATE: New Jersey
COUNTRY: USA
ZIP: 08543-4000

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,429
FILING DATE: 04-MAY-1998
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
NAME: Klein, Christopher A.
REGISTRATION NUMBER: 34,363
REFERENCE/DOCKET NUMBER: ON0141b
TELEPHONE: (609) 252-3714
TELEFAX: (609) 252-4526

INFORMATION FOR SEQ ID NO: 7;
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-072-429-7

Query Match 100.0%; Score 92; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWIFQNRRMKWK 16
|||||
DB 1 RQIKWIFQNRRMKWK 16

RESULT 5

US-08-964-302A-6
Sequence 6, Application US/08964302A
Patent No. 6015787

GENERAL INFORMATION:
APPLICANT: Potter, David A.
APPLICANT: Skolnik, Paul R.
TITLE OF INVENTION: CELL-PERMEABLE PROTEIN INHIBITORS OF CALPAIN
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESS: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/964,302A
FILING DATE: 04-NOV-1997

ATTORNEY/AGENT INFORMATION:
NAME: Meikiejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 00398/126001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154

INFORMATION FOR SEQ ID NO: 6;
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-964-302A-6

Query Match 100.0%; Score 92; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWIFQNRRMKWK 16
|||||
DB 1 RQIKWIFQNRRMKWK 16

RESULT 6

US-09-116-294-4
Sequence 4, Application US/09116294
Patent No. 6025140

GENERAL INFORMATION:
APPLICANT: Langel, Ulo
APPLICANT: Bartfal, Tamas
APPLICANT: Pooga, Margus
APPLICANT: Valkna, Andres
APPLICANT: Saar, Kulliki
APPLICANT: Hallbrink, Mattias
TITLE OF INVENTION: Conjugated Constructs of Peptides and
TITLE OF INVENTION: Nucleic Acid Analogs, and Their Transport Across Membranes
FILE REFERENCE: 4394
CURRENT APPLICATION NUMBER: US/09/116,294
CURRENT FILING DATE: 1998-07-16
EARLIER APPLICATION NUMBER: 60/052,678
EARLIER FILING DATE: 1997-07-24
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 16
TYPE: PPT
ORGANISM: drosophila

US-09-116-294-4

Query Match 100.0%; Score 92; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWQNRRMKWKK 16
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Db 1 RQIKWQNRRMKWKK 16

RESULT 7
US-08-964-614A-4
; Sequence 4, Application US/08964614A
; Patent No. 6057104
; GENERAL INFORMATION:
; APPLICANT: Hasty, Paul
; TITLE OF INVENTION: DISRUPTION OF THE MAMMALIAN
; TITLE OF INVENTION: RAD51 PROTEIN AND DISRUPTION OF PROTEINS THAT ASSOCIATE
; TITLE OF INVENTION: WITH MAMMALIAN RAD51 FOR HINDERING CELL PROLIFERATION
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds, LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FASTSEQ FOR Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/964,614A
; FILING DATE: 05-NOV-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/758,280
; FILING DATE: 05-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 8535-0019-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-964-614A-4

Query Match 100.0%; Score 92; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWQNRRMKWKK 16
| | | | | | | | | | | | | | | |
Db 1 RQIKWQNRRMKWKK 16

RESULT 8
US-08-849-486-1
; Sequence 1, Application US/08849486
; Patent No. 6080724
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PEPTIDES WHICH CAN BE USED AS VECTORS
; TITLE OF INVENTION: FOR THE INTRACELLULAR ADDRESSING OF ACTIVE MOLECULES
; NUMBER OF SEQUENCES: 10
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/849,486
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 95 11714
FILING DATE: 05-OCT-1995
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-849-486-1

Query Match 100.0%; Score 92; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWQNRRMKWKK 16
| | | | | | | | | | | | | | | |
Db 1 RQIKWQNRRMKWKK 16

RESULT 9
US-08-849-486-4
; Sequence 4, Application US/08849486
; Patent No. 6080724
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PEPTIDES WHICH CAN BE USED AS VECTORS
; TITLE OF INVENTION: FOR THE INTRACELLULAR ADDRESSING OF ACTIVE MOLECULES
; NUMBER OF SEQUENCES: 10
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/849,486
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 95 11714
FILING DATE: 05-OCT-1995
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..16
OTHER INFORMATION: /product= "amino acids of the D series"
US-08-849-486-4

Query Match 100.0%; Score 92; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWQNRRMKWKK 16
| | | | | | | | | | | | | | | |
Db 1 RQIKWQNRRMKWKK 16

RESULT 10
US-09-208-966-54


```
; Sequence 54, Application US/09208966
; Patent No. 6221355
; GENERAL INFORMATION:
; APPLICANT: Dowdy, Steven F.
; TITLE OF INVENTION: ANTI-PATHOGEN SYSTEM AND METHODS OF USE THEREOF
; FILE REFERENCE: 48891/1742
; CURRENT APPLICATION NUMBER: US/09/208,966
; EARLIER FILING DATE: 1998-12-10
; EARLIER APPLICATION NUMBER: 60/082,402
; EARLIER FILING DATE: 1998-04-20
; EARLIER APPLICATION NUMBER: 60/059,012
; EARLIER FILING DATE: 1997-12-10
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 54
; LENGTH: 16
; TYPE: PRT
; ORGANISM: human
US-09-208-966-54

Query Match      100.0%; Score 92; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RQIKWIFQNRRMKWK 16
Db      1 RQIKWIFQNRRMKWK 16

RESULT 11
US-09-308-935-8
; Sequence 8, Application US/09308935
; Patent No. 6268334
; GENERAL INFORMATION:
; APPLICANT: La Thangue, Nicholas B
; APPLICANT: Bandara, Lasantha R
; TITLE OF INVENTION: Peptide antagonists of DP transcription factors
; FILE REFERENCE: 620-67
; CURRENT APPLICATION NUMBER: US/09/308,935
; CURRENT FILING DATE: 1999-05-27
; EARLIER APPLICATION NUMBER: PCT/GB97/03506
; EARLIER FILING DATE: 1997-12-22
; EARLIER APPLICATION NUMBER: GB 9626589.7
; EARLIER FILING DATE: 1996-12-20
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 8
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-308-935-8

Query Match      100.0%; Score 92; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RQIKWIFQNRRMKWK 16
Db      1 RQIKWIFQNRRMKWK 16

RESULT 12
US-09-441-416A-6
; Sequence 6, Application US/09441416A
; Patent No. 6294518
; GENERAL INFORMATION:
; APPLICANT: Potter, David A.
; APPLICANT: Skolnik, Paul R.
; TITLE OF INVENTION: CELL-PERMEABLE PROTEIN INHIBITORS OF
; FILE REFERENCE: CALPAIN
; CURRENT APPLICATION NUMBER: 00398-140001
; CURRENT FILING DATE: 1999-11-16

US-09-419-826-35
; Sequence 35, Application US/09419826
; Patent No. 6306832
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PEPTIDE ANTISTROGEN COMPOSITIONS AND METHODS
; TITLE OF INVENTION: FOR TREATING BREAST CANCER
; NUMBER OF SEQUENCES: 39
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION NUMBER: US/09/419,826
; FILING DATE: 14-OCT-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US98/07711
; FILING DATE: 14-APR-1998
; APPLICATION NUMBER: US 60/043,545
; FILING DATE: 14-APR-1997
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
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; PRIOR APPLICATION NUMBER: US 08/964,302
; PRIOR FILING DATE: 1997-11-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-441-416A-6

Query Match      100.0%; Score 92; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RQIKWIFQNRRMKWK 16
Db      1 RQIKWIFQNRRMKWK 16

RESULT 13
US-09-296-089-33
; Sequence 33, Application US/09296089
; Patent No. 6303576
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Byers, Stephen
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; TITLE OF INVENTION: BETA-CATENIN MEDIATED GENE EXPRESSION
; FILE REFERENCE: 100086.411
; CURRENT APPLICATION NUMBER: US/09/296,089
; CURRENT FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 33
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-296-089-33

Query Match      100.0%; Score 92; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RQIKWIFQNRRMKWK 16
Db      1 RQIKWIFQNRRMKWK 16

RESULT 14
US-09-419-826-35
; Sequence 35, Application US/09419826
; Patent No. 6306832
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PEPTIDE ANTISTROGEN COMPOSITIONS AND METHODS
; TITLE OF INVENTION: FOR TREATING BREAST CANCER
; NUMBER OF SEQUENCES: 39
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION NUMBER: US/09/419,826
; FILING DATE: 14-OCT-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US98/07711
; FILING DATE: 14-APR-1998
; APPLICATION NUMBER: US 60/043,545
; FILING DATE: 14-APR-1997
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.0%; Pred. No. 2.1e-07; Indels 0; Gaps 0; Mismatches 0; Conservative 16; Matches 16; QY 1 ROIKWIFQNRMRKWK 16 Db 1 ROIKWIFQNRMRKWK 16

RESULT 17

US-09-346-847-25

Sequence 25, Application US/09346847

Patent No. 6472507

GENERAL INFORMATION:

APPLICANT: Fischer, M. Peter

APPLICANT: Wang, Shudong

TITLE OF INVENTION: Delivery System

FILE REFERENCE: CCI-009

CURRENT APPLICATION NUMBER: US/09/346,847

CURRENT FILING DATE: 1999-07-02

PRIOR APPLICATION NUMBER: GB 9814527

PRIOR FILING DATE: 1998-07-03

NUMBER OF SEQ ID NOS: 30

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 25

LENGTH: 16

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic

NAME/KEY: MOD RES

LOCATION: (16)

OTHER INFORMATION: AMIDATION

US-09-346-847-25

Query Match 100.0%; Score 92; DB 4; Length 16;

Best Local Similarity 100.0%; Pred. No. 2.1e-07; Indels 0; Gaps 0; Mismatches 0; Conservative 16; Matches 16; QY 1 ROIKWIFQNRMRKWK 16 Db 1 ROIKWIFQNRMRKWK 16

RESULT 18

US-09-057-363C-47

Sequence 47, Application US/09057363C

Patent No. 6551994

GENERAL INFORMATION:

APPLICANT: Blaschuk, Orest W.

Gour, Barbara J.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR INHIBITING THE INTERACTION BETWEEN ALPHA-CATENIN AND BETA-CATENIN

NUMBER OF SEQUENCES: 73

CORRESPONDENCE ADDRESS:

ADDRESSEE: Seed Intellectual Property Law Group

STREET: 701 Fifth Avenue, Suite 6300

CITY: Seattle

STATE: Washington

COUNTRY: USA

ZIP: 98104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/057,363C

FILING DATE: 08-Apr-1998

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Christiansen, William T.

REGISTRATION NUMBER: 44,614

LENGTH: 16 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

US-09-419-826-35

Query Match 100.0%; Score 92; DB 4; Length 16;

Best Local Similarity 100.0%; Pred. No. 2.1e-07; Indels 0; Gaps 0; Mismatches 0; Conservative 16; Matches 16; QY 1 ROIKWIFQNRMRKWK 16 Db 1 ROIKWIFQNRMRKWK 16

RESULT 15

US-09-302-305C-10

Sequence 10, Application US/09302305C

Patent No. 6350572

GENERAL INFORMATION:

APPLICANT: Bernards, Rene

APPLICANT: Zwijsen, Rene

TITLE OF INVENTION: Interaction Between Cyclin D1 and Steroid Receptor

FILE REFERENCE: 4238/80713

CURRENT APPLICATION NUMBER: US/09/302,305C

CURRENT FILING DATE: 1999-04-30

PRIOR APPLICATION NUMBER: PCT/GB99/00440

PRIOR FILING DATE: 1999-02-12

NUMBER OF SEQ ID NOS: 27

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 10

LENGTH: 16

TYPE: PRT

ORGANISM: Drosophila melanogaster

FEATURE:

NAME/KEY: PEPTIDE

LOCATION: (1)...(16)

OTHER INFORMATION: Translocation peptide derived from antennapedia

OTHER INFORMATION: homeodomain protein

US-09-302-305C-10

Query Match 100.0%; Score 92; DB 4; Length 16;

Best Local Similarity 100.0%; Pred. No. 2.1e-07; Indels 0; Gaps 0; Mismatches 0; Conservative 16; Matches 16; QY 1 ROIKWIFQNRMRKWK 16 Db 1 ROIKWIFQNRMRKWK 16

RESULT 16

US-09-346-847-1

Sequence 1, Application US/09346847

Patent No. 6472507

GENERAL INFORMATION:

APPLICANT: Fischer, M. Peter

APPLICANT: Wang, Shudong

TITLE OF INVENTION: Delivery System

FILE REFERENCE: CCI-009

CURRENT APPLICATION NUMBER: US/09/346,847

CURRENT FILING DATE: 1999-07-02

PRIOR APPLICATION NUMBER: GB 9814527

PRIOR FILING DATE: 1998-07-03

NUMBER OF SEQ ID NOS: 30

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 1

LENGTH: 16

TYPE: PRT

ORGANISM: Drosophila melanogaster

US-09-346-847-1

Query Match 100.0%; Score 92; DB 4; Length 16;

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/ REFERENCE/DOCKET NUMBER: 100086.406
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (206) 622-4900
/ TELEFAX: (206) 682-6031
/ INFORMATION FOR SEQ ID NO: 47:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 16 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: <Unknown>
/ TOPOLOGY: linear
/ SEQUENCE DESCRIPTION: SEQ ID NO: 47:
US-09-057-363C-47

Query Match          100.0%; Score 92; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RQIKWIFQNRRMKWK 16
Db 1 RQIKWIFQNRRMKWK 16

RESULT 19
US-09-043-560B-3
/ Sequence 3, Application US/09043560B
/ Patent No. 6569833
/ GENERAL INFORMATION:
/ APPLICANT: Fahraeus, Robin
/ TITLE OF INVENTION: Cyclin Dependent Kinase Binding Compounds
/ FILE REFERENCE: CCI-003US
/ CURRENT APPLICATION NUMBER: US/09/043,560B
/ CURRENT FILING DATE: 1999-04-07
/ PRIOR FILING DATE: 1999-04-07
/ NUMBER OF SEQ ID NOS: 16
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 3
/ LENGTH: 16
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-043-560B-3

Query Match          100.0%; Score 92; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RQIKWIFQNRRMKWK 16
Db 1 RQIKWIFQNRRMKWK 16

RESULT 20
US-09-648-400A-29
/ Sequence 29, Application US/09648400A
/ Patent No. 6593292
/ GENERAL INFORMATION:
/ APPLICANT: Rothbard, Jonathan B.
/ APPLICANT: Wender, Paul A.
/ APPLICANT: McGrane, P. Leo
/ APPLICANT: Sista, Lalitha V.S.
/ APPLICANT: Kirschberg, Thorsten A.
/ APPLICANT: Cellgate, Inc.
/ TITLE OF INVENTION: Compositions and Methods for Enhancing Drug Delivery
/ FILE REFERENCE: 019801-000210US
/ CURRENT APPLICATION NUMBER: US/09/648,400A
/ CURRENT FILING DATE: 2000-08-24
/ PRIOR FILING DATE: 1999-08-24
/ NUMBER OF SEQ ID NOS: 30
/ SOFTWARE: PatentIn Ver. 2.1
```

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/ SEQ ID NO 29
/ LENGTH: 16
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Antennapedia
/ OTHER INFORMATION: homeodomain, Antennapedia-43-58
US-09-648-400A-29

Query Match          100.0%; Score 92; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RQIKWIFQNRRMKWK 16
Db 1 RQIKWIFQNRRMKWK 16

RESULT 21
US-09-227-652B-4
/ Sequence 4, Application US/09227652B
/ Patent No. 6610495
/ GENERAL INFORMATION:
/ APPLICANT: TWV Telethon Institute for Child Health Research
/ TITLE OF INVENTION: PEPTIDE DETECTION METHOD
/ FILE REFERENCE: 1991209/MRO-PCT
/ CURRENT APPLICATION NUMBER: US/09/227,652B
/ CURRENT FILING DATE: 1999-01-08
/ PRIOR APPLICATION NUMBER: US 60/070989
/ PRIOR FILING DATE: 1998-01-09
/ NUMBER OF SEQ ID NOS: 4
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 4
/ LENGTH: 16
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Penetratin 16-mer.
US-09-227-652B-4

Query Match          100.0%; Score 92; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RQIKWIFQNRRMKWK 16
Db 1 RQIKWIFQNRRMKWK 16

RESULT 22
US-09-780-070-38
/ Sequence 38, Application US/09780070
/ Patent No. 6632616
/ GENERAL INFORMATION:
/ APPLICANT: Burke, James
/ APPLICANT: Strittmatter, Warren
/ APPLICANT: Nagai, Yoshitaka
/ TITLE OF INVENTION: COMPOUNDS THAT SELECTIVELY BIND TO EXPANDED POLYGLUTAMINE REPEAT I
/ TITLE OF INVENTION: AND METHODS OF USE THEREOF
/ FILE REFERENCE: 5405.242
/ CURRENT APPLICATION NUMBER: US/09/780,070
/ CURRENT FILING DATE: 2001-02-09
/ PRIOR APPLICATION NUMBER: 60/189,781
/ PRIOR FILING DATE: 2000-03-16
/ NUMBER OF SEQ ID NOS: 40
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 38
/ LENGTH: 16
/ TYPE: PRT
/ ORGANISM: Drosophila melanogaster
US-09-780-070-38

Query Match          100.0%; Score 92; DB 4; Length 16;
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us-09-830-779-7.ra1

Fri Oct 1 16:13:10 2004

Best Local Similarity 100.0%; Pred. No. 2.1e-07; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 0;

QY 1 RQIKWIFQNRMKWK 16
Db 1 RQIKWIFQNRMKWK 16

RESULT 23
US-08-610-220B-9
; Sequence 9, Application US/08610220B
; Patent No. 6635738
; GENERAL INFORMATION:
; APPLICANT: TIOY, Carol M.
; TITLE OF INVENTION: COMPOUNDS WHICH PREVENT NEURONAL CELL
; TITLE OF INVENTION: DEATH AND USES THEREOF
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/610,220B
; FILING DATE: MAR-04-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 48332/JFW/JML
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-610-220B-9

Query Match 100.0%; Score 92; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.1e-07; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 0;

QY 1 RQIKWIFQNRMKWK 16
Db 1 RQIKWIFQNRMKWK 16

RESULT 24
US-09-775-052A-54
; Sequence 54, Application US/09775052A
; Patent No. 6645501
; GENERAL INFORMATION:
; APPLICANT: Dowdy, Steven F.
; TITLE OF INVENTION: ANTI-PATHOGEN SYSTEM AND METHODS OF USE THEREOF
; FILE REFERENCE: 48881/1742
; CURRENT APPLICATION NUMBER: US/09/775,052A
; CURRENT FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/208,966
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-10
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/069,012
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-12-10
; NUMBER OF SEQ ID NOS: 57

SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 54
; LENGTH: 16
; TYPE: PRT
; ORGANISM: human
US-09-775-052A-54

Query Match 100.0%; Score 92; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.1e-07; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 0;

QY 1 RQIKWIFQNRMKWK 16
Db 1 RQIKWIFQNRMKWK 16

RESULT 25
US-09-155-165-22
; Sequence 22, Application US/09155165
; Patent No. 6660630
; GENERAL INFORMATION:
; APPLICANT: Radulescu, Razvan T
; TITLE OF INVENTION: PEPTIDES WITH ANTIPROLIFERATIVE PROPERTIES
; FILE REFERENCE: 201196/20
; CURRENT APPLICATION NUMBER: US/09/155,165
; CURRENT FILING DATE: 1999-06-07
; PRIOR APPLICATION NUMBER: 09/155,165
; PRIOR FILING DATE: 1998-09-22
; PRIOR APPLICATION NUMBER: PCT/DE97/00643
; PRIOR FILING DATE: 1997-03-26
; PRIOR APPLICATION NUMBER: DE 196 11 939.1
; PRIOR FILING DATE: 1996-03-26
; PRIOR APPLICATION NUMBER: DE 196 53 445.3
; PRIOR FILING DATE: 1996-12-20
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(16)
; OTHER INFORMATION: Peptide
US-09-155-165-22

Query Match 100.0%; Score 92; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.1e-07; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 0;

QY 1 RQIKWIFQNRMKWK 16
Db 1 RQIKWIFQNRMKWK 16

Search completed: October 1, 2004, 12:21:08
Job time : 19 secs

89 92 100.0 17 15 US-10-421-503-66 Sequence 66, Appl
 90 92 100.0 17 16 US-10-755-082-15 Sequence 15, Appl
 91 92 100.0 18 9 US-09-785-802A-14 Sequence 14, Appl
 92 92 100.0 18 16 US-10-364-645A-54 Sequence 54, Appl
 93 92 100.0 19 9 US-09-949-474-7 Sequence 7, Appl
 94 92 100.0 19 14 US-10-118-079-45 Sequence 45, Appl
 95 92 100.0 19 14 US-10-210-660-23 Sequence 23, Appl
 96 92 100.0 19 15 US-10-407-449-20 Sequence 20, Appl
 97 92 100.0 20 9 US-09-854-204-63 Sequence 63, Appl
 98 92 100.0 20 9 US-09-949-474-8 Sequence 8, Appl
 99 92 100.0 20 14 US-10-210-660-16 Sequence 16, Appl
 100 92 100.0 20 14 US-10-210-660-18 Sequence 18, Appl

ALIGNMENTS

RESULT 1
 US-08-610-220A-9
 ; Sequence 9, Application US/08610220A
 ; Publication No. US20030099638A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Troy, Carol M.
 ; TITLE OF INVENTION: COMPOUNDS WHICH PREVENT NEURONAL CELL
 ; DEATH AND USES THEREOF
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Cooper & Dunham LLP
 ; STREET: 1195 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/610,220A
 FILING DATE: MAR-04-1996
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: White, John P.
 REGISTRATION NUMBER: 28,678
 REFERENCE/DOCKET NUMBER: 48332/JFW/JWL
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-278-0400
 TELEFAX: 212-391-0525
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 16 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 ; MOLECULE TYPE: peptide

US-08-610-220A-9
 Query Match 100.0%; Score 92; DB 8; Length 16;
 Best Local Similarity 100.0%; Pred. No. 3.1e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RQIKWQNRRMKWKK 16
 |||||
 Db 1 RQIKWQNRRMKWKK 16

RESULT 2
 US-09-214-371-43
 ; Sequence 43, Application US/09214371B
 ; Patent No. US20010018511A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lane, David

; APPLICANT: Bottger, Volker
 ; APPLICANT: Bottger, Angelica
 ; APPLICANT: Picklesley, Stephen
 ; APPLICANT: Chene, Patrick
 ; APPLICANT: Hochkeppel, Heinz-Kurt
 ; APPLICANT: Garcia-Echeverria, Carlos
 ; APPLICANT: Furet, Pascal

; TITLE OF INVENTION: Inhibitors of the interaction of P53 and MDM2
 ; FILE REFERENCE: 4-20937/A/PCT
 ; CURRENT APPLICATION NUMBER: US/09/214,371B
 ; CURRENT FILING DATE: 1999-03-26
 ; PRIOR APPLICATION NUMBER: PCT/EP97/03549
 ; PRIOR FILING DATE: 1997-07-04
 ; NUMBER OF SEQ ID NOS: 83
 ; SOFTWARE: Patent in Ver. 2.0

; SEQ ID NO 43
 ; LENGTH: 16
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: peptide

US-09-214-371-43
 Query Match 100.0%; Score 92; DB 9; Length 16;
 Best Local Similarity 100.0%; Pred. No. 3.1e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RQIKWQNRRMKWKK 16
 |||||
 Db 1 RQIKWQNRRMKWKK 16

RESULT 3
 US-09-780-070-38
 ; Sequence 38, Application US/097800070
 ; Patent No. US20020009752A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Burke, James
 ; APPLICANT: Strittmatter, Warren

; APPLICANT: Nagai, Yoshitaka
 ; TITLE OF INVENTION: COMPOUNDS THAT SELECTIVELY BIND TO EXPANDED POLYGLUTAMINE REPEAT
 ; TITLE OF INVENTION: AND METHODS OF USE THEREOF
 ; FILE REFERENCE: 5405.242
 ; CURRENT APPLICATION NUMBER: US/09/780,070
 ; CURRENT FILING DATE: 2001-02-09
 ; PRIOR APPLICATION NUMBER: 60/189,781
 ; PRIOR FILING DATE: 2000-03-16
 ; NUMBER OF SEQ ID NOS: 40
 ; SOFTWARE: Patent in version 3.0

; SEQ ID NO 38
 ; LENGTH: 16
 ; TYPE: PRT
 ; ORGANISM: Drosophila melanogaster
 US-09-780-070-38
 Query Match 100.0%; Score 92; DB 9; Length 16;
 Best Local Similarity 100.0%; Pred. No. 3.1e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RQIKWQNRRMKWKK 16
 |||||
 Db 1 RQIKWQNRRMKWKK 16

RESULT 4
 US-09-150-623-9
 ; Sequence 9, Application US/09150623
 ; Patent No. US20020044931A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Troy, Carol M.
 ; TITLE OF INVENTION: COMPOUNDS WHICH PREVENT NEURONAL CELL
 ; DEATH AND USES THEREOF
 ; NUMBER OF SEQUENCES: 11

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Cooper & Dunham LLP
;; STREET: 1185 Avenue of the Americas
;; CITY: New York
;; STATE: New York
;; COUNTRY: U.S.A.
;; ZIP: 10036
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/150.623
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/610.220
;; FILING DATE: MAR-04-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: White, John P.
;; REGISTRATION NUMBER: 28,678
;; REFERENCE/DOCKET NUMBER: 48332/JFW/JML
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 212-278-0400
;; TELEFAX: 212-391-0525
;; INFORMATION FOR SEQ ID NOS:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 16 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-09-150-623-9

Query Match 100.0%; Score 92; DB 9; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWIFQNRRMKWK 16
DB 1 RQIKWIFQNRRMKWK 16

RESULT 5
US-09-731-023A-10
; Sequence 10, Application US/09731023A
; Patent No. US20020077283A1
; GENERAL INFORMATION:
; APPLICANT: Sessa, William
; TITLE OF INVENTION: Caveolin Peptides and Their Use as Therapeutics
; FILE REFERENCE: 44574-5076-US
; CURRENT APPLICATION NUMBER: US/09/731,023A
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/231,327
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1)..(16)
; OTHER INFORMATION: Homeodomain, internalization sequence
US-09-731-023A-10

Query Match 100.0%; Score 92; DB 9; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWIFQNRRMKWK 16

DB 1 RQIKWIFQNRRMKWK 16
RESULT 6
US-09-854-204-1
; Sequence 1, Application US/09854204-1
; Patent No. US20020098236A1
; GENERAL INFORMATION:
; APPLICANT: Fischer, Peter Martin
; APPLICANT: Zhelev, Nikolai
; TITLE OF INVENTION: Transport Vectors
; FILE REFERENCE: CCI-010
; CURRENT APPLICATION NUMBER: US/09/854,204
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 09/438,460
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: GB 9825000.4
; PRIOR FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: GB 9825001.2
; PRIOR FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: GB 9902525.6
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: GB 9902522.3
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: GB 9914578.1
; PRIOR FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: PCT/GB99/03750
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-854-204-1

Query Match 100.0%; Score 92; DB 9; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWIFQNRRMKWK 16
DB 1 RQIKWIFQNRRMKWK 16

RESULT 7
US-09-900-147-8
; Sequence 8, Application US/09900147
; Patent No. US20020103121A1
; GENERAL INFORMATION:
; APPLICANT: La Thangue, Nicholas B
; APPLICANT: Bandara, Lsantha R
; TITLE OF INVENTION: Peptide antagonists of DP transcription factors
; FILE REFERENCE: 620-67
; CURRENT APPLICATION NUMBER: US/09/900,147
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/308,935
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-05-27
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: GB 9626589.7
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-12-20
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-900-147-8

Query Match 100.0%; Score 92; DB 9; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

us-09-830-779-7.rapb

Fri Oct 1 16:13:10 2004

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QY 1 ROIKWFOQRMRMKWK 16
    |||||
Db 1 ROIKWFOQRMRMKWK 16

RESULT 10
US-09-785-802A-5
; Sequence 5, Application US/09785802A
; Patent No. US20020151004A1
; GENERAL INFORMATION:
; APPLICANT: Craig, Roger
; TITLE OF INVENTION: DELIVERY VEHICLES AND METHODS FOR USING THE SAME
; FILE REFERENCE: 11067/2035
; CURRENT APPLICATION NUMBER: US/09/785,802A
; CURRENT FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 09/748,06
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/748,789
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-785-802A-5
Query Match 100.0%; Score 92; DB 9; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ROIKWFOQRMRMKWK 16
    |||||
Db 1 ROIKWFOQRMRMKWK 16

RESULT 11
US-09-902-432-32
; Sequence 32, Application US/09902432
; Patent No. US20020160002A1
; GENERAL INFORMATION:
; APPLICANT: Irwin H. Gelman
; APPLICANT: Susan G. Jaken
; TITLE OF INVENTION: TUMOR SUPPRESSOR GENE
; FILE REFERENCE: A30558-A-FWC-A 070156.0597
; CURRENT APPLICATION NUMBER: US/09/902,432
; CURRENT FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: 08/978,277
; PRIOR FILING DATE: 1997-11-25
; PRIOR APPLICATION NUMBER: 08/665,401
; PRIOR FILING DATE: 1996-06-18
; PRIOR APPLICATION NUMBER: 08/635,121
; PRIOR FILING DATE: 1996-04-19
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Penetratin peptide
US-09-902-432-32
Query Match 100.0%; Score 92; DB 9; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ROIKWFOQRMRMKWK 16
    |||||
Db 1 ROIKWFOQRMRMKWK 16

RESULT 12
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QY 1 ROIKWFOQRMRMKWK 16
    |||||
Db 1 ROIKWFOQRMRMKWK 16

RESULT 8
US-09-792-480-29
; Sequence 29, Application US/09792480
; Patent No. US20020127198A1
; GENERAL INFORMATION:
; APPLICANT: Rothbard, Jonathan B.
; APPLICANT: Wender, Paul A.
; APPLICANT: McGrane, P. Leo
; APPLICANT: Sista, Lalitha V.S.
; APPLICANT: Kirschberg, Thorsten A.
; APPLICANT: CellGate, Inc.
; TITLE OF INVENTION: Compositions and Methods for Enhancing Drug Delivery
; TITLE OF INVENTION: Across and Into Epithelial Tissues
; FILE REFERENCE: 019801-000230US
; CURRENT APPLICATION NUMBER: US/09/792,480
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: US 09/648,400
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/150,510
; PRIOR FILING DATE: 1999-08-24
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Antennapedia
; OTHER INFORMATION: homeodomain, Antennapedia-43-58
US-09-792-480-29
Query Match 100.0%; Score 92; DB 9; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ROIKWFOQRMRMKWK 16
    |||||
Db 1 ROIKWFOQRMRMKWK 16

RESULT 9
US-09-785-802A-2
; Sequence 2, Application US/09785802A
; Patent No. US20020151004A1
; GENERAL INFORMATION:
; APPLICANT: Craig, Roger
; TITLE OF INVENTION: DELIVERY VEHICLES AND METHODS FOR USING THE SAME
; FILE REFERENCE: 11067/2035
; CURRENT APPLICATION NUMBER: US/09/785,802A
; CURRENT FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 09/748,06
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/748,789
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Membrane translocation sequence from Penetratin
US-09-785-802A-2
Query Match 100.0%; Score 92; DB 9; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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US-09-953-031A-10
; Sequence 10, Application US/09953031A
; Patent No. US2002017717A1
; GENERAL INFORMATION:
; APPLICANT: Bernards, Rene
; APPLICANT: Zwijsen, Renate
; TITLE OF INVENTION: Interaction Between Cyclin D1 and Steroid Receptor
; TITLE OF INVENTION: Co-Activators and Uses Thereof in Assays
; FILE REFERENCE: 4238/80713
; CURRENT APPLICATION NUMBER: US/09/953,031A
; CURRENT FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: US 09/302,305
; PRIOR FILING DATE: 1998-04-30
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 10
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(16)
; OTHER INFORMATION: Translocation peptide derived from antennapedia
; OTHER INFORMATION: homeodomain protein
US-09-953-031A-10

Query Match          100.0%; Score 92; DB 9; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWIFQNRRMKWK 16
DB 1 RQIKWIFQNRRMKWK 16

RESULT 13
US-09-981-286A-3
; Sequence 3, Application US/09981286A
; Publication No. US20020192799A1
; GENERAL INFORMATION:
; APPLICANT: Watowich, Stanley J.
; APPLICANT: Weaver, Robert A.
; TITLE OF INVENTION: Drug Discovery Methods
; FILE REFERENCE: 265.00260101
; CURRENT APPLICATION NUMBER: US/09/981,286A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: US 60/240,187
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 3
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cell-permeant polypeptide
US-09-981-286A-3

Query Match          100.0%; Score 92; DB 9; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWIFQNRRMKWK 16
DB 1 RQIKWIFQNRRMKWK 16

RESULT 14
US-09-962-967A-6
; Sequence 6, Application US/09962967A
; Publication No. US2003004112A1
; GENERAL INFORMATION:
; APPLICANT: Potter, David A.
; APPLICANT: Skolnik, Paul R.
; TITLE OF INVENTION: CELL-PERMEABLE PROTEIN INHIBITORS OF CALPAIN
; FILE REFERENCE: 00398-140002
; CURRENT APPLICATION NUMBER: US/09/962,967A
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: US 09/441,416
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: US 08/964,302
; PRIOR FILING DATE: 1997-11-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-962-967A-6

Query Match          100.0%; Score 92; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWIFQNRRMKWK 16
DB 1 RQIKWIFQNRRMKWK 16

RESULT 15
US-09-912-414-6
; Sequence 6, Application US/09912414
; Publication No. US20030013169A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Rolf
; APPLICANT: Kontermann, Roland E
; APPLICANT: Montigiani, Silvia
; TITLE OF INVENTION: Transcription factor E2F DNA-binding domain inhibitor
; TITLE OF INVENTION: Peptides and their use
; FILE REFERENCE: 620-151
; CURRENT APPLICATION NUMBER: US/09/912,414
; CURRENT FILING DATE: 2001-07-26
; PRIOR APPLICATION NUMBER: PCT/GB00/00227
; PRIOR FILING DATE: 2000-01-26
; PRIOR APPLICATION NUMBER: GB 9901710.5
; PRIOR FILING DATE: 1999-01-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 6
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-912-414-6

Query Match          100.0%; Score 92; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWIFQNRRMKWK 16
DB 1 RQIKWIFQNRRMKWK 16

RESULT 16
US-09-775-052-54
; Sequence 54, Application US/09775052
; Publication No. US20030054000A1
; GENERAL INFORMATION:
; APPLICANT: Dowdy, Steven F.
; TITLE OF INVENTION: ANTI-PATHOGEN SYSTEM AND METHODS OF USE THEREOF
; FILE REFERENCE: 48881/1742
; CURRENT APPLICATION NUMBER: US/09/775,052
; CURRENT FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: 09/208,966
; PRIOR FILING DATE: 1998-12-10
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; PRIOR APPLICATION NUMBER: 60/082,402
; PRIOR FILING DATE: 1998-04-20
; PRIOR APPLICATION NUMBER: 60/069,012
; PRIOR FILING DATE: 1997-12-10
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 54
; LENGTH: 16
; TYPE: PRT
; ORGANISM: human
US-09-775-052-54

Query Match      100.0%; Score 92; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ROIKWFOQRMRKWK 16
Db 1 ROIKWFOQRMRKWK 16

RESULT 17
US-09-295-189-4
; Sequence 4, Application US/09295189
; Publication No. US20030083273A1
; GENERAL INFORMATION:
; APPLICANT: Woolf, Tod M.
; TITLE OF INVENTION: Improved Antisense Oligomers
; FILE REFERENCE: SRI-004
; CURRENT APPLICATION NUMBER: US/09/295,189
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-295-189-4

Query Match      100.0%; Score 92; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ROIKWFOQRMRKWK 16
Db 1 ROIKWFOQRMRKWK 16

RESULT 18
US-09-965-876A-1
; Sequence 1, Application US/09965876A
; Publication No. US2003009243A1
; GENERAL INFORMATION:
; APPLICANT: Cellomics, Inc.
; APPLICANT: Busa, William B
; TITLE OF INVENTION: Methods and Reagents for Live-cell Gene Expression Quantification
; FILE REFERENCE: 00-789-A
; CURRENT APPLICATION NUMBER: US/09/965,876A
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US 60/236,407
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 16
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-09-965-876A-1

```

```

Query Match      100.0%; Score 92; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ROIKWFOQRMRKWK 16
Db 1 ROIKWFOQRMRKWK 16

RESULT 19
US-09-933-780C-2
; Sequence 2, Application US/09933780C
; Publication No. US20030229202A1
; GENERAL INFORMATION:
; APPLICANT: AVENTIS PHARMACEUTICALS INC.
; APPLICANT: GUO, Yong
; APPLICANT: MORSE, Clarence C
; APPLICANT: YAO, Zhengbin
; TITLE OF INVENTION: MEMBRANE PENETRATING PEPTIDES AND USES THEREOF
; FILE REFERENCE: HMR2053 PCT
; CURRENT APPLICATION NUMBER: US/09/933,780C
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 60/227,647
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: GB 0103110.3
; PRIOR FILING DATE: 2001-02-07
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Signal sequence peptide from Antennapedia homeodomain
US-09-933-780C-2

Query Match      100.0%; Score 92; DB 11; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ROIKWFOQRMRKWK 16
Db 1 ROIKWFOQRMRKWK 16

RESULT 20
US-10-286-964-3
; Sequence 3, Application US/10286964
; Publication No. US20040029791A1
; GENERAL INFORMATION:
; APPLICANT: Fahraeus, Robin
; APPLICANT: Lane, David P.
; TITLE OF INVENTION: Cyclin Dependent Kinase Binding Compounds
; FILE REFERENCE: CCI-003US
; CURRENT APPLICATION NUMBER: US/10/286,964
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US/09/043,560
; PRIOR FILING DATE: 1999-04-07
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-10-286-964-3

Query Match      100.0%; Score 92; DB 12; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 RQIKWIFQNRMRKWK 16
| | | | | | | | | | | | | | | | | |
DB 1 RQIKWIFQNRMRKWK 16

RESULT 21

US-10-432-291-6
; Sequence 6, Application US/104322291
; Publication No. US20040029281A1
; GENERAL INFORMATION:
; APPLICANT: Centre National de la Recherche Scientifique (CNRS)
; APPLICANT: Joliot, Alain
; APPLICANT: Dupont, Edmond
; APPLICANT: Prochiantz, Alain
; TITLE OF INVENTION: Carrier vectors through an epithelium with tight junctions
; FILE REFERENCE: 45636-5067-US
; CURRENT APPLICATION NUMBER: US/10/432,291
; CURRENT FILING DATE: 2003-05-20
; PRIOR APPLICATION NUMBER: PCT/FR01/03631
; PRIOR FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: FR 00/14945
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: penetratin sequence for transport vectors
US-10-432-291-6

Query Match 100.0%; Score 92; DB 12; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWIFQNRMRKWK 16
| | | | | | | | | | | | | | | | | |
DB 1 RQIKWIFQNRMRKWK 16

RESULT 22

US-10-357-826A-2
; Sequence 2, Application US/10357826A
; Publication No. US20040054155A1
; GENERAL INFORMATION:
; APPLICANT: WOOLF, TOD M.
; TITLE OF INVENTION: OLIGONUCLEOTIDE COMPOSITIONS WITH ENHANCED EFFICIENCY
; FILE REFERENCE: 089596/0403
; CURRENT APPLICATION NUMBER: US/10/357,826A
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: 60/353,381
; PRIOR FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 60/353,203
; PRIOR FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 60/436,238
; PRIOR FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: 60/438,608
; PRIOR FILING DATE: 2003-01-07
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 2.1
; SEQ ID NO 2
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Drosophila sp.
US-10-357-826A-2

Query Match 100.0%; Score 92; DB 12; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWIFQNRMRKWK 16
| | | | | | | | | | | | | | | | | |
DB 1 RQIKWIFQNRMRKWK 16

RESULT 23

US-10-603-409-12
; Sequence 12, Application US/10603409
; Publication No. US20040053849A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth Walter Bair
; APPLICANT: Yingnan Pan Chen
; APPLICANT: Timothy Michael Ramsey
; APPLICANT: Michael Lloyd Sabio
; APPLICANT: Sushill Kumar Sharma
; TITLE OF INVENTION: Inhibitors of the E2F-1/Cyclin
; TITLE OF INVENTION: Interaction for Cancer Therapy
; FILE REFERENCE: 4-33243/P1/N1
; CURRENT APPLICATION NUMBER: US/10/603,409
; CURRENT FILING DATE: 2003-06-25
; PRIOR APPLICATION NUMBER: 10/024,935
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: PCT/EP1 /15006
; PRIOR FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PROTEIN
US-10-603-409-12

Query Match 100.0%; Score 92; DB 12; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWIFQNRMRKWK 16
| | | | | | | | | | | | | | | | | |
DB 1 RQIKWIFQNRMRKWK 16

RESULT 24

US-09-748-063-3
; Sequence 3, Application US/09748063
; Publication No. US20010008758A1
; GENERAL INFORMATION:
; APPLICANT: McHale, Anthony P.
; APPLICANT: Craig, Roger
; APPLICANT: Haro, Anna Maria Rollan
; TITLE OF INVENTION: Delivery of an Agent
; FILE REFERENCE: 11067/1060
; CURRENT APPLICATION NUMBER: US/09/748,063
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: PCT/GB00/02848
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: US 60/146,556
; PRIOR FILING DATE: 2000-07-30
; PRIOR APPLICATION NUMBER: GB 9917416.1
; PRIOR FILING DATE: 1999-07-23
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Drosophila sp.
US-09-748-063-3

Query Match 100.0%; Score 92; DB 12; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Fri Oct 1 16:13:10 2004

Qy 1 RQIKWIFONRRMKWK 16
 Db 1 RQIKWIFONRRMKWK 16

RESULT 25
 US-09-779-791A-3
 ; Sequence 3, Application US/09779791A
 ; Publication No. US2001004417A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Mirus Corporation
 ; APPLICANT: Wolff, Jon A
 ; APPLICANT: Monahan, Sean D
 ; APPLICANT: Budker, Vladimir G
 ; APPLICANT: Stattum, Paul M
 ; APPLICANT: Rozema, David B
 ; TITLE OF INVENTION: A Compound Containing a Labile Disulfide Bond
 ; FILE REFERENCE: Mirus.006.03
 ; CURRENT APPLICATION NUMBER: US/09/779,791A
 ; CURRENT FILING DATE: 2001-02-08
 ; PRIOR APPLICATION NUMBER: 09/312,351
 ; PRIOR FILING DATE: 1999-05-14
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 3
 ; LENGTH: 16
 ; TYPE: PRT
 ; ORGANISM: Drosophila melanogaster
 US-09-779-791A-3

Query Match 100.0%; Score 92; DB 12; Length 16;
 Best Local Similarity 100.0%; Pred. No. 3.1e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RQIKWIFONRRMKWK 16
 Db 1 RQIKWIFONRRMKWK 16

Search completed: October 1, 2004, 12:48:41
 Job time : 65.4 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: October 1, 2004, 12:05:26 ; Search time 15.6 Seconds
(without alignments)
98.658 Million cell updates/sec

Title: US-09-830-779-7
Perfect score: 92
Sequence: 1 RQIKWIFQNRMKWKX 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : PIR_78.*

1: piri.*
2: piri2.*
3: piri3.*
4: piri4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	92	100.0	33	2 S57235	antennapedia prote
2	92	100.0	42	2 I65241	homeotic protein H
3	92	100.0	45	2 FC1216	homeotic protein D
4	92	100.0	48	2 I51439	homeobox protein -
5	92	100.0	66	2 S15536	homeotic protein H
6	92	100.0	66	2 S15538	homeotic protein H
7	92	100.0	71	2 JCL161	homeotic protein 3
8	92	100.0	71	2 A60084	homeotic protein H
9	92	100.0	74	2 D34310	homeotic protein H
10	92	100.0	75	2 I51341	homeo box protein
11	92	100.0	75	2 S58852	homeotic protein S
12	92	100.0	76	2 C43559	homeotic protein R
13	92	100.0	78	2 I51342	homeo box protein
14	92	100.0	81	2 S47605	homeotic protein H
15	92	100.0	81	2 B29585	homeotic protein H
16	92	100.0	82	2 S08302	homeotic protein H
17	92	100.0	83	2 S47603	homeotic protein H
18	92	100.0	83	2 S50066	homeotic protein H
19	92	100.0	86	2 A34510	homeotic protein H
20	92	100.0	86	2 J70489	homeotic protein Z
21	92	100.0	86	2 S08303	homeotic protein H
22	92	100.0	87	2 S00589	homeotic protein H
23	92	100.0	88	2 A03317	homeotic protein M
24	92	100.0	96	2 S08639	homeotic protein z
25	92	100.0	96	2 A05266	homeotic protein z
26	92	100.0	97	2 C27176	homeotic protein H
27	92	100.0	97	2 A24779	homeotic protein m
28	92	100.0	103	2 A32167	homeotic protein H
29	92	100.0	105	2 S47602	homeotic protein H

30	92	100.0	105	2 A27471	homeotic protein R
31	92	100.0	106	2 S36448	homeotic protein s
32	92	100.0	107	2 B61045	homeotic protein T
33	92	100.0	113	2 T10775	homeobox protein -
34	92	100.0	118	2 A24777	homeotic protein H
35	92	100.0	118	2 J70273	homeotic protein H
36	92	100.0	118	2 B24777	homeotic protein M
37	92	100.0	119	2 A03314	homeotic protein m
38	92	100.0	138	2 S20087	homeotic protein b
39	92	100.0	148	2 PC4071	homeobox A5 protei
40	92	100.0	153	1 WJHU3C	homeotic protein H
41	92	100.0	153	1 WJMSX6	homeotic protein H
42	92	100.0	158	2 A27348	homeotic protein H
43	92	100.0	209	2 A43553	homeotic protein H
44	92	100.0	217	1 WJHU2C	homeotic protein H
45	92	100.0	217	1 WJMSX2	homeotic protein H
46	92	100.0	220	2 A37371	homeotic protein H
47	92	100.0	220	2 S01063	Hox 2 protein type
48	92	100.0	222	2 S20029	homeotic protein H
49	92	100.0	224	2 S26400	homeotic protein H
50	92	100.0	224	2 A31324	homeotic protein H
51	92	100.0	227	2 S50067	homeotic protein H
52	92	100.0	228	2 S32563	homeotic protein H
53	92	100.0	229	2 A28329	homeotic protein H
54	92	100.0	230	2 S00592	homeotic protein H
55	92	100.0	232	1 A25108	homeotic protein H
56	92	100.0	232	2 S48125	homeotic protein H
57	92	100.0	233	2 I65197	hox1.3 protein - r
58	92	100.0	234	1 S02014	homeotic protein H
59	92	100.0	234	2 S00992	homeotic protein H
60	92	100.0	235	2 A55568	homeotic protein H
61	92	100.0	235	2 S74229	homeotic protein H
62	92	100.0	236	1 S09256	homeotic protein H
63	92	100.0	242	1 A39164	homeotic protein H
64	92	100.0	245	1 S10092	homeotic protein H
65	92	100.0	246	2 T46446	hypothetical prote
66	92	100.0	250	1 A36170	homeotic protein H
67	92	100.0	250	1 A31757	homeotic protein H
68	92	100.0	251	1 B60492	homeotic protein H
69	92	100.0	255	1 WJHU4B	homeotic protein H
70	92	100.0	264	1 S35219	homeotic protein H
71	92	100.0	264	1 S35219	homeotic protein H
72	92	100.0	269	1 A43551	homeotic protein H
73	92	100.0	269	1 A45578	homeotic protein H
74	92	100.0	270	1 WJHU1C	homeotic protein H
75	92	100.0	270	1 WJMS13	homeotic protein H
76	92	100.0	275	1 WJZFX2	homeotic protein H
77	92	100.0	295	2 S58850	homeotic protein a
78	92	100.0	378	2 A25399	homeotic protein A
79	92	100.0	394	2 S26492	homeotic protein S
80	92	100.0	413	1 S03631	homeotic protein S
81	92	100.0	590	2 A26638	homeotic protein D
82	91	98.9	60	2 PC2399	antennapedia-like
83	91	98.9	60	2 I51437	antennapedia-like
84	91	98.9	62	2 B32391	homeotic protein H
85	91	98.9	66	2 S15534	homeotic protein H
86	91	98.9	67	2 B27471	homeotic protein R
87	91	98.9	69	2 S13785	homeotic protein m
88	91	98.9	70	2 B37042	homeotic protein H
89	91	98.9	81	2 A25180	homeotic protein H
90	91	98.9	85	2 I51198	homeotic protein H
91	91	98.9	85	2 A24772	homeotic protein H
92	91	98.9	95	2 B32830	homeotic protein H
93	91	98.9	96	2 A55278	homeotic protein H
94	91	98.9	99	2 A41605	homeotic protein H
95	91	98.9	104	2 D43559	homeotic protein R
96	91	98.9	114	2 A43559	homeotic protein R
97	91	98.9	155	2 S25846	homeotic protein H
98	91	98.9	188	2 I50145	homeotic protein H
99	91	98.9	242	1 WJMSX3	homeotic protein H
100	91	98.9			

ALIGNMENTS

RESULT 1

S57235
antennapedia protein (clone pil05) - fruit fly (*Drosophila pseudoobscura*) (fragment)
C:Species: *Drosophila pseudoobscura*
C:Date: 10-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 15-Oct-1999
C:Accession: S57235
R:Randazzo, F.M.; Seeger, M.A.; Huss, C.A.; Sweeney, M.A.; Cecil, J.K.; Kaufman, T.C.
Genetics 133, 319-330, 1993
A:Title: Structural changes in the antennapedia complex of *Drosophila pseudoobscura*.
A:Reference number: S57224
A:Accession: S57235
A:Molecule type: DNA
A:Residues: 1-33 <RAN>
A:Cross-references: EMBL:X77711
C:Genetics:
A:Gene: FlyBase:Antp
A:Cross-references: FlyBase:FBgn0012693
C:Superfamily: unassigned homeobox proteins; homeobox homology
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation
F:1-22/Domain: homeobox homology (fragment) <HOX>

Query Match 100.0%; Score 92; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.4e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWIFQNRMKWK 16
|||
Db 7 RQIKWIFQNRMKWK 22

RESULT 2

I65241
homeotic protein Hox-A - rat (fragment)
C:Species: *Rattus norvegicus* (Norway rat)
C:Date: 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 15-Oct-1999
C:Accession: I65241
R:Sakayama, Y.; Mizuta, I.; Ogasawara, N.; Yoshikawa, H.
Biochem. Genet. 32, 351-360, 1994
A:Title: Cloning of rat homeobox genes.
A:Reference number: I52340; MUID:95217128; PMID:7702549
A:Accession: I65241
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-42 <RES>
A:Cross-references: GB:S76290; NID:g913077
C:Genetics:
A:Gene: Hox-A; Hox-1
C:Superfamily: unassigned homeobox proteins; homeobox homology
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation
F:1-40/Domain: homeobox homology (fragment) <HOX>

Query Match 100.0%; Score 92; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.8e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWIFQNRMKWK 16
|||
Db 25 RQIKWIFQNRMKWK 40

RESULT 3

PC1216
homeotic protein DfHx1 - planarian (*Dugesia tigrina*) (fragment)
C:Species: *Dugesia tigrina*
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 17-Oct-1997
C:Accession: PC1216
R:Oliver, G.; Vispo, M.; Mailhos, A.; Martinez, C.; Sosa-Pineda, B.; Fielitz, W.; Ehrlich
Gene 121, 337-342, 1992
A:Title: Homeoboxes in flatworms.
A:Reference number: JCI386; MUID:93077050; PMID:1359988

A:Accession: PC1216
A:Molecule type: DNA
A:Residues: 1-45 <OLI>
A:Cross-references: EMBL:X66822
C:Superfamily: unassigned homeobox proteins; homeobox homology
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation
F:1-45/Domain: homeobox homology (fragment) <HOX>

Query Match 100.0%; Score 92; DB 2; Length 45;
Best Local Similarity 100.0%; Pred. No. 1.9e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWIFQNRMKWK 16
|||
Db 30 RQIKWIFQNRMKWK 45

RESULT 4

I51439
homeobox protein - African clawed frog (fragment)
C:Species: *Xenopus laevis* (African clawed frog)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 15-Oct-1999
C:Accession: I51439
R:Heroy, P.; DeRobertis, E.M.
Dev. Dyn. 134, 21-32, 1992
A:Title: Effects of lithium chloride and retinoic acid on the expression of genes from the
A:Reference number: I51439; MUID:93043517; PMID:1384809
A:Accession: I51439
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-48 <LER>
A:Cross-references: GB:M91587; NID:G214257; PIDN:AAA49750.1; PID:G214258
C:Genetics:
A:Gene: Hox2.2
C:Superfamily: unassigned homeobox proteins; homeobox homology
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation
F:1-27/Domain: homeobox homology (fragment) <HOX>

Query Match 100.0%; Score 92; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWIFQNRMKWK 16
|||
Db 12 RQIKWIFQNRMKWK 27

RESULT 5

S15536
homeotic protein Hox A7 - human (fragment)
N:Alternate names: homeotic protein Hox 1A
C:Species: *Homo sapiens* (man)
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 29-Aug-1997
C:Accession: S15536
R:Boncinelli, B.; Acampora, D.; Pannese, M.; d'Esposito, M.; Somma, R.; Gaudino, G.; Stoll
Genome 31, 745-756, 1989
A:Title: Organization of human class I homeobox genes.
A:Reference number: S15036; MUID:90215256; PMID:2576652
A:Accession: S15536
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-66 <BON>
C:Genetics:
A:Gene: GDB:HOXA7
A:Cross-references: GDB:120647; OMIM:142950
A:Map position: 7p15.3-7p15.3
C:Superfamily: unassigned homeobox proteins; homeobox homology
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation
F:2-58/Domain: homeobox homology <HOX>

Query Match 100.0%; Score 92; DB 2; Length 66;
Best Local Similarity 100.0%; Pred. No. 2.8e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWQNRRMKWKK 16
 |||||
 DB 43 RQIKWQNRRMKWKK 58

RESULT 6

S15538
 homeotic protein Hox A6 - human (fragment)
 N;Alternate names: homeotic protein Hox 1B
 C;Species: Homo sapiens (man)
 C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 29-Aug-1997
 C;Accession: S15538
 R;Boncinelli, E.; Acampora, D.; Pannese, M.; d'Esposito, M.; Somma, R.; Gaudino, G.; Stoc
 Genome 31, 745-756, 1989
 A;Title: Organization of human class I homeobox genes.
 A;Reference number: S15036; MUID:90215256; PMID:2576652
 A;Accession: S15538
 A;Status: not compared with conceptual translation
 A;Molecule type: DNA
 A;Residues: 1-66 <BON>
 C;Genetics:
 A;Gene: GDB:H0XA6
 A;Cross-references: GDB:120648; OMIM:142951
 A;Map position: 7p15.3-7p15.3
 C;Superfamily: unassigned homeobox proteins; homeobox homology
 C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
 F;2-58/Domain: homeobox homology <Hox>

Query Match 100.0%; Score 92; DB 2; Length 66;
 Best Local Similarity 100.0%; Pred. No. 2.8e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWQNRRMKWKK 16
 |||||
 DB 43 RQIKWQNRRMKWKK 58

RESULT 7

JC1161
 homeotic protein 3.4 - eastern newt (fragment)
 C;Species: Notophthalmus viridescens, Triturus viridescens (eastern newt)
 C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 23-May-1997
 C;Accession: JC1161
 R;Belleville, S.; Beauchemin, M.; Tremblay, M.; Noiseux, N.; Savard, P.
 Gene 114, 179-186, 1992
 A;Title: Homeobox-containing genes in the newt are organized in clusters similar to other
 A;Reference number: JC1161; MUID:92290273; PMID:1351019
 A;Accession: JC1161
 A;Molecule type: DNA
 A;Residues: 1-71 <BEL>
 A;Cross-references: GB:M84001
 C;Genetics:
 A;Gene: NVHBox-3.4
 C;Superfamily: unassigned homeobox proteins; homeobox homology
 C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
 F;5-61/Domain: homeobox homology <Hox>

Query Match 100.0%; Score 92; DB 2; Length 71;
 Best Local Similarity 100.0%; Pred. No. 3e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWQNRRMKWKK 16
 |||||
 DB 46 RQIKWQNRRMKWKK 61

RESULT 8

A60084
 homeotic protein Hox 3.4 - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 20-Feb-1993 #sequence_revision 20-Feb-1993 #text_change 07-May-1999
 C;Accession: A60084

R;Gaunt, S.J.; Coletta, P.L.; Pravtcheva, D.; Sharpe, P.T.
 Development 109, 329-339, 1990
 A;Title: Mouse Hox-3.4: homeobox sequence and embryonic expression patterns compared with
 A;Reference number: A60084; MUID:90382249; PMID:1976088
 A;Accession: A60084
 A;Status: not compared with conceptual translation
 A;Molecule type: DNA
 A;Residues: 1-71 <GAU>
 C;Genetics:
 A;Map position: 15
 C;Superfamily: unassigned homeobox proteins; homeobox homology
 C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
 F;5-61/Domain: homeobox homology <Hox>

Query Match 100.0%; Score 92; DB 2; Length 71;
 Best Local Similarity 100.0%; Pred. No. 3e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWQNRRMKWKK 16
 |||||
 DB 46 RQIKWQNRRMKWKK 61

RESULT 9

D34510
 homeotic protein H90 - honeybee (fragment)
 C;Species: Apis mellifera (honeybee)
 C;Date: 22-Jun-1990 #sequence_revision 09-Oct-1992 #text_change 24-Sep-1999
 C;Accession: D34510
 R;Walldorf, U.; Fleig, R.; Gehring, W.J.
 Proc. Natl. Acad. Sci. U.S.A. 86, 9971-9975, 1989
 A;Title: Comparison of homeobox-containing genes of the honeybee and Drosophila.
 A;Reference number: A34510; MUID:90099384; PMID:2574865
 A;Accession: D34510
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-74 <WAL>

A;Cross-references: GB:M29493; NID:9155675; PIDN:AAA27728.1; PID:9155676
 A;Note: the authors mistranslated the codons for residues 68-74
 C;Superfamily: unassigned homeobox proteins; homeobox homology
 C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
 F;9-65/Domain: homeobox homology <Hox>

Query Match 100.0%; Score 92; DB 2; Length 74;
 Best Local Similarity 100.0%; Pred. No. 3.1e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWQNRRMKWKK 16
 |||||
 DB 50 RQIKWQNRRMKWKK 65

RESULT 10

IS1341
 homeo box protein - Atlantic salmon (fragment)
 C;Species: Salmo salar (Atlantic salmon)
 C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 24-Sep-1999
 C;Accession: IS1341
 R;Fjose, A.; Moiven, A.; Eiken, H.G.
 Gene 82, 141-152, 1988
 A;Title: Molecular cloning and characterization of homeobox-containing genes from Atlantic
 A;Reference number: IS1341; MUID:88226009; PMID:2897318
 A;Accession: IS1341
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-75 <FJO>
 A;Cross-references: GB:M18903; NID:9213797; PIDN:AAA49559.1; PID:9213798
 C;Superfamily: unassigned homeobox proteins; homeobox homology
 C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
 F;2-58/Domain: homeobox homology <Hox>

Query Match 100.0%; Score 92; DB 2; Length 75;
 Best Local Similarity 100.0%; Pred. No. 3.1e-07;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWFWQNRMKWK 16
 Db 43 RQIKWFWQNRMKWK 58

RESULT 11

S58852
 homeotic protein Scr homolog - Junonia coenia (fragment)
 N;Alternate names: sex combs reduced homeodomain protein
 C;Species: Junonia coenia
 C;Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 24-Sep-1999
 C;Accession: S58852
 R;Warren, R. W.; Nagy, L.; Selegue, J.; Gates, J.; Carroll, S.
 Nature 372, 458-461, 1994
 A;Title: Evolution of homeotic gene regulation and function in flies and butterflies.
 A;Reference number: S58850; MUID:95075456; PMID:7840822
 A;Accession: S58852
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: mRNA
 A;Residues: 1-75 <WAR>

A;Cross-references: EMBL:L42136; NID:G806495; PIDN:AAA68462.1; PID:G806496
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1995
 C;Superfamily: unassigned homeobox proteins; homeobox homology
 C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
 F;1-40/Domain: homeobox homology (fragment) <HOX>

Query Match 100.0%; Score 92; DB 2; Length 75;
 Best Local Similarity 100.0%; Pred. No. 3.2e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWFWQNRMKWK 16
 Db 25 RQIKWFWQNRMKWK 40

RESULT 12

C43559
 homeotic protein R3 - rat (fragment)
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 24-Sep-1999
 C;Accession: C43559
 R;Falzon, M.; Chung, S. Y.
 Development 103, 601-610, 1988
 A;Title: The expression of rat homeobox-containing genes is developmentally regulated and
 A;Reference number: A43559; MUID:89231502; PMID:2907739
 A;Accession: C43559
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-76 <FAL>

A;Cross-references: GB:M37567; NID:9204634; PIDN:AAA41343.1; PID:G204635
 C;Superfamily: unassigned homeobox proteins; homeobox homology
 C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
 F;20-76/Domain: homeobox homology (fragment) <HOX>

Query Match 100.0%; Score 92; DB 2; Length 76;
 Best Local Similarity 100.0%; Pred. No. 3.2e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWFWQNRMKWK 16
 Db 53 RQIKWFWQNRMKWK 68

RESULT 13

I51342
 homeo box protein - Atlantic salmon (fragment)
 C;Species: Salmo salar (Atlantic salmon)
 C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 24-Sep-1999
 C;Accession: I51342
 R;Jose, A.; Molven, A.; Eiken, H. G.
 Gene 62, 141-152, 1988

A;Title: Molecular cloning and characterization of homeobox-containing genes from Atlantic
 A;Reference number: I51341; MUID:88226009; PMID:2897318

A;Accession: I51342
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-78 <FUO>
 A;Cross-references: GB:M18904; NID:G213799; PIDN:AAA49560.1; PID:G213800
 C;Superfamily: unassigned homeobox proteins; homeobox homology
 C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
 F;2-58/Domain: homeobox homology <HOX>

Query Match 100.0%; Score 92; DB 2; Length 78;
 Best Local Similarity 100.0%; Pred. No. 3.2e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWFWQNRMKWK 16
 Db 43 RQIKWFWQNRMKWK 58

RESULT 14

S47605
 homeotic protein Hox-7 - Florida lancelet (fragment)
 C;Species: Branchiostoma floridae (Florida lancelet)
 C;Date: 01-Feb-1995 #sequence_revision 26-May-1995 #text_change 24-Sep-1999
 C;Accession: S47605
 R;Garcia-Fernandez, J.; Holland, P. W. H.
 Nature 370, 563-566, 1994

A;Title: Archetypal organization of the amphioxus Hox gene cluster.
 A;Reference number: S47599; MUID:94329179; PMID:7914353
 A;Accession: S47605
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-81 <GAR>

A;Cross-references: EMBL:Z35147; NID:G520617; PIDN:CAA84519.1; PID:G520618
 C;Superfamily: unassigned homeobox proteins; homeobox homology
 C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
 F;4-60/Domain: homeobox homology <HOX>

Query Match 100.0%; Score 92; DB 2; Length 81;
 Best Local Similarity 100.0%; Pred. No. 3.4e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWFWQNRMKWK 16
 Db 45 RQIKWFWQNRMKWK 60

RESULT 15

B29585
 homeotic protein Hox 2.2 precursor - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 15-Dec-1988 #sequence_revision 30-Sep-1991 #text_change 17-Oct-1997
 C;Accession: B29585
 R;Lonai, P.; Arman, E.; Czesnek, H.; Ruddle, F. H.; Blatt, C.
 DNA 6, 409-418, 1987

A;Title: New murine homeoboxes: structure, chromosomal assignment, and differential expression
 A;Reference number: A29585; MUID:88054465; PMID:2890503
 A;Accession: B29585
 A;Molecule type: DNA
 A;Residues: 1-81 <LON>

A;Cross-references: GB:M18167
 A;Note: the authors translated the codon CAG for residue 69 as Glu
 C;Superfamily: unassigned homeobox proteins; homeobox homology
 C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
 F;4-60/Domain: homeobox homology <HOX>

Query Match 100.0%; Score 92; DB 2; Length 81;
 Best Local Similarity 100.0%; Pred. No. 3.4e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWFWQNRMKWK 16
 Db 45 RQIKWFWQNRMKWK 60

Db 45 RQIKWFOQRNRMKWK 60

RESULT 16

S08302
homeotic protein Hox 2.1 - chicken (fragment)
C:Species: Gallus gallus (chicken)
C:Date: 02-Dec-1993 #sequence_revision 03-Nov-1995 #text_change 20-Jun-2000
C:Accession: S08302
R:Wedden, S.E.; Pang, K.; Eichele, G.
Development 105, 639-650, 1989
A:Title: Expression pattern of homeobox-containing genes during chick embryogenesis.
A:Reference number: S08302; MUID:90126373; PMID:2575515
A:Accession: S08302
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-82 <MED>
A:Cross-references: EMBL:X16846; NID:G62905; PIDN:CAA34743.1; PID:gl3334633
A>Note: the authors translated the codon GGA for residue 4 as Arg
C:Superfamily: homeotic protein Hox A5; homeobox homology
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation
F:8-64/Domain: homeobox homology <HOX>

Query Match 100.0%; Score 92; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 3.4e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWFOQRNRMKWK 16

Db 49 RQIKWFOQRNRMKWK 64

RESULT 17

S47603
homeotic protein Hox-5 - Florida lancelet (fragment)
C:Species: Branchiostoma floridae (Florida lancelet)
C:Date: 01-Feb-1995 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C:Accession: S47603
R:Garcia-Fernandez, J.; Holland, P.W.H.
Nature 370, 563-566, 1994
A:Title: Archetypal organization of the amphioxus Hox gene cluster.
A:Reference number: S47599; MUID:94329179; PMID:7914353
A:Accession: S47603
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-83 <GAR>
A:Cross-references: EMBL:Z35145
C:Superfamily: unassigned homeobox proteins; homeobox homology
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation
F:7-63/Domain: homeobox homology <HOX>

Query Match 100.0%; Score 92; DB 2; Length 83;
Best Local Similarity 100.0%; Pred. No. 3.4e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWFOQRNRMKWK 16

Db 48 RQIKWFOQRNRMKWK 63

RESULT 18

S50066
homeotic protein Hox-5 - Florida lancelet (fragment)
C:Species: Branchiostoma floridae (Florida lancelet)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 24-Sep-1999
C:Accession: S50066
R:Holland, P.W.
submitted to the EMBL Data Library, July 1994
A:Reference number: S50066
A:Accession: S50066
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-83 <HOL>

A:Cross-references: EMBL:Z35145; NID:9520613; PIDN:CAA84517.1; PID:gs20614
C:Superfamily: unassigned homeobox proteins; homeobox homology
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation
F:7-63/Domain: homeobox homology <HOX>

Query Match 100.0%; Score 92; DB 2; Length 83;
Best Local Similarity 100.0%; Pred. No. 3.4e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWFOQRNRMKWK 16

Db 48 RQIKWFOQRNRMKWK 63

RESULT 19

A34510
homeotic protein H55 - honeybee (fragment)
C:Species: Apis mellifera (honeybee)
C:Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 24-Sep-1999
C:Accession: A34510
R:Waldorf, U.; Fleig, R.; Gehring, W.J.
Proc. Natl. Acad. Sci. U.S.A. 86, 9971-9975, 1989
A:Title: Comparison of homeobox-containing genes of the honeybee and Drosophila.
A:Reference number: A34510; MUID:90093384; PMID:2574865
A:Accession: A34510
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-86 <WAL>
A:Cross-references: GB:M29488; NID:G155665; PIDN:AAA27723.1; PID:gl55666
C:Superfamily: unassigned homeobox proteins; homeobox homology
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation
F:9-65/Domain: homeobox homology <HOX>

Query Match 100.0%; Score 92; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWFOQRNRMKWK 16

Db 50 RQIKWFOQRNRMKWK 65

RESULT 20

JT0489
homeotic protein ZP-13 - zebra fish
C:Species: Brachydanio rerio (zebra fish)
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 17-Oct-1997
C:Accession: JT0489
R:Njoelstad, P.R.; Molven, A.; Eiken, H.G.; Fjose, A.
Gene 73, 33-46, 1988
A:Title: Structure and neural expression of a zebrafish homeobox sequence.
A:Reference number: JT0489; MUID:89211958; PMID:2468579
A:Accession: JT0489
A:Molecule type: DNA
A:Residues: 1-86 <NJO>
C:Genetics:
A:Gene: ZP-13
C:Superfamily: unassigned homeobox proteins; homeobox homology
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation
F:11-67/Domain: homeobox homology <HOX>

Query Match 100.0%; Score 92; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWFOQRNRMKWK 16

Db 52 RQIKWFOQRNRMKWK 67

RESULT 21

S08103
homeotic protein Hox 2.2 - chicken (fragment)

C:Species: Gallus gallus (Chicken)
 C:Date: 02-Dec-1993 #sequence_revision 03-Aug-1995 #text_change 17-Oct-1997
 C:Accession: S08303
 R:Wedden, S.E.; Pang, K.; Bichele, G.
 Development 105, 639-650, 1989
 A:Title: Expression pattern of homeobox-containing genes during chick embryogenesis.
 A:Reference number: S08302; MUID:90126373; PMID:2575515
 A:Accession: S08303
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-86 <WEB>
 A:Cross-references: EMBL:X16847
 C:Superfamily: unassigned homeobox proteins; homeobox homology
 C:Keywords: DNA binding; homeobox; nucleus; transcription regulation
 F:10-66/Domain: homeobox homology <HOX>

Query Match 100.0%; Score 92; DB 2; Length 86;
 Best Local Similarity 100.0%; Pred. No. 3.6e-07; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 0

QY 1 RQIKWIFQNRMRMKWK 16
 |||||
 DB 51 RQIKWIFQNRMRMKWK 66

RESULT 22

S00589
 homeotic protein Hox 5 - African clawed frog (fragment)
 C:Species: Xenopus laevis (African clawed frog)
 C:Date: 01-Dec-1999 #sequence_revision 01-Dec-1989 #text_change 24-Sep-1999
 C:Accession: S00589
 R:Fritz, A.; de Robertis, E.M.
 Nucleic Acids Res. 16, 1453-1469, 1988
 A:Title: Xenopus homeobox-containing cDNAs expressed in early development.
 A:Reference number: S00589; MUID:88157707; PMID:2894634
 A:Accession: S00589
 A:Molecule type: mRNA
 A:Residues: 1-87 <FRI>
 A:Cross-references: EMBL:X07105; NID:964757; PIDN:CAA30126.1; PID:e12307; PID:g1334653
 C:Superfamily: unassigned homeobox proteins; homeobox homology
 C:Keywords: DNA binding; homeobox; nucleus; transcription regulation
 F:21-77/Domain: homeobox homology <HOX>

Query Match 100.0%; Score 92; DB 2; Length 87;
 Best Local Similarity 100.0%; Pred. No. 3.6e-07; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 0

QY 1 RQIKWIFQNRMRMKWK 16
 |||||
 DB 62 RQIKWIFQNRMRMKWK 77

RESULT 23

A03317
 homeotic protein WM3 - African clawed frog (fragment)
 C:Species: Xenopus laevis (African clawed frog)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 24-Sep-1999
 C:Accession: A03317
 R:Muller, M.M.; Carrasco, A.B.; DeRobertis, E.M.
 Cell 39, 157-162, 1984
 A:Title: A homeo-box-containing gene expressed during oogenesis in Xenopus.
 A:Reference number: A03317; MUID:85024889; PMID:6207937
 A:Accession: A03317
 A:Molecule type: DNA
 A:Residues: 1-88 <MUL>
 A:Cross-references: GB:K02616; NID:9214254; PIDN:AAA49749.1; PID:g214255
 C:Comment: This protein is expressed in oocytes.
 C:Genetics:

A:Gene: WM3
 C:Superfamily: unassigned homeobox proteins; homeobox homology
 C:Keywords: alternative splicing; DNA binding; homeobox; nucleus; oocyte; transcription
 F:9-65/Domain: homeobox homology <HOX>

Query Match 100.0%; Score 92; DB 2; Length 88;
 Best Local Similarity 100.0%; Pred. No. 3.6e-07; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 0

QY 1 RQIKWIFQNRMRMKWK 16
 |||||
 DB 50 RQIKWIFQNRMRMKWK 65

RESULT 24

S08639
 homeotic protein zf-61 - zebra fish
 C:Species: Brachydanio rerio (zebra fish)
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-Sep-1999
 C:Accession: S08639
 R:Njolstad, P.R.; Molven, A.; Apold, J.; Fjose, A.
 EMBO J. 9, 515-524, 1990
 A:Title: The zebrafish homeobox gene hox-2.2: transcription unit, potential regulatory re
 A:Reference number: S08639; MUID:90151628; PMID:1968004
 A:Accession: S08639
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-96 <NGO>
 A:Cross-references: EMBL:X17266; NID:962538; PIDN:CAA35170.1; PID:e16657; PID:g1334622
 C:Superfamily: unassigned homeobox proteins; homeobox homology
 C:Keywords: DNA binding; homeobox; nucleus; transcription regulation
 F:8-64/Domain: homeobox homology <HOX>

Query Match 100.0%; Score 92; DB 2; Length 96;
 Best Local Similarity 100.0%; Pred. No. 4e-07; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 0

QY 1 RQIKWIFQNRMRMKWK 16
 |||||
 DB 49 RQIKWIFQNRMRMKWK 64

RESULT 25

A05266
 homeotic protein Hox B6 - human (fragment)
 N:Alternate names: homeotic protein Hox 2B; homeotic protein Hu2
 C:Species: Homo sapiens (man)
 C:Date: 05-Jun-1987 #sequence_revision 30-Sep-1991 #text_change 17-Oct-1997
 C:Accession: A05266; S15337
 R:Levine, M.; Rubin, G.M.; Tjian, R.
 Cell 38, 667-673, 1984
 A:Title: Human DNA sequences homologous to a protein coding region conserved between home
 A:Reference number: A05265; MUID:85024858; PMID:6091895
 A:Accession: A05266
 A:Molecule type: DNA
 A:Residues: 1-96 <LEV>
 A:Cross-references: EMBL:K02571
 A:Note: this reading frame extends between two stop codons and does not begin with a sta
 R:Bocinelli, E.; Acampora, D.; Pannese, M.; d'Esposito, M.; Somma, R.; Gaudino, G.; Stoi

Genome 31, 745-756, 1989
 A:Title: Organization of human class I homeobox genes.
 A:Reference number: S15036; MUID:90215256; PMID:2576652
 A:Accession: S15337
 A:Molecule type: DNA
 A:Residues: 18-19, 'R', 21-83 <BON>
 C:Genetics:
 A:Gene: GDB:HOXB6
 A:Cross-references: GDB:120659; OMIM:142961
 A:Map position: 17q21.3-17q21.3
 C:Superfamily: unassigned homeobox proteins; homeobox homology
 C:Keywords: DNA binding; homeobox; nucleus; transcription regulation
 F:19-75/Domain: homeobox homology <HOX>

Query Match 100.0%; Score 92; DB 2; Length 96;
 Best Local Similarity 100.0%; Pred. No. 4e-07; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 0

QY 1 RQIKWIFQNRMRMKWK 16

Fri Oct 1 16:13:11 2004

us-09-830-779-7.rpr

Page 7

Db 60 ROIKWFOQRRMKWK 75

Search completed: October 1, 2004, 12:19:36
Job time : 16.6 secs

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OM protein - protein search, using sw model

Run on: October 1, 2004, 12:04:01 ; Search time 8.8 Seconds

(without alignments)
94.673 Million cell updates/sec

Title: US-09-830-779-7

Perfect score: 92

Sequence: 1 RQIKWIFQNRRMKWKX 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	92	100.0	48	1	HXB6_XENLA
2	92	100.0	49	1	HXA7_SHEEP
3	92	100.0	71	1	HXA7_SHEEP
4	92	100.0	71	1	HXA7_SHEEP
5	92	100.0	71	1	HXA7_SHEEP
6	92	100.0	75	1	HXA7_SHEEP
7	92	100.0	76	1	HXA7_SHEEP
8	92	100.0	78	1	HXA7_SHEEP
9	92	100.0	80	1	HXA7_SHEEP
10	92	100.0	81	1	HXA7_SHEEP
11	92	100.0	82	1	HXA7_SHEEP
12	92	100.0	84	1	HXA7_SHEEP
13	92	100.0	86	1	HXA7_SHEEP
14	92	100.0	87	1	HXA7_SHEEP
15	92	100.0	93	1	HXA7_SHEEP
16	92	100.0	96	1	HXA7_SHEEP
17	92	100.0	105	1	HXA7_SHEEP
18	92	100.0	105	1	HXA7_SHEEP
19	92	100.0	112	1	HXA7_SHEEP
20	92	100.0	148	1	HXA7_SHEEP
21	92	100.0	153	1	HXA7_SHEEP
22	92	100.0	208	1	HXA7_SHEEP
23	92	100.0	209	1	HXA7_SHEEP
24	92	100.0	217	1	HXA7_SHEEP
25	92	100.0	217	1	HXA7_SHEEP
26	92	100.0	217	1	HXA7_SHEEP
27	92	100.0	220	1	HXA7_SHEEP
28	92	100.0	220	1	HXA7_SHEEP
29	92	100.0	222	1	HXA7_SHEEP
30	92	100.0	222	1	HXA7_SHEEP
31	92	100.0	224	1	HXA7_SHEEP
32	92	100.0	224	1	HXA7_SHEEP
33	92	100.0	225	1	HXA7_SHEEP

RESULT 1

ALIGNMENTS

34	92	100.0	228	1	HXB6_BRARE	P15861 brachydanio
35	92	100.0	229	1	HXA6_HETFR	Q91a24 heterodontu
36	92	100.0	229	1	HXA7_MOUSE	P02830 mus musculus
37	92	100.0	230	1	HXA7_HUMAN	P31268 homo sapien
38	92	100.0	230	1	HXB5_XENLA	P09019 xenopus lae
39	92	100.0	232	1	HXA6_MOUSE	P09092 mus musculus
40	92	100.0	232	1	HXB4_XENLA	P09070 xenopus lae
41	92	100.0	232	1	HXB5_BRARE	P09074 brachydanio
42	92	100.0	233	1	HXB5_RAT	P52949 rattus norv
43	92	100.0	233	1	HXA6_HUMAN	P14267 homo sapien
44	92	100.0	234	1	HXA6_NOTVI	P14858 notophthalm
45	92	100.0	234	1	HXB6_XENLA	P02832 xenopus lae
46	92	100.0	235	1	HXB6_HUMAN	P09630 homo sapien
47	92	100.0	235	1	HXB6_MOUSE	P10629 mus musculus
48	92	100.0	235	1	HXB4_CHICK	P17278 gallus gall
49	92	100.0	236	1	HXB4_BRARE	O57374 brachydanio
50	92	100.0	242	1	HXA7_COTJA	P24061 coturnix co
51	92	100.0	245	1	HXB4_CHICK	P14840 gallus gall
52	92	100.0	250	1	HXB4_MOUSE	P10628 mus musculus
53	92	100.0	251	1	HXB4_FUGRU	O13074 fugu rubrip
54	92	100.0	251	1	HXB4_HUMAN	P17483 homo sapien
55	92	100.0	252	1	HXB5_HETFR	Q91a11 heterodontu
56	92	100.0	255	1	HXB4_HUMAN	P09016 homo sapien
57	92	100.0	261	1	HXB4_ORYLA	Q98V84 oryzias lat
58	92	100.0	264	1	HXB4_HUMAN	P09017 homo sapien
59	92	100.0	264	1	HXB4_MOUSE	Q08624 mus musculus
60	92	100.0	269	1	HXB5_HUMAN	P09067 homo sapien
61	92	100.0	269	1	HXB5_MOUSE	P09075 mus musculus
62	92	100.0	270	1	HXA5_MOUSE	P20719 homo sapien
63	92	100.0	270	1	HXA5_MOUSE	P09021 mus musculus
64	92	100.0	275	1	HXB5_HETFR	Q91a23 heterodontu
65	92	100.0	275	1	HXB5_BRARE	P09014 brachydanio
66	92	100.0	281	1	HXA5_MORSA	Q9PwD3 morone saxa
67	92	100.0	378	1	HMAN_DROME	P02833 drosophila
68	92	100.0	394	1	HMAN_DROME	Q24645 drosophila
69	92	100.0	415	1	SCR_DROME	P09077 drosophila
70	92	100.0	415	1	SCR_DROME	P09078 drosophila
71	92	100.0	590	1	HMDP_DROME	P09635 rattus norv
72	91	98.9	67	1	HXA4_RAT	P18863 rattus norv
73	91	98.9	92	1	HXB8_RAT	P18866 rattus norv
74	91	98.9	108	1	HXB8_RAT	P23459 gallus gall
75	91	98.9	108	1	HXB8_CHICK	Q91a12 heterodontu
76	91	98.9	240	1	HXB8_HUMAN	P31273 homo sapien
77	91	98.9	242	1	HXB8_MOUSE	P09025 mus musculus
78	91	98.9	242	1	HXB8_HUMAN	P17481 homo sapien
79	91	98.9	243	1	HXB8_MOUSE	P09632 mus musculus
80	91	98.9	243	1	HXB8_MOUSE	Q91a22 heterodontu
81	91	98.9	247	1	HXA4_HETFR	Q9PwD2 morone saxa
82	91	98.9	248	1	HXA4_MORSA	P06798 mus musculus
83	91	98.9	285	1	HXB4_MOUSE	P23463 mus musculus
84	91	98.9	289	1	HXB8_MOUSE	P13378 homo sapien
85	91	98.9	290	1	HXB8_HUMAN	P17277 gallus gall
86	91	98.9	309	1	HXA4_CHICK	Q00056 homo sapien
87	91	98.9	320	1	HXA4_HUMAN	P10178 tripneustes
88	89	96.7	108	1	HXB3_TRIGR	P17138 helobdella
89	87	94.6	60	1	HXA2_HETFR	P32442 mus musculus
90	87	94.6	253	1	MOX1_MOUSE	P50221 homo sapien
91	87	94.6	254	1	MOX1_HUMAN	P14827 xenopus lae
92	87	94.6	271	1	HMB_XENLA	P52945 h insulatu
93	87	94.6	283	1	IPF1_HUMAN	P70118 mesocricatu
94	87	94.6	283	1	IPF1_MESAU	P52947 rattus norv
95	87	94.6	283	1	IPF1_RAT	P52946 mus musculus
96	87	94.6	284	1	IPF1_MOUSE	P52947 rattus norv
97	87	94.6	298	1	MOX2_XENLA	P52946 mus musculus
98	87	94.6	303	1	MOX2_HUMAN	P50222 homo sapien
99	87	94.6	303	1	MOX2_MOUSE	P32443 mus musculus
100	87	94.6	303	1	MOX2_RAT	P39020 rattus norv

```

XHB6 XENLA
ID XHB6_XENLA STANDARD; PRT; 48 AA.
AC P31256;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Homeobox protein Hox-B6 (XlHox-2.2) (Fragment).
GN HXB6 OR XLHox-2.2
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93043517; PubMed=1384809;
RA Leroy P., de Robertis E.M.;
RT Effects of lithium chloride and retinoic acid on the expression of
RT genes from the Xenopus laevis Hox 2 complex.;
RL Dev. Dyn. 194:21-32(1992).
CC -!- FUNCTION: Sequence-specific transcription factor which is part of
CC a developmental regulatory system that provides cells with
CC specific positional identities on the anterior-posterior axis.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: Belongs to the Antp homeobox family.
CC
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CC
CC EMBL; M91587; AAA9750.1; -.
CC F1R; I51439; I51439.
CC DR InterPro; IPR001827; Antennapedia.
CC DR InterPro; IPR001356; Homeobox.
CC DR Pfam; PF00046; homeobox; 1.
CC DR PRINTS; PR00024; HOMEBOX.
CC DR ProDom; PD000010; Homeobox; 1.
CC DR SMART; SM00389; HOX; 1.
CC DR PROSITE; PS00027; HOMEBOX 1; 1.
CC DR PROSITE; PS00071; HOMEBOX 2; 1.
CC DR Homeobox; DNA-binding; Developmental protein; Nuclear protein;
CC Transcription regulation.
CC FT NON_TER 1 1
CC FT DNA_BIND <1 29 HOMEBOX.
CC FT NON_TER 1 1
CC SQ SEQUENCE 48 AA; 5716 MW; BC39B36822EDDD2A CRC64;

Query Match 100.0%; Score 92; DB 1; Length 48;
Best Local Similarity 100.0%; Pred. No. 2.5e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWQNRRMKWKK 16
DB 12 RQIKWQNRRMKWKK 27

RESULT 2
HXAS SHEEP
ID HXA5_SHEEP STANDARD; PRT; 49 AA.
AC Q28559;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Homeobox protein Hox-A5 (Fragment).
GN HXA5 OR HOXA-5.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RX Roche P.J.;
RA Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Sequence-specific transcription factor which is part of
CC a developmental regulatory system that provides cells with
CC specific positional identities on the anterior-posterior axis.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: Belongs to the Antp homeobox family.
CC
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OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RA Roche P.J.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Sequence-specific transcription factor which is part of
CC a developmental regulatory system that provides cells with
CC specific positional identities on the anterior-posterior axis.
CC Also binds to its own promoter. Binds specifically to the motif:
CC 5'-CYNATTA[GTG]-3'.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: Belongs to the Antp homeobox family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U61378; AAB04754.1; -.
CC HSP; P02833; LHOM.
CC DR InterPro; IPR001356; Homeobox.
CC DR Pfam; PF00046; homeobox; 1.
CC DR PRINTS; PR00024; HOMEBOX.
CC DR ProDom; PD000010; Homeobox; 1.
CC DR SMART; SM00389; HOX; 1.
CC DR PROSITE; PS00027; HOMEBOX 1; 1.
CC DR PROSITE; PS00071; HOMEBOX 2; 1.
CC DR Homeobox; DNA-binding; Developmental protein; Nuclear protein;
CC Transcription regulation.
CC FT NON_TER 1 1
CC FT DNA_BIND <1 49 HOMEBOX.
CC FT NON_TER 49 49
CC SQ SEQUENCE 49 AA; 6331 MW; 1EE702315E7C099B CRC64;

Query Match 100.0%; Score 92; DB 1; Length 49;
Best Local Similarity 100.0%; Pred. No. 2.6e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWQNRRMKWKK 16
DB 32 RQIKWQNRRMKWKK 47

RESULT 3
HXA7 SHEEP
ID HXA7_SHEEP STANDARD; PRT; 71 AA.
AC Q28500;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Homeobox protein Hox-A7 (Fragment).
GN HXA7 OR HOXA-7.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RX Roche P.J.;
RA Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Sequence-specific transcription factor which is part of
CC a developmental regulatory system that provides cells with
CC specific positional identities on the anterior-posterior axis.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: Belongs to the Antp homeobox family.
CC
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CC -----

DR EMBL; U61979; AAB04755.1; -.
DR HSP; P02833; 9ANT.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR000047; HTH lambdarepressr.
DR Pfam; PF000046; homeobox; 1.
DR PRINTS; PR000024; HOMEBOX.
DR PRINTS; PR000031; HTHREPRESSR.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX 1; 1.
DR PROSITE; PS00071; HOMEBOX 2; 1.
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KW Transcription regulation.
FT NON_TER 1 1
FT DNA_BIND 4 63 HOMEBOX.
FT NON_TER 71 71
FT SEQUENCE 71 AA; 8888 MW; 931049FAC1BAACB7 CRC64;
SQ

Query Match 100.0%; Score 92; DB 1; Length 71;
Best Local Similarity 100.0%; Pred. No. 3.9e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWIFQNRMKWK 16
DB 46 RQIKWIFQNRMKWK 61

RESULT 4

HXC5 NOTVI
ID HXC5 NOTVI STANDARD; PRT; 71 AA.
AC P31262;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Homeobox protein Hox-C5 (Nrbbox-3.4) (Fragment).
OS Notophthalmus viridescens (Eastern newt) (Triturus viridescens).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae;
OC Notophthalmus.
OC NCBI_TaxID=8316;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92290273; PubMed=1351019;
RA Belleville S., Beauchemin M., Tremblay M., Noiseux N., Savard P.;
RT "Homeobox-containing genes in the newt are organized in clusters
RT similar to other vertebrates.";
RL Gene 114:179-186 (1992).

CC -1- FUNCTION: Sequence-specific transcription factor which is part of
CC a developmental regulatory system that provides cells with
CC specific positional identities on the anterior-posterior axis.

CC -1- SUBCELLULAR LOCATION: Nuclear.

CC -1- SIMILARITY: Belongs to the Antp homeobox family.

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CC -----

DR EMBL; M84001; AAA49397.1; ALT_INIT.
DR PIR; JCI1161; JCI1161.
DR HSP; P02833; ISAN.
DR InterPro; IPR001827; Antennapedia.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF000046; homeobox; 1.
DR PRINTS; PR00024; HOMEBOX.
SQ

DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX 1; 1.
DR PROSITE; PS00032; ANTENNAPEdia; PARTIAL.
DR PROSITE; PS00071; HOMEBOX 2; 1.
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KW Transcription regulation.
FT NON_TER 1 1
FT DNA_BIND 4 63 HOMEBOX.
FT NON_TER 71 71
FT SEQUENCE 71 AA; 8979 MW; 079999FDE89995B42 CRC64;
SQ

Query Match 100.0%; Score 92; DB 1; Length 71;
Best Local Similarity 100.0%; Pred. No. 3.9e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWIFQNRMKWK 16
DB 46 RQIKWIFQNRMKWK 61

RESULT 5

HM90 APIME
ID HM90 APIME STANDARD; PRT; 74 AA.
AC P15850;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Homeobox protein H90 (Fragment).
OS Apis mellifera (Honeybee).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Prterygota;
OC Neoptera; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Apidae; Apis.
OC NCBI_TaxID=7460;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90099384; PubMed=2574865;
RA Walldorf U., Fleig R., Gehring W.J.;
RT "Comparison of homeobox-containing genes of the honeybee and
RT Drosophila."
RL Proc. Natl. Acad. Sci. U.S.A. 86:9971-9975 (1989).
CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -1- SIMILARITY: Belongs to the Antp homeobox family.
CC -1- SIMILARITY: Contains 1 homeobox domain.

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CC -----

DR EMBL; M29493; AAA27728.1; -.
DR PIR; D34510; D34510.
DR HSP; P02833; IHOM.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF000046; homeobox; 1.
DR PRINTS; PR00024; HOMEBOX.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX 1; 1.
DR PROSITE; PS00071; HOMEBOX 2; 1.
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein.
FT NON_TER 1 1
FT DNA_BIND 8 67 HOMEBOX.
FT NON_TER 74 74
FT SEQUENCE 74 AA; 9263 MW; 5FC8FB4F723D3837 CRC64;
SQ

Query Match 100.0%; Score 92; DB 1; Length 74;
Best Local Similarity 100.0%; Pred. No. 4e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ROIKWQFQNRKWK 16
DB 50 ROIKWQFQNRKWK 65

RESULT 6
HMSA_SALSA
ID HMSA_SALSA STANDARD; PRT; 75 AA.
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Homeobox protein Hox-A (Fragment)
OS Salmo salar (Atlantic salmon)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
OX NCBI_TaxID=8030;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88226009; PubMed=2897318;
RA Fjose A., Molven A., Eiken H.G.;
RT "Molecular cloning and characterization of homeo-box-containing genes from Atlantic salmon";
RL Gene 62:141-152(1988).
CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -1- SIMILARITY: Belongs to the Antp homeobox family.
CC -1- SIMILARITY: Contains 1 homeobox domain.
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CC -----
DR EMBL; M18903; AAA49559.1; --
DR PIR; I51341; I51341.
DR HSP; P02833; 9ANT.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; homeobox; 1.
DR PRINTS; PR00024; HOMEBOX.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX 1; 1.
DR PROSITE; PS50071; HOMEBOX 2; 1.
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein.
KW Transcription regulation.
FT NON_TER 1 1 HOMEBOX.
FT DNA_BIND 75 75
FT NON_TER 75 75
FT NON_TER 75 75
SQ SEQUENCE 75 AA; 9330 MW; FC02C3672F35475D CRC64;
Query Match 100.0%; Score 92; DB 1; Length 75;
Best Local Similarity 100.0%; Pred. No. 4.1e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ROIKWQFQNRKWK 16
DB 43 ROIKWQFQNRKWK 58

RESULT 7
HXC4_RAT
ID HXC4_RAT STANDARD; PRT; 76 AA.
AC P18855;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Homeobox protein Hox-C4 (R3) (Fragment)
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Sprague-Dawley;
RX MEDLINE=89231502; PubMed=2907739;
RA Falzon M., Chung S.Y.;
RT "The expression of rat homeobox-containing genes is developmentally regulated and tissue specific";
RL Development 103:601-610(1988).
CC -1- FUNCTION: Sequence-specific transcription factor which is part of a developmental regulatory system that provides cells with specific positional identities on the anterior-posterior axis.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- TISSUE SPECIFICITY: Predominantly spinal cord and kidney.
CC -1- SIMILARITY: Belongs to the Antp homeobox family. Deformed subfamily.
CC -----
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CC -----
DR EMBL; M37567; AAA41343.1; --
DR PIR; C43559; C43559.
DR HSP; P02833; 9ANT.
DR InterPro; IPR001827; Antennapedia.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR000047; HTH lambdarepress.
DR Pfam; PF00046; homeobox; 1.
DR PRINTS; PR00024; HOMEBOX.
DR PRINTS; PR00031; HTHREPRESS.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00032; ANTENNAPEDIA; PARTIAL.
DR PROSITE; PS00027; HOMEBOX 1; 1.
DR PROSITE; PS50071; HOMEBOX 2; 1.
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KW Transcription regulation.
FT NON_TER 1 1 HOMEBOX.
FT DNA_BIND 11 70
FT NON_TER 11 70
SQ SEQUENCE 76 AA; 9293 MW; 5235F665C0672385 CRC64;
Query Match 100.0%; Score 92; DB 1; Length 76;
Best Local Similarity 100.0%; Pred. No. 4.2e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ROIKWQFQNRKWK 16
DB 53 ROIKWQFQNRKWK 68

RESULT 8
HXA5_SALSA
ID HXA5_SALSA STANDARD; PRT; 78 AA.
AC P09637;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Homeobox protein Hox-A5 (S12-B) (Fragment)
GN HXA5.
OS Salmo salar (Atlantic salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
OX NCBI_TaxID=8030;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88226009; PubMed=2897318;
RA Fjose A., Molven A., Eiken H.G.;


```

RT "Molecular cloning and characterization of homeo-box-containing genes
RL from Atlantic salmon."
RL Gene 62:141-152(1988).
CC -1- FUNCTION: Sequence-specific transcription factor which is part of
CC a developmental regulatory system that provides cells with
CC specific positional identities on the anterior-posterior axis.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: Belongs to the Antp homeobox family.
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CC -----
DR EMBL: M18904; AAA49560.1; -.
DR PIR: I51342; I51342.
DR HSSP: P02833; 9ANT.
DR InterPro: IPR001827; Antennapedia.
DR InterPro: IPR001356; Homeobox.
DR Pfam: PF00046; homeobox; 1.
DR PRINTS: PR00024; HOMEBOX.
DR ProDom: PD000010; Homeobox; 1.
DR SMART: SM00389; HOX; 1.
DR PROSITE: PS00027; HOMEBOX_1; 1.
DR PROSITE: PS00032; ANTENNAPEDIA; PARTIAL.
DR PROSITE: PS00071; HOMEBOX_2; 1.
DR Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KW Transcription regulation.
FT NON_TER 1
FT DNA_BIND 1 60 HOMEBOX.
FT NON_TER 1
SQ SEQUENCE 78 AA; 9489 MW; 828DEBDDF78AC920 CRC64;

Query Match 100.0%; Score 92; DB 1; Length 78;
Best Local Similarity 100.0%; Pred. No. 4.3e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ROIKWIFQNRMRKWK 16
Db 43 ROIKWIFQNRMRKWK 58

RESULT 9
HX4 LINS4 STANDARD; PRT; 80 AA.
AC P81192;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Homeobox protein Hox-A4 (LsHox 4) (Fragment).
GN HOXA4.
OS Lineus sanguineus (Ribbon worm).
OC Eukaryota; Metazoa; Anopla; Heteronemertea; Lineidae;
OC Lineus.
OX NCBI_TaxID=48190;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98169491; PubMed=9501210;
RA Kmita-Cunisse M., Loosli F., Bierre J., Gehring W.J.;
RT "Homeobox genes in the ribbonworm Lineus sanguineus: evolutionary
RT implications."
RL Proc. Natl. Acad. Sci. U.S.A. 95:3030-3035(1998).
CC -1- FUNCTION: Sequence-specific transcription factor which is part of
CC a developmental regulatory system that provides cells with
CC specific positional identities on the anterior-posterior axis (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -1- SIMILARITY: Belongs to the Antp homeobox family. Deformed
CC subfamily.
DR HSSP: P02833; 9ANT.
DR InterPro: IPR001827; Antennapedia.

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DR InterPro: IPR001356; Homeobox.
DR InterPro: IPR000047; HTH_lambrepreser.
DR Pfam: PF00046; homeobox; 1.
DR PRINTS: PR00024; HOMEBOX.
DR PRINTS: PR00031; HTHREPRESSR.
DR ProDom: PD000010; Homeobox; 1.
DR SMART: SM00389; HOX; 1.
DR PROSITE: PS00027; HOMEBOX_1; 1.
DR PROSITE: PS00071; HOMEBOX_2; 1.
DR PROSITE: PS00032; ANTENNAPEDIA; PARTIAL.
DR Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KW Transcription regulation.
FT NON_TER 1
FT DNA_BIND 21 80 HOMEBOX.
FT NON_TER 80
SQ SEQUENCE 80 AA; 9860 MW; F2CE1B01CB8042F1 CRC64;

Query Match 100.0%; Score 92; DB 1; Length 80;
Best Local Similarity 100.0%; Pred. No. 4.4e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ROIKWIFQNRMRKWK 16
Db 53 ROIKWIFQNRMRKWK 68

RESULT 10
HX5L BRARE STANDARD; PRT; 81 AA.
AC P09013;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Homeobox protein Hox-B5 like (ZF-54) (Fragment).
GN HOXB5B OF ZF54 OR ZF-54.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89016617; PubMed=2902580;
RA Njolstad P.R., Molven A., Hordvik I., Apold J., Fjose A.;
RT "Primary structure, developmentally regulated expression and
RT potential duplication of the zebrafish homeobox gene ZF-21."
RL Nucleic Acids Res. 16:9097-9113(1988).
CC -1- FUNCTION: Sequence-specific transcription factor which is part of
CC a developmental regulatory system that provides cells with
CC specific positional identities on the anterior-posterior axis.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: Belongs to the Antp homeobox family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X12803; CA331291.1; -.
DR HSSP: P02833; 1SAN.
DR ZFIN: ZDB-GENE-000823-6; hoxb5b.
DR InterPro: IPR001356; Homeobox.
DR Pfam: PF00046; homeobox; 1.
DR PRINTS: PR00024; HOMEBOX.
DR ProDom: PD000010; Homeobox; 1.
DR SMART: SM00389; HOX; 1.
DR PROSITE: PS00027; HOMEBOX_1; 1.
DR PROSITE: PS00071; HOMEBOX_2; 1.
DR Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KW Transcription regulation.

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```

FT NON_TER 1 1 HOMEBOX.
FT DNA_BIND 6 65
SQ SEQUENCE 81 AA; 9977 MW; B7698AEFFB3C654 CRC64;

Query Match 100.0%; Score 92; DB 1; Length 81;
Best Local Similarity 100.0%; Pred. No. 4.4e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWQNRRMKWKK 16
DB 48 RQIKWQNRRMKWKK 63

RESULT 11
HXB6 CHICK STANDARD; PRT; 82 AA.
AC P14838;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Homeobox protein Hox-B5 (Hox-2.1) (Fragment).
GN HOXB5 OR HOX-2.1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Erythrocyte;
RX MEDLINE=90126373; PubMed=2575515;
RA Wedden S.E., Pang K., Eichele G.;
RT "Expression pattern of homeobox-containing genes during chick
embryogenesis.";
RL Development 105:639-650(1999).
CC -!- FUNCTION: Sequence-specific transcription factor which is part of
a developmental regulatory system that provides cells with
specific positional identities on the anterior-posterior axis.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: Belongs to the Antp homeobox family.
CC
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CC
CC EMBL; X16846; CAA34743.1; -
CC F1R; S08302; S08302.
CC HSP; P02833; 1S0N.
CC InterPro; IPR001827; Antennapedia.
CC InterPro; IPR001356; Homeobox.
CC InterPro; IPR000047; ETH lambrepresr.
CC Pfam; PF00046; homeobox; 1.
CC PRINTS; PR00024; HOMEBOX.
CC PRINTS; PR00031; HTHRSPRESSR.
CC PRDOM; PD000010; Homeobox; 1.
CC SMART; SM00389; HOX; 1.
CC PROSITE; PS00027; HOMEBOX 1; 1.
CC PROSITE; PS00032; ANTENNAPEDIA; PARTIAL.
CC PROSITE; PS00071; HOMEBOX 2; 1.
CC Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KW Transcription regulation.
FT NON_TER 1 1 HOMEBOX.
FT DNA_BIND 7 65
SQ SEQUENCE 82 AA; 9877 MW; 53F70ACDC9FDF8F CRC64;

Query Match 100.0%; Score 92; DB 1; Length 82;
Best Local Similarity 100.0%; Pred. No. 4.5e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWQNRRMKWKK 16
DB 49 RQIKWQNRRMKWKK 64

RESULT 13
HXB6 CHICK STANDARD; PRT; 86 AA.
AC P15859;
DT 01-APR-1990 (Rel. 14, Created)

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DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Homeobox protein H55 (Fragment).
OS Apis mellifera (Honeybee).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Apidae; Apis.
RN NCBI_TaxID=7460;
RX NCBI TaxID=7460;
RP SEQUENCE FROM N.A.
RX MEDLINE=9009384; PubMed=2574865;
RA Walldorf U., Fleig R., Gehring W.J.;
RT "Comparison of homeobox-containing genes of the honeybee and
RT Drosophila.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:9971-9975(1989).
CC -!- FUNCTION: Sequence-specific transcription factor which is part of
CC a developmental regulatory system that provides cells with
CC specific positional identities on the anterior-posterior axis.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY. STRONGEST, TO SCR
CC OF DROSOPHILA.
CC -----
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CC -----
DE EMBL; M29486; AAA27723.1; -.
DR PIR; A34510; A34510.
DR HSP; P02833; ISAN.
DR InterPro; IPR001827; Antennapedia.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; homeobox; 1.
DR PRINTS; PR00024; HOMEOBOX.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00032; ANTENNAPEDIA; PARTIAL.
DR PROSITE; PS00027; HOMEOBOX_1; 1.
DR PROSITE; PS50071; HOMEOBOX_2; 1.
DR Homeobox; DNA-binding; Developmental protein; Nuclear protein.
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein.
FT NON_TER 1
FT DNA_BIND 8 67 HOMEOBOX.
FT NON_TER 86
FT NON_TER 86
SQ SEQUENCE 86 AA; 10713 MW; 2A49AB857C138AB8 CRC64;

Query Match 100.0%; Score 92; DB 1; Length 86;
Best Local Similarity 100.0%; Pred. No. 4.7e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RQIKWIFQNRMRKWK 16
Db 50 RQIKWIFQNRMRKWK 65

RESULT 14
HXCS_XENLA STANDARD; PRT; 87 AA.
ID HXC5_XENLA
AC P09020;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Homeobox protein Hox-C5 (XlHox-5) (Fragment).
GN HXC5 OR XLHXC5.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
RN NCBI_TaxID=8355;
RX NCBI TaxID=8355;
RP SEQUENCE FROM N.A.

DT 01-APR-1990 (Rel. 14, Last sequence update);
DT 28-FEB-2003 (Rel. 41, Last annotation update);
DE Homeobox-containing cDNAs expressed in early development.";
OS "Xenopus homeobox-containing cDNAs expressed in early development.";
RL Nucleic Acids Res. 16:1453-1469(1988).
CC -!- FUNCTION: Sequence-specific transcription factor which is part of
CC a developmental regulatory system that provides cells with
CC specific positional identities on the anterior-posterior axis.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- DEVELOPMENTAL STAGE: EXPRESSED EXCLUSIVELY IN EARLY EMBRYOS.
CC -!- SIMILARITY: Belongs to the Antp homeobox family.
CC -----
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CC -----
DE EMBL; X07105; CAA30126.1; -.
DR PIR; S00589; S00589.
DR HSP; P02833; 9ANT.
DR TRANSFAC; T03765; -.
DR InterPro; IPR001827; Antennapedia.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; homeobox; 1.
DR PRINTS; PR00025; ANTENNAPEDIA.
DR PRINTS; PR00024; HOMEOBOX.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEOBOX_1; 1.
DR PROSITE; PS00032; ANTENNAPEDIA; 1.
DR PROSITE; PS50071; HOMEOBOX_2; 1.
DR Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein.
FT NON_TER 1
FT DNA_BIND 20 79 ANTP-TYPE HEXAPEPTIDE.
FT NON_TER 5 10 HOMEOBOX.
FT DNA_BIND 20 79
SQ SEQUENCE 87 AA; 11058 MW; E67939E334E2BA43 CRC64;

Query Match 100.0%; Score 92; DB 1; Length 87;
Best Local Similarity 100.0%; Pred. No. 4.8e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RQIKWIFQNRMRKWK 16
Db 62 RQIKWIFQNRMRKWK 77

RESULT 15
HXB8_PIG STANDARD; PRT; 93 AA.
ID HXB8_PIG
AC P09078;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Homeobox protein Hox-B8 (Hox-2.4) (Fragment).
GN HXB8 OR Hox-2.4.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
RX NCBI_TaxID=9823;
RP SEQUENCE FROM N.A.
RX MEDLINE=89057478; PubMed=2904133;
RA Miller J.R., Gaunt S.J., Sharpe P.T.;
RT "Pig Hox-2.4 has accumulated a frameshift mutation relative to mouse
RT Hox-2.4.";
RL Nucleic Acids Res. 16:10364-10364(1988).
CC -!- FUNCTION: Sequence-specific transcription factor which is part of
CC a developmental regulatory system that provides cells with
CC specific positional identities on the anterior-posterior axis.
CC -!- SUBCELLULAR LOCATION: Nuclear.

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CC -!- SIMILARITY: Belongs to the Antp homeobox family.
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 CC -----
 CC ENBL; X06688; CAB57825.1; ALT SEQ.
 CC HSSP; P02834; I881.
 CC InterPro; IPR001827; Antennapedia.
 CC InterPro; IPR001356; Homeobox.
 CC InterPro; IPR000047; HTH lambrapress.
 CC Pfam; PF00046; homeobox; 1.
 CC PRINTS; PR00024; HOMEBOX.
 CC PROSITE; PS00031; HTHREPRESS.
 CC ProDom; PD000010; Homeobox; 1.
 CC SMART; SM00389; HOX; 1.
 CC PROSITE; PS00032; ANTENNAPEDIA; PARTIAL.
 CC PROSITE; PS00027; HOMEBOX; 1; 1.
 CC PROSITE; PS00071; HOMEBOX; 2; 1.
 CC Homeobox; DNA-binding; Developmental protein; Nuclear protein;
 CC Transcription regulation.
 CC NON_TER 1 1
 CC DNA_BIND 7 66 HOMEBOX.
 CC SEQUENCE 93 AA; 10872 MW; 7841DD6D17634BEC CRC64;
 CC -----
 CC Query Match 100.0%; Score 92; DB 1; Length 93;
 CC Best Local Similarity 100.0%; Pred. No. 5.1e-08;
 CC Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC -----
 CC QY 1 RQIKWIFQNRKMKWK 16
 CC DB 49 RQIKWIFQNRKMKWK 64
 CC -----
 CC RESULT 16
 CC HXC6 BRARE
 CC ID HXC6 BRARE STANDARD; PRT; 96 AA.
 CC PL582;
 CC DT 01-APR-1990 (Rel. 14, Created)
 CC DT 01-APR-1990 (Rel. 14, Last sequence update)
 CC DE 28-FEB-2003 (Rel. 41, Last annotation update)
 CC DE Homeobox protein Hox-C6 (ZF-61) (Fragment).
 CC GN HXC6 OR HXC6A OR HXC6-6 OR ZF-61.
 CC OS Brachydanio rerio (Zebrafish) (Danio rerio).
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;
 CC OC Cyprinidae; Danio.
 CC OC NCBI_TaxID=7955;
 CC [1]
 CC SEQUENCE FROM N.A.
 CC TISSUE=Embryo;
 CC RC MEDLINE=90151628; PubMed=1968004;
 CC RA Njolstad P.R., Mølvén A., Apold J., Fjose A.;
 CC RT "The zebrafish homeobox gene hox-2.2: transcription unit, potential
 CC regulatory regions and in situ localization of transcripts.";
 CC RL EMBO J. 9:515-524 (1990).
 CC -!- FUNCTION: Sequence-specific transcription factor which is part of
 CC a developmental regulatory system that provides cells with
 CC specific positional identities on the anterior-posterior axis.
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- SIMILARITY: Belongs to the Antp homeobox family.
 CC -----
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 CC -----

CC EMBL; X17266; CAA35170.1; --
 CC PIR; S08639; S08639.
 CC HSSP; P02833; 9ANT.
 CC ZFIN; ZDB-GENE-990415-113; hoxc6a.
 CC InterPro; IPR001827; Antennapedia.
 CC InterPro; IPR001356; Homeobox.
 CC Pfam; PF00046; homeobox; 1.
 CC PRINTS; PR00024; HOMEBOX.
 CC ProDom; PD000010; Homeobox; 1.
 CC SMART; SM00389; HOX; 1.
 CC PROSITE; PS00027; HOMEBOX; 1; 1.
 CC PROSITE; PS00032; ANTENNAPEDIA; PARTIAL.
 CC PROSITE; PS00071; HOMEBOX; 2; 1.
 CC Homeobox; DNA-binding; Developmental protein; Nuclear protein;
 CC Transcription regulation.
 CC NON_TER 1 1
 CC DNA_BIND 7 66 HOMEBOX.
 CC SEQUENCE 96 AA; 11638 MW; F1ED7AF3A3B640C0 CRC64;
 CC -----
 CC Query Match 100.0%; Score 92; DB 1; Length 96;
 CC Best Local Similarity 100.0%; Pred. No. 5.3e-08;
 CC Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC -----
 CC QY 1 RQIKWIFQNRKMKWK 16
 CC DB 49 RQIKWIFQNRKMKWK 64
 CC -----
 CC RESULT 17
 CC HXA7 RAT
 CC ID HXA7 RAT STANDARD; PRT; 105 AA.
 CC P09634;
 CC DT 01-MAR-1989 (Rel. 10, Created)
 CC DT 01-MAR-1989 (Rel. 10, Last sequence update)
 CC DE 28-FEB-2003 (Rel. 41, Last annotation update)
 CC DE Homeobox protein Hox-A7 (Hox-1.1) (R5) (Fragment).
 CC GN HXA7 OR HOXA-7.
 CC OS Rattus norvegicus (Rat).
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 CC OC NCBI_TaxID=10116;
 CC [1]
 CC SEQUENCE FROM N.A.
 CC RC STRAIN=Sprague-Dawley;
 CC RX MEDLINE=87277429; PubMed=2886401;
 CC RA Falzon M., Sanderson N., Chung S.Y.;
 CC RT "Cloning and expression of rat homeo-box-containing sequences.";
 CC RL Gene 54:23-32 (1987).
 CC -!- FUNCTION: Sequence-specific transcription factor which is part of
 CC a developmental regulatory system that provides cells with
 CC specific positional identities on the anterior-posterior axis.
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- SIMILARITY: Belongs to the Antp homeobox family.
 CC -----
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 CC -----
 CC EMBL; M16807; -- NOT ANNOTATED_CDS.
 CC PIR; A27471; A27471.
 CC HSSP; P02833; 9ANT.
 CC TRANSFAC; T01707; --
 CC InterPro; IPR001827; Antennapedia.
 CC InterPro; IPR001356; Homeobox.
 CC Pfam; PF00046; homeobox; 1.
 CC PRINTS; PR00024; HOMEBOX.
 CC ProDom; PD000010; Homeobox; 1.
 CC SMART; SM00389; HOX; 1.
 CC -----

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DR PROSITE; PS00032; ANTENNAPEDIA; PARTIAL.
DR Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KW Transcription regulation.
FT NON_TER 1 1
FT DNA_BIND 10 69 HOMEBOX.
SQ SEQUENCE 105 AA; 12262 MW; B0EFD84D909289F1 CRC64;

Query Match 100.0%; Score 92; DB 1; Length 105;
Best Local Similarity 100.0%; Pred. No. 5.9e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RQIKWFOQRMRMKWK 16
Db 52 RQIKWFOQRMRMKWK 67

RESULT 19
HXB7_RAT
ID HXB7_RAT STANDARD; PRT; 112 AA.
AC P18864;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Homeobox protein Hox-B7 (R1B) (Fragment).
GN HOXB7 OR HOXB-7.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RC MEDLINE=89231502; PubMed=2907739;
EA Falzon M., Chung S.Y.;
RT "The expression of rat homeobox-containing genes is developmentally
regulated and tissue specific.";
RL Development 103:601-610(1988).
CC -!- FUNCTION: Sequence-specific transcription factor which is part of
a developmental regulatory system that provides cells with
specific positional identities on the anterior-posterior axis.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- TISSUE SPECIFICITY: Predominantly spinal cord and kidney.
CC -!- SIMILARITY: Belongs to the Antp homeobox family.
CC
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CC
CC EMBL; M37566; AAA41342.2; -.
CC HSP; P02833; 9ANT.
CC InterPro; IPR001827; Antennapedia.
CC InterPro; IPR001356; Homeobox.
CC Pfam; PF00046; homeobox; 1.
CC PRINTS; PR00024; HOMEBOX.
CC ProDom; PD000010; Homeobox; 1.
CC SMART; SMC0389; HOX; 1.
CC PROSITE; PS00032; ANTENNAPEDIA; PARTIAL.
CC PROSITE; PS00027; HOMEBOX_1; 1.
CC PROSITE; PS50071; HOMEBOX_2; 1.
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KW Transcription regulation.
FT NON_TER 1 1
FT DNA_BIND 10 69 HOMEBOX.
SQ SEQUENCE 112 AA; 13910 MW; 099B6F064DC47C28 CRC64;

Query Match 100.0%; Score 92; DB 1; Length 112;
Best Local Similarity 100.0%; Pred. No. 6.3e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RQIKWFOQRMRMKWK 16
Db 47 RQIKWFOQRMRMKWK 62

RESULT 18
HXB4_BRAE
ID HXB4_BRAE STANDARD; PRT; 105 AA.
AC P22574; O42369;
DT 01-AUG-1991 (Rel. 19, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Homeobox protein Hox-B4 (ZF-13) (Fragment).
GN HOXB4 OR HOXB4 OR Hox-B4 OR ZF-13.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE OF 1-86 FROM N.A.
RC MEDLINE=89211958; PubMed=2468579;
RA Njoelestad P.R., Molven A., Eiken H.G., Fjose A.;
RT "Structure and neural expression of a zebrafish homeobox sequence.";
RL Gene 73:33-45(1988).
CC [2]
CC SEQUENCE OF 44-105 FROM N.A.
CC PRINCE V.E., Means C.B., Kimmel C.B., Ho R.K.;
CC "Zebrafish hox genes: expression in the hindbrain region of wild-type
and mutants of the segmentation gene, valentino.";
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Sequence-specific transcription factor which is part of
a developmental regulatory system that provides cells with
specific positional identities on the anterior-posterior axis.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: Belongs to the Antp homeobox family. Deformed
subfamily.
CC
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CC
CC EMBL; M24085; AAA56866.1; ALT INIT.
CC EMBL; Y13946; CAA74284.1; -.
CC PIR; JTO489; JTO489.
CC ZFIN; ZDB-GENE-990415-105; hoxb4a.
CC InterPro; IPR001827; Antennapedia.
CC InterPro; IPR001356; Homeobox.
CC Pfam; PF00046; homeobox; 1.
CC PRINTS; PR00024; HOMEBOX.
CC ProDom; PD000010; Homeobox; 1.
CC SMART; SMC0389; HOX; 1.
CC PROSITE; PS00027; HOMEBOX_1; 1.
CC PROSITE; PS50071; HOMEBOX_2; 1.

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QY 1 RQIKWIFQNRMKWKX 16
 DB 52 RQIKWIFQNRMKWKX 67

RESULT 20
 ID HXAS AMBME STANDARD; PRT; 148 AA.
 AC P50208;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Homeobox protein Hox-A5 (Fragment).
 GN HoxA5.
 OS Ambystoma mexicanum (Axolotl).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Ambystomidae;
 OC Amphibia; Batrachia; Caudata; Salamandroides;
 OC Ambystoma.
 NCBI_TaxID=8296;
 RN [1]

SEQUENCE FROM N.A.
 RX MEDLINE=96032352; PubMed=7557438;
 RA Gaur A.F., Lemanski L.F., Dube D.K.;
 RT "Identification and expression of a homologue of the murine HoxA5
 gene in the Mexican axolotl (Ambystoma mexicanum).";
 RL Gene 162:249-253(1995).
 CC -!- FUNCTION: Sequence-specific transcription factor which is part of
 CC a developmental regulatory system that provides cells with
 CC specific positional identities on the anterior-posterior axis (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- SIMILARITY: Belongs to the Antp homeobox family.

EMBL; U19239; AAA01634.1; --
 DR PIR; PC4071; PC4071.
 DR HSP; P02833; ISAN.
 DR TRANSFAC; T03305; --
 DR InterPro; IPR001827; Antennapedia.
 DR InterPro; IPR001356; Homeobox.
 DR Pfam; PF00046; homeobox; 1.
 DR PRINTS; PR00025; ANTENNAPEDIA.
 DR PRODOM; PD000010; Homeobox; 1.
 DR SMART; SM00389; Hox; 1.
 DR PROSITE; PS00027; HOMEBOX 1; 1.
 DR PROSITE; PS00032; ANTENNAPEDIA; 1.
 DR PROSITE; PS50071; HOMEBOX 2; 1.
 DR Homeobox; DNA-binding; Developmental protein; Nuclear protein;
 KW Transcription regulation.
 FT DNA_BIND 73 132 HOMEBOX.
 FT NON_TER 1 1
 FT SEQUENCE 148 AA; 16758 MW; C1893F0E9B5086 CRC64;

Query Match 100.0%; Score 92; DB 1; Length 148;
 Best Local Similarity 100.0%; Pred. No. 8.4e-08;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWIFQNRMKWKX 16
 DB 115 RQIKWIFQNRMKWKX 130

RESULT 21
 HXC6 SHEEP STANDARD; PRT; 153 AA.
 ID HXC6_SHEEP STANDARD; PRT; 153 AA.

P49925;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Homeobox protein Hox-C6.
 GN HoxC6.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 NCBI_TaxID=9940;
 RN [1]

SEQUENCE FROM N.A.
 RA Cosby N.C., Hernandez-Ledezma J., Mathialagan N., Roberts R.;
 RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Sequence-specific transcription factor which is part of
 CC a developmental regulatory system that provides cells with
 CC specific positional identities on the anterior-posterior axis.
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- SIMILARITY: Belongs to the Antp homeobox family.

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 or send an email to license@isb-sib.ch).

EMBL; U33049; AAA75473.1; --
 DR HSP; P02833; 9ANT.
 DR InterPro; IPR001827; Antennapedia.
 DR InterPro; IPR001356; Homeobox.
 DR Pfam; PF00046; homeobox; 1.
 DR PRINTS; PR00025; ANTENNAPEDIA.
 DR PRODOM; PD000010; Homeobox; 1.
 DR SMART; SM00389; Hox; 1.
 DR PROSITE; PS00027; HOMEBOX 1; 1.
 DR PROSITE; PS00032; ANTENNAPEDIA; 1.
 DR PROSITE; PS50071; HOMEBOX 2; 1.
 DR Homeobox; DNA-binding; Developmental protein; Nuclear protein;
 KW Transcription regulation.
 FT SITE 40 45 ANTP-TYPE HEXAPEPTIDE.
 FT DNA_BIND 59 118 HOMEBOX.
 FT DOMAIN 86 89 POLY-ARG.
 FT DOMAIN 126 130 POLY-GLY.
 FT DOMAIN 139 153 GLU/LYS-RICH.
 FT SEQUENCE 153 AA; 17804 MW; 291E24399159621E CRC64;

Query Match 100.0%; Score 92; DB 1; Length 153;
 Best Local Similarity 100.0%; Pred. No. 8.7e-08;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWIFQNRMKWKX 16
 DB 101 RQIKWIFQNRMKWKX 116

RESULT 22
 HXA7 HETFR STANDARD; PRT; 208 AA.
 ID HXA7 HETFR STANDARD; PRT; 208 AA.
 AC Q91A25;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Homeobox protein Hox-A7.
 GN HoxA7.
 OS Heterodontus francisci (Horn shark).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
 OC Elasmobranchii; Galeomorphi; Heterodontidae; Heterodontiformes;
 OC Heterodontidae; Heterodontus.
 NCBI_TaxID=7792;

```

RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=20144096; PubMed=10677514;
RA  Kim C.S., Ameyya C., Bailey W., Kawasaki K., Mezey J., Miller W.,
RA  Minoshima S., Shimizu N., Wagner G., Ruddle F.;
RL  "Hox cluster genomics in the horn shark, Heterodontus francisci."
RL  Proc. Natl. Acad. Sci. U.S.A. 97:1655-1660(2000).
CC  -!- FUNCTION: Sequence-specific transcription factor which is part of
CC  a developmental regulatory system that provides cells with
CC  specific positional identities on the anterior-posterior axis (By
CC  similarity).
CC  -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC  -!- SIMILARITY: Belongs to the Antp homeobox family.
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CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  EMBL; AF224262; AAF44645.1; -
CC  HSP; P02833; 9ANT.
CC  TRANSFAC; T04478; -
CC  InterPro; IPR001827; Antennapedia.
CC  Pfam; PF00046; homeobox; 1.
CC  PRINTS; PR00025; ANTENNAPEDIA.
CC  PRINTS; PR00024; HOMEBOX.
CC  P-CDOM; PD000010; Homeobox; 1.
CC  SMART; SM00389; HOX; 1.
CC  PROSITE; PS00032; ANTENNAPEDIA; 1.
CC  PROSITE; PS00027; HOMEBOX_1; 1.
CC  PROSITE; PS00071; HOMEBOX_2; 1.
CC  Homeobox; DNA-binding; Developmental protein; Nuclear protein;
CC  Transcription regulation.
CC  SITE 124 129 ANTP-TYPE HEXAPEPTIDE.
CC  SITE 124 129 HOMEBOX.
CC  FT DNA BIND 135 194
CC  SQ SEQUENCE 208 AA; 23786 MW; 71B661AB78E064D0 CRC64;

Query Match 100.0%; Score 92; DB 1; Length 208;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RQIKWQNRRMKWKK 16
Db 177 RQIKWQNRRMKWKK 192

RESULT 23
HXAF_XENLA STANDARD; PRT; 209 AA.
AC P09071;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Homeobox protein Hox-A7 (XlHox-3) (XlHox-36).
GN HOXA7 OR XLHBOX3.
OS Xenopus laevis (African clawed frog).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
CC Xenopodinae; Xenopus.
CC NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86211489; PubMed=2452727;
RA Cordie B.G., Harland R.M.;
RL "Posterior expression of a homeobox gene in early Xenopus embryos.";
RL Development 101:93-105(1987).
RN [2]
RP SEQUENCE OF 119-209 FROM N.A.
RX MEDLINE=88157707; PubMed=2894634;

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RA Fritz A., de Robertis E.M.;
RL "Xenopus homeobox-containing cDNAs expressed in early development.";
RL Nucleic Acids Res. 16:1453-1463(1988).
CC -!- FUNCTION: Sequence-specific transcription factor which is part of
CC a developmental regulatory system that provides cells with
CC specific positional identities on the anterior-posterior axis.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- DEVELOPMENTAL STAGE: EXPRESSED EXCLUSIVELY IN THE POSTERIOR
CC MESODERM AND ECTODERM OF EARLY XENOPUS EMBRYOS.
CC -!- SIMILARITY: Belongs to the Antp homeobox family.
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CC or send an email to license@isb-sib.ch).
CC EMBL; M24752; AAA49753.1; -
CC EMBL; X07103; CAA30124.1; ALT_INIT.
CC PIR; A43553; 9ANT.
CC HSP; P02833; 9ANT.
CC TRANSFAC; T01704; -
CC InterPro; IPR001827; Antennapedia.
CC InterPro; IPR001356; Homeobox.
CC Pfam; PF00046; homeobox; 1.
CC PRINTS; PR00025; ANTENNAPEDIA.
CC PRINTS; PR00024; HOMEBOX.
CC P-CDOM; PD000010; Homeobox; 1.
CC SMART; SM00389; HOX; 1.
CC PROSITE; PS00027; HOMEBOX_1; 1.
CC PROSITE; PS00032; ANTENNAPEDIA; 1.
CC PROSITE; PS00071; HOMEBOX_2; 1.
CC Homeobox; DNA-binding; Developmental protein; Nuclear protein;
CC Transcription regulation.
CC SITE 111 116 ANTP-TYPE HEXAPEPTIDE.
CC SITE 122 181 HOMEBOX.
CC FT DNA BIND 122 181
CC SQ SEQUENCE 209 AA; 23984 MW; 4EAC0A052F05D70D CRC64;

Query Match 100.0%; Score 92; DB 1; Length 209;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RQIKWQNRRMKWKK 16
Db 164 RQIKWQNRRMKWKK 179

RESULT 24
HXAF_BOVIN STANDARD; PRT; 217 AA.
AC Q9TTR9;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Homeobox protein Hox-B7.
GN HXB7.
OS Bos taurus (Bovine).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
CC Bovidae; Bovinae; Bos.
CC NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20302721; PubMed=10842316;
RA Bostrom K., Tintut Y., Kao S.C., Stanford W.P., Demer L.L.;
RL "HOXB7 overexpression promotes differentiation of C3H10T1/2 cells to
RL smooth muscle cells."
RL J. Cell. Biochem. 78:210-221(2000).
CC -!- FUNCTION: Sequence-specific transcription factor which is part of
CC a developmental regulatory system that provides cells with
CC specific positional identities on the anterior-posterior axis.

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CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- SIMILARITY: Belongs to the Antp homeobox family.
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 CC
 CC EMBL; AF200721; AAF17552.1; -;
 CC HSP; P02833; IHOM.
 CC InterPro; IPR001827; Antennapedia.
 CC InterPro; IPR001356; Homeobox.
 CC Pfam; PF00046; homeobox; 1.
 CC PRINTS; PR00025; ANTENNAPEDIA.
 CC ProDom; PD000010; Homeobox; 1.
 CC SMART; SM00389; HOX; 1.
 CC PROSITE; PS00032; ANTENNAPEDIA; 1.
 CC PROSITE; PS00027; HOMEBOX 1; 1.
 CC PROSITE; PS00071; HOMEBOX 2; 1.
 CC Homeobox; DNA-binding; Developmental protein; Nuclear protein;
 CC Transcription regulation.
 CC SITE 126 131 ANTP-TYPE HEXAPEPTIDE.
 CC FT DNA_BIND 137 196 HOMEBOX.
 CC FT DOMAIN 210 217 GLU-RICH (ACIDIC).
 CC
 CC QUERY MATCH 100.0%; Score 92; DB 1; Length 217;
 CC Best Local Similarity 100.0%; Pred. No. 1.3e-07;
 CC Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 CC QY 1 RQIKWIFQNRKMKWK 16
 CC Db 179 RQIKWIFQNRKMKWK 194
 CC
 CC RESULT 25
 CC HXB7 HUMAN STANDARD; PRT; 217 AA.
 CC AC P09629; Q15957.
 CC DT 01-MAR-1989 (Rel. 10, Created)
 CC DT 01-AUG-1990 (Rel. 15, Last sequence update)
 CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
 CC DE Homeobox protein Hox-B7 (Hox-2C) (HBO.C1).
 CC GN HOXB7 OR HOXC2C.
 CC OS Homo sapiens (Human).
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 CC OX NCBI_TaxID=9606;
 CC RN [1]
 CC RP MEDLINE=87260899; PubMed=2885844;
 CC RA Simeone A., Mavilio F., Acampora D., Giampaolo A., Faiella A.,
 CC RA Zappavigna V., D'Esposito M., Rannese M., Russo G., Boncinelli E.,
 CC RA Reschle C.;
 CC RT "Two human homeobox genes, c1 and c8: structure analysis and
 CC RT expression in embryonic development.";
 CC Proc. Natl. Acad. Sci. U.S.A. 84:4914-4918 (1987).
 CC [2]
 CC RP MEDLINE=91329816; PubMed=1678287;
 CC RA Baier L.J., Hannibal M.C., Hanley E.W., Nabel G.J.;
 CC RT "Lymphoid expression and TATAA binding of a human protein containing
 CC RT an Antennapedia homeodomain.";
 CC RL Blood 78:1047-1055 (1991).
 CC [3]
 CC RP MEDLINE=90046832; PubMed=2573064;
 CC RA Shen W.-F., Largman C., Lowney P., Corral J.C., Detmer K.,
 CC HAUSER C.A., Simonitch T.A., Hack F.M., Lawrence H.J.;

RT "Lineage-restricted expression of homeobox-containing genes in human
 RT hematopoietic cell lines.";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:8536-8540 (1989).
 RN [4]
 RP SEQUENCE OF 137-202 FROM N.A.
 RX MEDLINE=90215256; PubMed=2576652;
 RA Boncinelli E., Acampora D., Rannese M., D'Esposito M., Somma R.,
 RA Caudino G., Scornaiuolo A., Cafiero M., Faiella A., Simeone A.;
 RT "Organization of human class I homeobox genes.";
 RL Genome 31:745-756 (1989).
 CC -!- FUNCTION: Sequence-specific transcription factor which is part of
 CC a developmental regulatory system that provides cells with
 CC specific positional identities on the anterior-posterior axis.
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- SIMILARITY: Belongs to the Antp homeobox family.
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 CC
 CC EMBL; M16937; AAA36003.1; -;
 CC EMBL; S49765; AAB19469.2; -;
 CC EMBL; M30598; AAA36005.1; -;
 CC EIR; A28030; WJHU2C.
 CC HSP; P02833; IHOM.
 CC TRANSFAC; T01734; -;
 CC Gensu; HGNC:5118; HOXB7.
 CC MIM; 142962; -;
 CC GO; GO:0005634; C:nucleus; NAS.
 CC GO; GO:0003700; F:transcription factor activity; NAS.
 CC GO; GO:0007275; P:development; NAS.
 CC GO; GO:0006355; P:regulation of transcription, DNA-dependent; NAS.
 CC InterPro; IPR001827; Antennapedia.
 CC InterPro; IPR001356; Homeobox.
 CC Pfam; PF00046; homeobox; 1.
 CC PRINTS; PR00025; ANTENNAPEDIA.
 CC PRINTS; PR00024; HOMEBOX.
 CC ProDom; PD000010; Homeobox; 1.
 CC SMART; SM00389; HOX; 1.
 CC PROSITE; PS00027; HOMEBOX 1; 1.
 CC PROSITE; PS00032; ANTENNAPEDIA; 1.
 CC PROSITE; PS00071; HOMEBOX 2; 1.
 CC Homeobox; DNA-binding; Developmental protein; Nuclear protein;
 CC Transcription regulation.
 CC SITE 126 131 ANTP-TYPE HEXAPEPTIDE.
 CC FT DNA_BIND 137 196 HOMEBOX.
 CC FT DOMAIN 212 217 GLU-RICH (ACIDIC).
 CC FT CONFLICT 108 108 A -> G (IN REF. 2).
 CC FT CONFLICT 118 118 L -> F (IN REF. 2).
 CC FT CONFLICT 129 129 W -> S (IN REF. 1).
 CC FT CONFLICT 154 154 K -> N (IN REF. 2).
 CC FT CONFLICT 173 173 T -> A (IN REF. 1 AND 2).
 CC FT CONFLICT 194 194 K -> N (IN REF. 2).
 CC FT CONFLICT 200 202 GPG -> APA (IN REF. 2).
 CC SEQUENCE 217 AA; 23970 MW; 99509FE700BE76A7 CRC64;
 CC
 CC QUERY MATCH 100.0%; Score 92; DB 1; Length 217;
 CC Best Local Similarity 100.0%; Pred. No. 1.3e-07;
 CC Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 1 RQIKWIFQNRKMKWK 16
 CC Db 179 RQIKWIFQNRKMKWK 194
 CC
 CC Search completed: October 1, 2004, 12:18:12
 CC Job time : 9.8 secs

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OM protein - protein search, using sw model

Run on: October 1, 2004, 11:56:56 ; Search time 50.8 seconds
(without alignments)
99.376 Million cell updates/sec

Title: US-09-830-779-7

Perfect score: 92

Sequence: 1 RQIKWIFQNRRMKWK 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phase:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriap:*

17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	92	100.0	33	5 Q86FU0	Q86FU0 drosophila
2	92	100.0	39	13 C57368	C57368 brachydanio
3	92	100.0	42	11 Q80WH6	Q80WH6 rattus sp.
4	92	100.0	43	13 C57359	C57359 brachydanio
5	92	100.0	46	13 Q9PVR9	Q9PVR9 oryzias lat
6	92	100.0	51	5 Q27413	Q27413 ctenodrilus
7	92	100.0	51	5 Q23743	Q23743 ctenodrilus
8	92	100.0	51	5 Q26407	Q26407 ctenodrilus
9	92	100.0	57	13 Q9PVR8	Q9PVR8 oryzias lat
10	92	100.0	58	5 Q9Y188	Q9Y188 priapulid c
11	92	100.0	58	5 Q25208	Q25208 junonia coe
12	92	100.0	58	13 C57362	C57362 brachydanio
13	92	100.0	59	5 Q8WRM9	Q8WRM9 lithobius a
14	92	100.0	59	5 Q9NB42	Q9NB42 anopheles g
15	92	100.0	59	13 Q9PVR5	Q9PVR5 oryzias lat
16	92	100.0	60	5 Q77143	Q77143 archegozete

17	92	100.0	60	5 Q77139	Q77139 archegozete
18	92	100.0	60	11 Q80WH7	Q80WH7 rattus sp.
19	92	100.0	60	11 Q80WH4	Q80WH4 rattus sp.
20	92	100.0	60	13 Q8QGL5	Q8QGL5 petromyzon
21	92	100.0	60	13 Q8QGL3	Q8QGL3 petromyzon
22	92	100.0	60	13 Q8QGL6	Q8QGL6 petromyzon
23	92	100.0	60	13 Q8QGL2	Q8QGL2 petromyzon
24	92	100.0	60	13 Q8QGL8	Q8QGL8 petromyzon
25	92	100.0	60	13 Q8QGL7	Q8QGL7 petromyzon
26	92	100.0	61	5 Q27910	Q27910 polyandroc
27	92	100.0	63	5 Q77138	Q77138 archegozete
28	92	100.0	63	5 Q8MXB2	Q8MXB2 holopneuste
29	92	100.0	66	13 C57356	C57356 brachydanio
30	92	100.0	69	5 Q9U9T4	Q9U9T4 nereis vire
31	92	100.0	69	5 Q9BMF7	Q9BMF7 halotis as
32	92	100.0	70	5 Q967W5	Q967W5 folsonia ca
33	92	100.0	70	13 Q801B4	Q801B4 latimeria m
34	92	100.0	71	13 Q9PVS3	Q9PVS3 oryzias lat
35	92	100.0	71	13 Q9PVS1	Q9PVS1 oryzias lat
36	92	100.0	73	5 Q9Y186	Q9Y186 priapulid c
37	92	100.0	73	5 Q86D93	Q86D93 spadella ce
38	92	100.0	74	13 C57367	C57367 brachydanio
39	92	100.0	75	5 Q25209	Q25209 junonia coe
40	92	100.0	75	13 Q9PVR6	Q9PVR6 oryzias lat
41	92	100.0	76	5 Q44257	Q44257 ethmostigm
42	92	100.0	76	5 Q86NS1	Q86NS1 calanus hel
43	92	100.0	77	5 Q44260	Q44260 ethmostigm
44	92	100.0	77	5 Q9Y187	Q9Y187 priapulid c
45	92	100.0	77	5 Q9U924	Q9U924 lingula ung
46	92	100.0	78	5 Q720F3	Q720F3 lysagittif
47	92	100.0	79	5 Q967V2	Q967V2 lithobius f
48	92	100.0	79	5 Q9U9T9	Q9U9T9 nereis vire
49	92	100.0	80	5 Q05008	Q05008 artemia san
50	92	100.0	81	5 Q9BN27	Q9BN27 porcellio s
51	92	100.0	81	5 P91769	P91769 manduca sex
52	92	100.0	81	5 Q17142	Q17142 brachiosco
53	92	100.0	81	13 Q9PVR7	Q9PVR7 oryzias lat
54	92	100.0	82	5 Q24758	Q24758 drosophila
55	92	100.0	82	13 Q9PVS0	Q9PVS0 oryzias lat
56	92	100.0	82	13 Q801B8	Q801B8 latimeria m
57	92	100.0	83	5 Q17140	Q17140 brachiosco
58	92	100.0	85	13 Q801B9	Q801B9 latimeria m
59	92	100.0	86	13 Q9W7P8	Q9W7P8 paralichthy
60	92	100.0	87	13 Q8QFV4	Q8QFV4 lampetra fl
61	92	100.0	88	5 Q967W7	Q967W7 folsonia ca
62	92	100.0	89	5 Q967V4	Q967V4 lithobius f
63	92	100.0	90	5 Q94576	Q94576 heliocidari
64	92	100.0	90	5 Q817C9	Q817C9 ciona intes
65	92	100.0	92	13 C57377	C57377 brachydanio
66	92	100.0	93	5 Q9U925	Q9U925 lingula ung
67	92	100.0	93	5 Q8WQR9	Q8WQR9 euryymna sc
68	92	100.0	94	5 Q967V6	Q967V6 lithobius f
69	92	100.0	96	5 Q9U9T8	Q9U9T8 nereis vire
70	92	100.0	96	5 Q62550	Q62550 lineus sang
71	92	100.0	97	5 Q9U923	Q9U923 lingula ung
72	92	100.0	98	5 Q8MX73	Q8MX73 sacculina c
73	92	100.0	100	5 Q9GTN5	Q9GTN5 tribolium c
74	92	100.0	100	5 Q8WQS0	Q8WQS0 euryymna sc
75	92	100.0	100	5 Q8WQS1	Q8WQS1 euryymna sc
76	92	100.0	101	13 Q9PVS5	Q9PVS5 gallus gall
77	92	100.0	103	5 Q62551	Q62551 lineus sang
78	92	100.0	105	5 Q17139	Q17139 brachiosco
79	92	100.0	106	5 Q26498	Q26498 schistocerc
80	92	100.0	107	5 Q8W3M8	Q8W3M8 lithobius a
81	92	100.0	108	11 Q8UZW2	Q8UZW2 mus musculu
82	92	100.0	109	5 Q94575	Q94575 heliocidari
83	92	100.0	109	5 Q05011	Q05011 artemia san
84	92	100.0	115	5 Q44258	Q44258 ethmostigm
85	92	100.0	115	13 Q801B5	Q801B5 latimeria m
86	92	100.0	120	5 Q44268	Q44268 acanthokaza
87	92	100.0	140	13 Q801D0	Q801D0 latimeria m
88	92	100.0	146	5 Q05009	Q05009 artemia san
89	92	100.0	150	11 Q61679	Q61679 mus musculu

90 92 100.0 172 5 076844
 91 92 100.0 203 5 024681
 92 92 100.0 217 4 096BQ6
 93 92 100.0 218 5 09XY03
 94 92 100.0 219 13 090VZ9
 95 92 100.0 220 5 018313
 96 92 100.0 222 11 08BJW4
 97 92 100.0 223 13 0801A6
 98 92 100.0 224 13 08JH54
 99 92 100.0 225 13 0801C0
 100 92 100.0 227 5 017141

ALIGNMENTS

RESULT 1

Q86FU0 PRELIMINARY; PRT; 33 AA.
 AC Q86FU0;
 DT 01-JUN-2003 (TREMELrel. 24, Created)
 DT 01-JUN-2003 (TREMELrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
 DE Antennapedia complex (Fragment).
 GN ANT-C.
 OS Drosophila pseudoobscura (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 CX NCBI_TaxID=7237;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9322933; PubMed=8098982;
 RA Randazzo F.W., Seeger M.A., Hues C.A., Sweeney M.A., Cecil J.K.,
 RA Kaufman T.C.;
 RT "Structural changes in the antennapedia complex of Drosophila
 pseudobscura";
 RL Genetics 134:319-330(1993).
 DR EMBL; S63455; AAP13946.1; -.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR001356; Homeobox.
 DR PRINTS; PR00024; HOMEBOX.
 DR ProDom; PD000010; Homeobox; 1.
 DR PROSITE; PS50071; HOMEBOX_2; 1.
 FT NON_TER 1 1
 FT NON_TER 33 33
 SQ SEQUENCE 33 AA; 3863 MW; D78E37ED81PD45DF CRC64;

Query Match 100.0%; Score 92; DB 5; Length 33;
 Best Local Similarity 100.0%; Pred. No. 1.3e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWIFQNRKMKWK 16

Db 7 RQIKWIFQNRKMKWK 22

RESULT 2

Q57368 PRELIMINARY; PRT; 39 AA.
 AC Q57368;
 DT 01-JUN-1998 (TREMELrel. 06, Created)
 DT 01-JUN-1998 (TREMELrel. 06, Last sequence update)
 DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
 DE Hoxc5 protein (Fragment).
 GN HOXC5A OR HOXC5.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 CX NCBI_TaxID=7955;

RN [1]
 RP SEQUENCE FROM N.A.
 RA Prince V.E., Joly L., Ekker M., Ho R.K.;
 RT "zebrafish hox genes; genomic organization and modified colinear
 expression patterns in the trunk";
 RL submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- SURCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 DR EMBL; Y14539; CA74874.1; -.
 DR ZFIN; ZDB-GENE-980526-533; hoxc5a.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR001356; Homeobox.
 DR InterPro; IPR000047; HTH_lambrepreser.
 DR Pfam; PF00046; homeobox_1.
 DR PRINTS; PR00024; HOMEBOX.
 DR PRINTS; PR00031; HTHREPRESSR.
 DR ProDom; PD000010; Homeobox; 1.
 DR SMART; SM00389; HOX; 1.
 DR PROSITE; PS00027; HOMEBOX_1; 1.
 DR PROSITE; PS00071; HOMEBOX_2; 1.
 KW DNA-binding; Homeobox; Nuclear protein.
 FT NON_TER 1 1
 FT NON_TER 39 39
 SQ SEQUENCE 39 AA; 4827 MW; 592A0FEC12E58860 CRC64;

Query Match 100.0%; Score 92; DB 13; Length 39;
 Best Local Similarity 100.0%; Pred. No. 1.6e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWIFQNRKMKWK 16

Db 14 RQIKWIFQNRKMKWK 29

RESULT 3

Q80WH6 PRELIMINARY; PRT; 42 AA.
 ID Q80WH6;
 AC Q80WH6;
 DT 01-JUN-2003 (TREMELrel. 24, Created)
 DT 01-JUN-2003 (TREMELrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
 DE Hox-A|Hox-1 (Fragment).
 GN HOX-A|Hox-1.
 OS Rattus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 CX NCBI_TaxID=10118;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95217128; PubMed=7702549;
 RA Sakoyama Y., Mizuta I., Ogasawara N., Yoshikawa H.;
 RT "Cloning of rat homeobox genes";
 RL Biochem. Genet. 32:351-360(1994).
 DR EMBL; S76290; AAP31864.1; -.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR001356; Homeobox.
 DR InterPro; IPR000047; HTH_lambrepreser.
 DR Pfam; PF00046; homeobox_1.
 DR PRINTS; PR00024; HOMEBOX.
 DR PRINTS; PR00031; HTHREPRESSR.
 DR ProDom; PD000010; Homeobox; 1.
 DR SMART; SM00389; HOX; 1.
 DR PROSITE; PS00027; HOMEBOX_1; 1.
 DR PROSITE; PS00071; HOMEBOX_2; 1.
 FT NON_TER 1 1
 FT NON_TER 42 42
 SQ SEQUENCE 42 AA; 5494 MW; 38E5153B92216FE9 CRC64;

Query Match 100.0%; Score 92; DB 11; Length 42;
 Best Local Similarity 100.0%; Pred. No. 1.7e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 RQIKWIFQNRMMKWK 16
Db 25 RQIKWIFQNRMMKWK 40

RESULT 4
OS 57359 PRELIMINARY; PRT; 43 AA.
AC 057359;
DT 01-JUN-1998 (Tremblrel. 06, Created)
DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Hoxas protein (Fragment).
GN HOXC5A OR HOXA5.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
CX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Prince V.E., Joly L., Ekker M., Ho R.K.;
RT "Zebrafish hox genes: genomic organization and modified colinear
expression patterns in the trunk.";
RL Submitted (AUG-1997) to the EMBL/GenBank/DBSJ databases.
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL; Y14526; CAA74861.1; -.
DR ZFIN; ZDB-GENE-000823-6; hoxb5b.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; homeobox; 1.
DR PRINTS; PR00024; HOMEBOX.
DR ProDom; PD00010; Homeobox; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS00071; HOMEBOX_2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
FT NON_TER 1
SQ SEQUENCE 43 AA; 5050 MW; 53034C37F3DFA596 CRC64;

Query Match 100.0%; Score 92; DB 13; Length 43;
Best Local Similarity 100.0%; Pred. No. 1.7e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWIFQNRMMKWK 16
Db 10 RQIKWIFQNRMMKWK 25

RESULT 5
OS 9PVR9 PRELIMINARY; PRT; 46 AA.
AC 09PVR9;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE HOXC5A (Fragment).
GN HOXC5A.
OS Oryzias latipes (Medaka fish) (Japanese ricefish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
CX NCBI_TaxID=8090;
RN [1]
RP SEQUENCE FROM N.A.
RA Kondo S., Naruse K., Shima A.;
RT "Hox genes of the medakafish Oryzias latipes.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBSJ databases.
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL; AB026960; BAA86243.1; -.

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DR HSP; P02833; IHOM.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; homeobox; 1.
DR PRINTS; PR00024; HOMEBOX.
DR ProDom; PD00010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS00071; HOMEBOX_2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
FT NON_TER 1
SQ SEQUENCE 46 AA; 5955 MW; 60399999ED4294DD3 CRC64;

Query Match 100.0%; Score 92; DB 13; Length 46;
Best Local Similarity 100.0%; Pred. No. 1.8e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWIFQNRMMKWK 16
Db 23 RQIKWIFQNRMMKWK 38

RESULT 6
OS 027413 PRELIMINARY; PRT; 51 AA.
AC 027413;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE LOX5 ORTHOLOG homeobox (Fragment).
GN CTS-LOX5.
OS Ctenodrilus serratus.
OC Eukaryota; Metazoa; Annelida; Polychaeta; Palpata; Canalipalpata;
OC Terebellida; Ctenodrilidae; Ctenodrilus.
CX NCBI_TaxID=40316;
RN [1]
RP SEQUENCE FROM N.A.
RA Dick M.H., Buss L.W.;
RT "A PCR-based survey of homeobox genes in Ctenodrilus serratus
(Annelida: Polychaeta).";
RL Mol. Phylogenet. Evol. 3:146-158(1994).
RN [2]
RP SEQUENCE FROM N.A.
RA Dick M.H., Buss L.W.;
RL Submitted (MAY-1995) to the EMBL/GenBank/DBSJ databases.
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL; U26629; AAC46851.1; -.
DR EMBL; S76226; AAB31777.1; -.
DR HSP; P02833; 9ANT.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR000047; HTH lambrpressor.
DR Pfam; PF00046; homeobox; 1.
DR PRINTS; PR00024; HOMEBOX.
DR PRINTS; PR00031; HTHREPRESSR.
DR ProDom; PD00010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS00071; HOMEBOX_2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
FT NON_TER 1
FT NON_TER 51
SQ SEQUENCE 51 AA; 6278 MW; 88C8F65161E94A22 CRC64;

Query Match 100.0%; Score 92; DB 5; Length 51;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 RQIKWFOQRMMKWK 16
 DB 23 RQIKWFOQRMMKWK 38

RESULT 7

Q23743 ID Q23743 PRELIMINARY; PRT; 51 AA.
 AC Q23743;
 DT 01-NOV-1996 (TREMELrel. 01, Created)
 DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
 DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
 DE Deformed ortholog homeobox (Fragment).
 GN CTS-DFD.
 OS Ctenodrilus serratus.
 OC Eukaryota; Metazoa; Annelida; Polychaeta; Palpata; Canaliculipalata;
 OC Terebellida; Ctenodrilidae; Ctenodrilus.
 OC NCBI_TaxID=40316;
 [1]
 RN RP
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94356262; PubMed=7915607;
 RA Dick M.H., Buss L.W.;
 RT "A PCR-based survey of homeobox genes in Ctenodrilus serratus
 (Annelida: Polychaeta).";
 RL Mol. Phylogenet. Evol. 3:146-158(1994).
 [2]

SEQUENCE FROM N.A.

QY 1 RQIKWFOQRMMKWK 16
 DB 23 RQIKWFOQRMMKWK 38

RESULT 8

Q26407 ID Q26407 PRELIMINARY; PRT; 51 AA.
 AC Q26407;
 DT 01-NOV-1996 (TREMELrel. 01, Created)
 DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
 DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
 DE CTS-DFD protein (Fragment).
 GN CTS-DFD.
 OS Ctenodrilus serratus.
 OC Eukaryota; Metazoa; Annelida; Polychaeta; Palpata; Canaliculipalata;
 OC Terebellida; Ctenodrilidae; Ctenodrilus.
 OC NCBI_TaxID=40316;
 [1]
 RN RP
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94356262; PubMed=7915607;

RA Dick M.H., Buss L.W.;
 RT "A PCR-based survey of homeobox genes in Ctenodrilus serratus
 (Annelida: Polychaeta).";
 RL Mol. Phylogenet. Evol. 3:146-158(1994).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 DR EMBL; S76416; AAB31775.1; -;
 DR HSSP; P02833; 9ANT.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR001356; Homeobox.
 DR InterPro; IPR000047; HTH_lambrepres.
 DR Pfam; PF00046; homeobox; 1.
 DR PRINTS; PR00024; HOMEBOX.
 DR PRINTS; PR00031; HTHREPRESS.
 DR ProDom; PD000010; Homeobox; 1.
 DR SMART; SM00389; HOX; 1.
 DR PROSITE; PS00027; HOMEBOX_1; 1.
 DR PROSITE; PS00071; HOMEBOX_2; 1.
 KW DNA-binding; Homeobox; Nuclear protein.
 FT NON TER 1
 SQ SEQUENCE 51 AA; 6533 MW; 9EDB50C927FBCBD5 CRC64;

Query Match 100.0%; Score 92; DB 5; Length 51;

Best Local Similarity 100.0%; Pred. No. 2e-07; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWFOQRMMKWK 16

DB 23 RQIKWFOQRMMKWK 38

RESULT 9

Q9PVR8 ID Q9PVR8 PRELIMINARY; PRT; 57 AA.
 AC Q9PVR8;
 DT 01-MAY-2000 (TREMELrel. 13, Created)
 DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
 DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
 DE HOXA5A (Fragment).
 GN HOXA5A.
 OS Oryzias latipes (Medaka fish) (Japanese ricefish).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
 OC Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
 OC NCBI_TaxID=8090;
 [1]
 RN RP
 RP SEQUENCE FROM N.A.
 RA Kondo S., Naruse K., Shima A.;
 RT "Hox genes of the medakafish Oryzias latipes.";
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 DR EMBL; AB026961; BAA86244.1; -;
 DR HSSP; P02833; 1HOM.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR001356; Homeobox.
 DR Pfam; PF00046; Homeobox; 1.
 DR PRINTS; PR00024; HOMEBOX.
 DR ProDom; PD000010; Homeobox; 1.
 DR SMART; SM00389; HOX; 1.
 DR PROSITE; PS00027; HOMEBOX_1; 1.
 DR PROSITE; PS00071; HOMEBOX_2; 1.
 KW DNA-binding; Homeobox; Nuclear protein.
 FT NON TER 1
 SQ SEQUENCE 57 AA; 6891 MW; 54A6430320F68C04 CRC64;

Query Match 100.0%; Score 92; DB 13; Length 57;

Best Local Similarity 100.0%; Pred. No. 2.3e-07; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWFOQRMMKWK 16

DB 23 RQIKWFOQRMMKWK 38

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QY 1 RQIKWIFQNRMKWK 16
DB 23 RQIKWIFQNRMKWK 38

RESULT 10
QY188 PRELIMINARY; PRT; 58 AA.
ID QY188
AC QY188
DT 01-NOV-1999 (TEMBLrel. 12, Created)
DT 01-NOV-1999 (TEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)
DE HBI homeodomain protein (Fragment).
GN HBI.
OS Priapulus caudatus.
OC Eukaryota; Metazoa; Priapulida; Priapulidae; Priapulidae; Priapulidae.
OX NCBI_TaxID=37621;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=93318125; PubMed=10391241;
RA de Rosa R., Grenier J.K., Andreeva T., Cook C.E., Adoutte A., Akam M.,
RA Carroll S.B., Balavoine G.;
RT "Hox genes in brachiopods and priapulids and protostome evolution.";
RL Nature 399:772-776(1999).
CC -|- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL; AF14888; AAD40644.1; -.
DR HSP; P02833; 9ANT.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR000047; HTH_lambdarepressr.
DR Pfam; PF00046; homeobox; 1.
DR PRINTS; PR00024; HOMEBOX.
DR PROSITE; PS00031; HTHREPRESSR.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS00071; HOMEBOX_2; 1.
DR DNA-binding; Homeobox; Nuclear protein.
FT NON_TER 1
FT NON_TER 58
SQ SEQUENCE 58 AA; 7333 MW; 572F30DA57C9A613 CRC64;

Query Match 100.0%; Score 92; DB 5; Length 58;
Best Local Similarity 100.0%; Pred. No. 2.3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWIFQNRMKWK 16
DB 24 RQIKWIFQNRMKWK 39

RESULT 11
ID QY208 PRELIMINARY; PRT; 58 AA.
AC QY208
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)
DE Antennapedia protein (Fragment).
GN ANTENNAPEDIA.
OS Junonia coenia (Peacock butterfly) (Precis coenia).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysa;
OC Papilionoidea; Nymphalidae; Nymphalidae; Junonia.
OX NCBI_TaxID=39708;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=95075456; PubMed=7840822;
RA Warren R.W., Nagy L., Selegue J., Carroll S.;
RT "Evolution of homeotic gene regulation and function in flies and
RT butterflies.";
RL Nature 372:458-461(1994).

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CC -|- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL; L42135; AAG8461.1; -.
DR PIR; S5850; S5850.
DR HSP; P02833; 1HOM.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR000047; HTH_lambdarepressr.
DR Pfam; PF00046; homeobox; 1.
DR PRINTS; PR00024; HOMEBOX.
DR PROSITE; PS00031; HTHREPRESSR.
DR PROSITE; PS00071; HOMEBOX_2; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS00071; HOMEBOX_2; 1.
DR DNA-binding; Homeobox; Nuclear protein.
FT NON_TER 1
FT NON_TER 58
SQ SEQUENCE 58 AA; 7583 MW; BD69B4875BAE565E CRC64;

Query Match 100.0%; Score 92; DB 5; Length 58;
Best Local Similarity 100.0%; Pred. No. 2.3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWIFQNRMKWK 16
DB 43 RQIKWIFQNRMKWK 58

RESULT 12
ID QY7362 PRELIMINARY; PRT; 58 AA.
AC QY7362
DT 01-JUN-1998 (TEMBLrel. 06, Created)
DT 01-JUN-1998 (TEMBLrel. 06, Last sequence update)
DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)
DE Hoxb7 protein (Fragment).
GN HOXB7A OR HOXB7.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Prince V.E., Joly L., Ekker M., Ho R.K.;
RT "Zebrafish hox genes: genomic organization and modified colinear
RT expression patterns in the trunk.";
RL Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
CC -|- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL; Y14533; CAA74868.1; -.
DR TRANSFAC; T03635; -.
DR ZFIN; ZDB-GENE-000329-2; hoxb7a.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR000047; HTH_lambdarepressr.
DR Pfam; PF00046; homeobox; 1.
DR PRINTS; PR00024; HOMEBOX.
DR PRINTS; PR00031; HTHREPRESSR.
DR PROSITE; PS00031; HTHREPRESSR.
DR PROSITE; PS00071; HOMEBOX_2; 1.
DR PROSITE; PS00071; HOMEBOX_2; 1.
DR DNA-binding; Homeobox; Nuclear protein.
FT NON_TER 1
FT NON_TER 58
SQ SEQUENCE 58 AA; 6863 MW; 41EA6F14488DA1E5 CRC64;

Query Match 100.0%; Score 92; DB 13; Length 58;
Best Local Similarity 100.0%; Pred. No. 2.3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ROIKWQNRMRKWK 16
 DB 14 ROIKWQNRMRKWK 29

RESULT 13

Q8WRM9 ID Q8WRM9 PRELIMINARY; PRT; 59 AA.
 AC Q8WRM9
 DT 01-MAR-2002 (TREMELrel. 20, Created)
 DT 01-MAR-2002 (TREMELrel. 20, Last sequence update)
 DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
 DE Antennapedia (Fragment).
 GN ANTP.
 OS Lithobius atkinsoni.
 OC Eukaryota; Metazoa; Arthropoda; Myriapoda; Chilopoda;
 OC Pleurostigmophora; Lithobiomorpha; Lithobiidae; Lithobius.
 OX NCBI_TaxID=177213;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hughes C.L., Kaufman T.C.;
 RT "Exploring the myriapod body plan: expression patterns of the ten Hox
 RT genes in a centipede."
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 DR EMBL; AF434996; AAL36901.1;
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR001356; Homeobox.
 DR Pfam; PF00046; Homeobox; 1.
 DR PRINTS; PR00024; HOMEBOX.
 DR PROSITE; PS00031; HTHREPRESSOR.
 DR PRODOM; PD000010; Homeobox; 1.
 DR SMART; SM00389; HOX; 1.
 DR PROSITE; PS00027; HOMEBOX 1; 1.
 DR PROSITE; PS00071; HOMEBOX 2; 1.
 DR DNA-binding; Homeobox; Nuclear protein.
 FT NON_TER 1
 SQ SEQUENCE 59 AA; 7093 MW; 9E60036CE0D515C1 CRC64;

Query Match 100.0%; Score 92; DB 5; Length 59;
 Best Local Similarity 100.0%; Pred. No. 2.3e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ROIKWQNRMRKWK 16
 DB 23 ROIKWQNRMRKWK 38

RESULT 14

Q9NB42 ID Q9NB42 PRELIMINARY; PRT; 59 AA.
 AC Q9NB42
 DT 01-OCT-2000 (TREMELrel. 15, Created)
 DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
 DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
 DE Transcription factor deformed (Fragment).
 GN DFD.
 OS Anopheles gambiae (African malaria mosquito).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoides; Anopheles.
 OX NCBI_TaxID=7165;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=21150895; PubMed=11256376;
 RX Powers T.P., Hogan J., Ke Z., Dymkowski K., Wang X., Collins F.H.,
 RA Kaufman T.C.;
 RT "Characterization of the Hox cluster from the mosquito Anopheles
 RT gambiae (Diptera: Culicidae).";
 RL Evol. Dev. 2:311-325 (2000).

CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 DR EMBL; AF269155; AAF91400.1;
 DR HSSP; P02833; 1SAN.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR001356; Homeobox.
 DR Pfam; PF00046; Homeobox; 1.
 DR PRINTS; PR00024; HOMEBOX.
 DR PRODOM; PD000010; Homeobox; 1.
 DR SMART; SM00389; HOX; 1.
 DR PROSITE; PS00027; HOMEBOX 1; 1.
 DR PROSITE; PS00071; HOMEBOX 2; 1.
 DR DNA-binding; Homeobox; Nuclear protein.
 FT NON_TER 1
 SQ SEQUENCE 59 AA; 7621 MW; C38A2505A81D9952 CRC64;

Query Match 100.0%; Score 92; DB 5; Length 59;
 Best Local Similarity 100.0%; Pred. No. 2.3e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ROIKWQNRMRKWK 16
 DB 43 ROIKWQNRMRKWK 58

RESULT 15

Q9PVR5 ID Q9PVR5 PRELIMINARY; PRT; 59 AA.
 AC Q9PVR5
 DT 01-MAY-2000 (TREMELrel. 13, Created)
 DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
 DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
 DE HOXB6B (Fragment).
 DR HOXB6B.
 OS Oryzias latipes (Medaka fish) (Japanese ricefish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
 OC Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
 OX NCBI_TaxID=8090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kondo S., Naruse K., Shima A.;
 RT "Hox genes of the medakafish Oryzias latipes."
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ Databases.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 DR EMBL; AB026964; BAA86247.1;
 DR HSSP; P02833; 1HQM.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR001356; Homeobox.
 DR Pfam; PF00046; Homeobox; 1.
 DR PRINTS; PR00024; HOMEBOX.
 DR PRODOM; PD000010; Homeobox; 1.
 DR SMART; SM00389; HOX; 1.
 DR PROSITE; PS00027; HOMEBOX 1; 1.
 DR PROSITE; PS00071; HOMEBOX 2; 1.
 DR DNA-binding; Homeobox; Nuclear protein.
 FT NON_TER 1
 SQ SEQUENCE 59 AA; 7425 MW; AA2181EC556B968D CRC64;

Query Match 100.0%; Score 92; DB 13; Length 59;
 Best Local Similarity 100.0%; Pred. No. 2.3e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ROIKWQNRMRKWK 16
 DB 23 ROIKWQNRMRKWK 38

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RESULT 16
ID 077143 PRELIMINARY; PRT; 60 AA.
AC 077143;
DT 01-NOV-1998 (TEMBLrel. 08, Created)
DT 01-NOV-1998 (TEMBLrel. 08, Last sequence update)
DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)
DE Sex comps reduced (Fragment).
GN SCR.
OS Archegozetes longisetosus.
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Acariformes; Sarcopitiformes; Oribatida; Desmonomata;
OC Trhypochthonioides; Trhypochthoniidae; Archegozetes.
OX NCBI_TaxID=66560;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98393703; PubMed=9724762;
RA Telford M.J., Thomas R.H.;
RT "Expression of homeobox genes shows chelicerate arthropods retain
RT their deutocerebral segment.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:10671-10675(1998).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL; AF071407; AAC35936.1; -.
DR HSSP; P02833; ISAN.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR000047; HTH lambdarepressor.
DR Pfam; PF00046; homeobox_1.
DR PRINTS; PR00024; HOMEBOX.
DR PRINTS; PR00031; HTHREPRESSR.
DR PRODOM; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS00071; HOMEBOX_2; 1.
KM DNA-binding; Homeobox; Nuclear protein.
FT NON_TER 1 1
FT NON_TER 60 60
SQ SEQUENCE 60 AA; 7807 MW; 0A228B7CA4C98143 CRC64;

Query Match 100.0%; Score 92; DB 5; Length 60;
Best Local Similarity 100.0%; Pred. No. 2.4e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWFWQRNMKWK 16
DB 43 RQIKWFWQRNMKWK 58

RESULT 17
ID 077139 PRELIMINARY; PRT; 60 AA.
AC 077139;
DT 01-NOV-1998 (TEMBLrel. 08, Created)
DT 01-NOV-1998 (TEMBLrel. 08, Last sequence update)
DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)
DE Deformed (Fragment).
GN DPD.
OS Archegozetes longisetosus.
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Acariformes; Sarcopitiformes; Oribatida; Desmonomata;
OC Trhypochthonioides; Trhypochthoniidae; Archegozetes.
OX NCBI_TaxID=66560;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98393703; PubMed=9724762;
RA Telford M.J., Thomas R.H.;
RT "Expression of homeobox genes shows chelicerate arthropods retain
RT their deutocerebral segment.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:10671-10675(1998).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL; AF071403; AAC35932.1; -.

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DR HSSP; P02833; ISAN.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR000047; HTH lambdarepressor.
DR Pfam; PF00046; homeobox_1.
DR PRINTS; PR00024; HOMEBOX.
DR PRINTS; PR00031; HTHREPRESSR.
DR PRODOM; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS00071; HOMEBOX_2; 1.
KM DNA-binding; Homeobox; Nuclear protein.
FT NON_TER 1 1
FT NON_TER 60 60
SQ SEQUENCE 60 AA; 7755 MW; 32678A250BDEP74 CRC64;

Query Match 100.0%; Score 92; DB 5; Length 60;
Best Local Similarity 100.0%; Pred. No. 2.4e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWFWQRNMKWK 16
DB 43 RQIKWFWQRNMKWK 58

RESULT 18
ID 080WH7 PRELIMINARY; PRT; 60 AA.
AC 080WH7;
DT 01-JUN-2003 (TEMBLrel. 24, Created)
DT 01-JUN-2003 (TEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE Hox-A|Hox-1 (Fragment).
GN Hox-A|Hox-1.
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95217128; PubMed=7702549;
RA Sakoyama Y., Mizuta I., Ogasawara N., Yoshikawa H.;
RT "Cloning of rat homeobox genes.";
RL Biochem. Genet. 32:351-360(1994).
DR EMBL; S76287; AAP31863.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR000047; HTH lambdarepressor.
DR Pfam; PF00046; homeobox_1.
DR PRINTS; PR00024; HOMEBOX.
DR PRINTS; PR00031; HTHREPRESSR.
DR PRODOM; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS00071; HOMEBOX_2; 1.
FT NON_TER 1 1
FT NON_TER 60 60
SQ SEQUENCE 60 AA; 7849 MW; 1334ED6984875BAE CRC64;

Query Match 100.0%; Score 92; DB 11; Length 60;
Best Local Similarity 100.0%; Pred. No. 2.4e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWFWQRNMKWK 16
DB 43 RQIKWFWQRNMKWK 58

RESULT 19

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Q80WH4
ID Q80WH4 PRELIMINARY; PRT; 60 AA.
AC Q80WH4;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hox-B Hox-2 (Fragment).
GN Hox-B Hox-2.
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95217128; PubMed=7702549;
RA Sakoyama Y., Mizuta I., Ogasawara N., Yoshikawa H.;
RT "Cloning of rat homeobox genes.";
RL Biochem. Genet. 32:351-360(1994).
DR EMBL; S76297; AAP31867.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR000047; HTH lambrpressor.
DR Pfam; PF00046; homeobox; 1.
DR PRINTS; PR00024; HOMEBOX.
DR PRINTS; PR00031; HTHREPRESSR.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS00071; HOMEBOX_2; 1.
FT NON TER 1
FT NON TER 60
SQ SEQUENCE 60 AA; 7842 MW; 3407ED69B4874816 CRC64;

Query Match 100.0%; Score 92; DB 11; Length 60;
Best Local Similarity 100.0%; Pred. No. 2.4e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ROIKWQNRKMKWK 16
DB 43 ROIKWQNRKMKWK 58

RESULT 20
Q80GL5 PRELIMINARY; PRT; 60 AA.
AC Q80GL5;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Hox15/6 homeobox (Fragment).
OS Petromyzon marinus (Sea lamprey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
OC Petromyzontiformes; Petromyzontidae; Petromyzon.
OX NCBI_TaxID=7757;
RN [1]
RP SEQUENCE FROM N.A.
RX Irvine S.Q., Carr J.L., Bailey W.J., Kawasaki K., Shimizu N.,
RA Amemiya C.T., Ruddle F.H.;
RT "Genomic analysis of Hox clusters in the sea lamprey Petromyzon
marinus.";
RL J. Exp. Zool. 0:0-0(2002).
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL; AF410916; AAM19472.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR000047; HTH lambrpressor.
DR Pfam; PF00046; homeobox; 1.
DR PRINTS; PR00024; HOMEBOX.
DR PRINTS; PR00031; HTHREPRESSR.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS00071; HOMEBOX_2; 1.
FT NON TER 1
FT NON TER 60
SQ SEQUENCE 60 AA; 7863 MW; 1334F475B49847PE CRC64;

Query Match 100.0%; Score 92; DB 13; Length 60;
Best Local Similarity 100.0%; Pred. No. 2.4e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ROIKWQNRKMKWK 16
DB 43 ROIKWQNRKMKWK 58

RESULT 22
Q80GL6 PRELIMINARY; PRT; 60 AA.
AC Q80GL6;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE HoxK6 homeobox (Fragment).
OS Petromyzon marinus (Sea lamprey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
OC Petromyzontiformes; Petromyzontidae; Petromyzon.
OX NCBI_TaxID=7757;
RN [1]
RP SEQUENCE FROM N.A.
RX Irvine S.Q., Carr J.L., Bailey W.J., Kawasaki K., Shimizu N.,
RA Amemiya C.T., Ruddle F.H.;
RT "Genomic analysis of Hox clusters in the sea lamprey Petromyzon
marinus.";
RL J. Exp. Zool. 0:0-0(2002).
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL; AF410914; AAM19472.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR000047; HTH lambrpressor.
DR Pfam; PF00046; homeobox; 1.
DR PRINTS; PR00024; HOMEBOX.
DR PRINTS; PR00031; HTHREPRESSR.

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OS Petromyzon marinus (Sea lamprey).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
 OC Petromyzontiformes; Petromyzontidae; Petromyzon.
 OX NCBI_TaxID=7757;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Irvine S.O., Carr J.L., Bailey W.J., Kawasaki K., Shimizu N.,
 RA Ameniya C.T., Ruddle F.H.,
 RT "Genomic analysis of Hox clusters in the sea lamprey Petromyzon
 RT marinus";
 RL J. Exp. Zool. 0:0-0(2002).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 DR EMBL; AF410913; AAM19475.1;
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR000047; HTH_lambrepres.
 DR Pfam; PF00046; homeobox; 1.
 DR PRINTS; PR00024; HOMEBOX.
 DR PRODOM; PD00010; Homeobox; 1.
 DR SMART; SM00389; HOX; 1.
 DR PROSITE; PS00027; HOMEBOX_1; 1.
 DR PROSITE; PS00071; HOMEBOX_2; 1.
 KW Homeobox; DNA-binding; Nuclear protein.
 FT NON TER 1
 FT NON TER 60
 SQ SEQUENCE 60 AA; 7715 MW; 17A6ED79EF76A4F5 CRC64;

Query Match 100.0%; Score 92; DB 13; Length 60;
 Best Local Similarity 100.0%; Pred. No. 2.4e-07; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 0;

Qy 1 RQIKWIFQNRMRKWK 16
 Db 43 RQIKWIFQNRMRKWK 58

RESULT 23

Q8QGL2 PRELIMINARY; PRT; 60 AA.
 ID Q8QGL2
 AC Q8QGL2
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hox7 homeobox (Fragment)
 OS Petromyzon marinus (Sea lamprey).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
 OC Petromyzontiformes; Petromyzontidae; Petromyzon.
 OX NCBI_TaxID=7757;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Irvine S.O., Carr J.L., Bailey W.J., Kawasaki K., Shimizu N.,
 RA Ameniya C.T., Ruddle F.H.,
 RT "Genomic analysis of Hox clusters in the sea lamprey Petromyzon
 RT marinus";
 RL J. Exp. Zool. 0:0-0(2002).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 DR EMBL; AF410917; AAM19475.1;
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR000047; HTH_lambrepres.
 DR Pfam; PF00046; homeobox; 1.
 DR PRINTS; PR00024; HOMEBOX.
 DR PRODOM; PD00010; Homeobox; 1.
 DR SMART; SM00389; HOX; 1.
 DR PROSITE; PS00027; HOMEBOX_1; 1.
 DR PROSITE; PS00071; HOMEBOX_2; 1.
 KW Homeobox; DNA-binding; Nuclear protein.
 FT NON TER 1
 FT NON TER 60

FT NON TER 60
 SQ SEQUENCE 60 AA; 7863 MW; 1334F475B49B47FE CRC64;
 Query Match 100.0%; Score 92; DB 13; Length 60;
 Best Local Similarity 100.0%; Pred. No. 2.4e-07; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 0;
 Qy 1 RQIKWIFQNRMRKWK 16
 Db 43 RQIKWIFQNRMRKWK 58

RESULT 24

Q8QGL8 PRELIMINARY; PRT; 60 AA.
 ID Q8QGL8
 AC Q8QGL8
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE HoxG4 homeobox (Fragment)
 OS Petromyzon marinus (Sea lamprey).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
 OC Petromyzontiformes; Petromyzontidae; Petromyzon.
 OX NCBI_TaxID=7757;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Irvine S.O., Carr J.L., Bailey W.J., Kawasaki K., Shimizu N.,
 RA Ameniya C.T., Ruddle F.H.,
 RT "Genomic analysis of Hox clusters in the sea lamprey Petromyzon
 RT marinus";
 RL J. Exp. Zool. 0:0-0(2002).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 DR EMBL; AF410911; AAM19469.1;
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR001356; Homeobox.
 DR InterPro; IPR000047; HTH_lambrepres.
 DR Pfam; PF00046; homeobox; 1.
 DR PRINTS; PR00024; HOMEBOX.
 DR PRODOM; PD00010; Homeobox; 1.
 DR SMART; SM00389; HOX; 1.
 DR PROSITE; PS00027; HOMEBOX_1; 1.
 DR PROSITE; PS00071; HOMEBOX_2; 1.
 KW Homeobox; DNA-binding; Nuclear protein.
 FT NON TER 1
 FT NON TER 60
 SQ SEQUENCE 60 AA; 7704 MW; 08BBB642C24DEC6E CRC64;

Query Match 100.0%; Score 92; DB 13; Length 60;
 Best Local Similarity 100.0%; Pred. No. 2.4e-07; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 0;

Qy 1 RQIKWIFQNRMRKWK 16
 Db 43 RQIKWIFQNRMRKWK 58

RESULT 25

Q8QGL7 PRELIMINARY; PRT; 60 AA.
 ID Q8QGL7
 AC Q8QGL7
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE HoxJ5 homeobox (Fragment)
 OS Petromyzon marinus (Sea lamprey).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
 OC Petromyzontiformes; Petromyzontidae; Petromyzon.
 OX NCBI_TaxID=7757;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Irvine S.O., Carr J.L., Bailey W.J., Kawasaki K., Shimizu N.,
 RA Anemiyu C.T., Ruddle P.H.,
 RT "Genomic analysis of Hox clusters in the sea lamprey Petromyzon
 RT marinus";
 RL J. Exp. Zool. 0:0-0(2002).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 DR EMBL; AF410912; AA019470.1; -.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR001356; Homeobox.
 DR Pfam; PF00046; homeobox; 1.
 DR PRINTS; PR00024; HOMEBOX.
 DR PRODOM; PD000010; Homeobox; 1.
 DR SMART; SM00389; HOX; 1.
 DR PROSITE; PS00027; HOMEBOX_1; 1.
 DR PROSITE; PS00071; HOMEBOX_2; 1.
 KW Homeobox; DNA-binding; Nuclear protein.
 FT NON_TER 1 1
 FT NON_TER 60 60
 SQ SEQUENCE 60 AA; 7635 MW; E1F1209C5ACDF866 CRC64;

Query Match 100.0%; Score 92; DB 13; Length 60;
 Best Local Similarity 100.0%; Pred. No. 2.4e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWIFQNRKMKKK 16
 DB 43 RQIKWIFQNRKMKKK 58

Search completed: October 1, 2004, 12:17:25
 Job time : 54.8 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 1, 2004, 11:56:15 ; Search time 63.2 Seconds

(without alignments)
71.531 Million cell updates/sec

Title: US-09-830-779-8

Perfect score: 75

Sequence: 1 MEKVQLTRSAIRAS 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 segs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

A Genesepc29Jan04:*
1: Genesepc1980s:*
2: Genesepc1990s:*
3: Genesepc2000s:*
4: Genesepc2001s:*
5: Genesepc2002s:*
6: Genesepc2003as:*
7: Genesepc2003bs:*
8: Genesepc2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	75	100.0	16	3	AAY71009 Human Pho
2	75	100.0	35	3	AAY71012 Penetrati
3	75	100.0	36	3	AAY71011 Penetrati
4	75	100.0	36	8	ADE45175 Human SER
5	75	100.0	52	3	AAY71003 Human mut
6	75	100.0	52	3	AAY71002 Human Pho
7	75	100.0	52	5	ABP06592 Human ORF
8	75	100.0	52	8	ADE45172 Mouse SER
9	75	100.0	52	8	ADE45170 Rabbit SE
10	75	100.0	52	8	ADE45171 Rat SERCA
11	75	100.0	52	8	ADE45167 Human SER
12	75	100.0	79	3	AAY71019 H6 tagged
13	75	100.0	79	3	AAY71017 Hexahisti
14	72	96.0	52	3	AAY71006 Human mut
15	72	96.0	52	8	ADE45168 Pig SERCA
16	72	96.0	52	8	ADE45169 Dog SERCA
17	71	94.7	35	3	AAY71014 Penetrati
18	71	94.7	36	3	AAY71013 Penetrati
19	71	94.7	52	5	ABB79404 Human pho
20	71	94.7	52	8	ADE45173 Chicken S
21	71	94.7	79	3	AAY71018 H6 tagged
22	70	93.3	52	3	AAY71005 Human mut
23	69	92.0	52	3	AAY71004 Human mut
24	66	88.0	52	3	AAY71007 Human mut
25	41	54.7	116	7	ADC67928 Ribosomal

26	41	54.7	451	4	AAB96582	Putative
27	40	53.3	121	6	ABU19318	Protein e
28	39	52.0	364	5	ABF29187	Streptoco
29	38	50.7	113	6	ABU26060	Protein e
30	38	50.7	389	2	AAR29657	TGF-beta
31	38	50.7	390	2	AAR27522	TGF-beta
32	38	50.7	408	5	ABP27526	Streptoco
33	37	49.3	339	4	ABP27526	Streptoco
34	37	49.3	376	5	ABP27525	Streptoco
35	37	49.3	369	4	ABG24741	Novel hum
36	36.5	48.7	331	2	AAW71592	Human mye
37	36	48.0	96	6	AAU47163	Propionib
38	36	48.0	96	6	ABM43682	Propionib
39	36	48.0	113	4	AAG91979	C Glutami
40	36	48.0	114	6	ABU24669	Protein e
41	36	48.0	155	5	ABP04260	Human ORF
42	36	48.0	207	6	ABU43491	Protein e
43	36	48.0	275	4	ABU52746	Human met
44	36	48.0	387	4	ABB5660	Drosophil
45	36	48.0	401	4	ABB5661	Drosophil
46	36	48.0	409	6	ABU38335	Protein e
47	36	48.0	434	4	AAE01344	Arabidops
48	36	48.0	434	4	AAE01348	Arabidops
49	36	48.0	434	6	AAE36344	Arabidops
50	36	48.0	465	6	ABU20943	Protein e
51	36	48.0	486	7	ADES8782	Human Pro
52	36	48.0	511	4	AAU59773	Propionib
53	36	48.0	511	6	ABM56292	Propionib
54	36	48.0	596	6	ABM65049	Propionib
55	36	48.0	720	5	AAE25100	Human kin
56	36	48.0	765	4	ABE5514	Human pro
57	36	48.0	924	2	AAW37430	Rat hexok
58	36	48.0	924	2	AAW37443	Rat hexok
59	36	48.0	2400	6	ABM70712	Phototrab
60	35.5	47.3	319	4	ABE369696	Drosophil
61	35	46.7	24	2	AAY36671	Fragment
62	35	46.7	24	6	ADA11925	Human nov
63	35	46.7	61	4	AAV21036	Peptide #
64	35	46.7	61	4	ABE43216	Peptide #
65	35	46.7	61	4	ABE41248	Peptide #
66	35	46.7	61	4	AAW35032	Peptide #
67	35	46.7	61	4	AAW37056	Peptide #
68	35	46.7	61	4	ABE25244	Protein #
69	35	46.7	61	4	ABE26300	Protein #
70	35	46.7	61	4	AAW74917	Human bon
71	35	46.7	61	4	AAW76948	Human bon
72	35	46.7	61	4	AAW64123	Human bra
73	35	46.7	61	4	AAW62113	Human bra
74	35	46.7	61	4	ABG58610	Human liv
75	35	46.7	61	5	ABG46055	Human pep
76	35	46.7	62	4	AAW94354	Human rep
77	35	46.7	69	4	AAU47311	Propionib
78	35	46.7	69	6	ABM43830	Propionib
79	35	46.7	76	5	ABP07326	Human ORF
80	35	46.7	96	5	ABP33456	Human ORF
81	35	46.7	113	6	ABU33987	Protein e
82	35	46.7	131	2	AAY36660	Fragment
83	35	46.7	131	6	ADA11914	Human nov
84	35	46.7	137	3	AAW08267	Arabidops
85	35	46.7	137	3	AAW48859	Arabidops
86	35	46.7	137	3	AAW14887	Arabidops
87	35	46.7	137	3	AAW48819	Arabidops
88	35	46.7	144	4	ABE58335	Drosophil
89	35	46.7	147	4	ABU46685	Propionib
90	35	46.7	147	6	AAU23404	Propionib
91	35	46.7	156	4	AAU23445	Novel hum
92	35	46.7	190	4	ABU2490	Human pro
93	35	46.7	207	6	ABU43247	Protein e
94	35	46.7	209	4	ABG02969	Novel hum
95	35	46.7	211	5	ABP40291	Staphyloc
96	35	46.7	220	3	AAW48818	Arabidops
97	35	46.7	220	3	AAW48858	Arabidops
98	35	46.7	220	3	AAW14886	Arabidops

99 35 46.7 220 3 ANG08266 AAGC8266 Arabidops
100 35 46.7 234 6 ABU29277 ABU29277 Protein e

ALIGNMENTS

RESULT 1
ID AAY71009 standard; peptide; 16 AA.
XX AC AAY71009;
XX DT 29-AUG-2000 (first entry)
XX DE Human Phospholamban (PLB) cargo peptide.
XX KW Phospholamban; PLB; human; sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a;
KW cardiant; cardiomyocyte; transport peptide; penetratin; cargo peptide;
KW contractilin; cardiac contractility; inhibitor; cardiac disease;
KW treatment; heart failure; myocardial dysfunction.
XX OS Homo sapiens.
XX WO200025804-A2.
XX PD 11-MAY-2000.
XX PF 02-NOV-1999; 99WO-US025692.
XX PR 02-NOV-1998; 98US-0106718P.
XX PR 27-JUL-1999; 99US-0145883P.
XX PA (REGC) UNIV CALIFORNIA.
XX PI Chien K, Dillman W, Minamisawa S, He H, Hoshijima M, Meyer M;
XX PI Scott C, Wang Y, Silverman GJ;
XX DR WPI; 2000-365393/31.
XX PT Treating cardiac diseases, e.g. heart failure or myocardial dysfunction
XX PT comprises enhancing cardiac contractility by inhibiting interaction
XX PT between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine
XX PT triphosphatase.
XX PS Example 4; Page 50; 56pp; English.

The patent discloses a method for the treatment of heart failure, using small peptide complexes and recombinant proteins, that induces phospholamban (PLB) deficiency and inhibits the interaction between PLB and sarcoplasmic reticulum Ca 2+ ATPase (SERCA2a) within cardiomyocytes. The peptide complex comprises of transport peptide like penetratin and cargo peptide selected from mutant PLB, native PLB or antibody against PLB protein (contractilin). Penetratin-PLB peptide functions as a dominant negative inhibitor of PLB-SERCA2a interaction, enhances cardiac contractility and reduces blood pressure. This method is useful for the treatment of cardiac disease e.g. heart failure and myocardial dysfunction. The present amino acid sequence is the cargo peptide from human PLB amino terminal residues 1-16. It could be derived from any segment of wild type or mutant PLB protein. The cargo peptide is linked to the transport peptide by a covalent linkage

Sequence 16 AA;

Query Match 100.0%; Score 75; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 1e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQLTRSAIRRAS 16
Db 1 MEKVQLTRSAIRRAS 16

RESULT 2
ID AAY71012 standard; peptide; 35 AA.
XX AC AAY71012;
XX DT 29-AUG-2000 (first entry)
XX DE Penetratin-based recombinant phospholamban peptide, TAT-PLB.
XX KW Phospholamban; PLB; human; sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a;
KW cardiant; cardiomyocyte; transport peptide; penetratin; cargo peptide;
KW contractilin; cardiac contractility; inhibitor; cardiac disease;
KW treatment; heart failure; myocardial dysfunction; recombinant peptide;
KW HIV; TAT protein.
XX OS Homo sapiens.
XX OS Human immunodeficiency virus.
XX FH Key Location/Qualifiers
XX FT Region 5..15
XX FT /note= "Corresponds to denatured human immunodeficiency virus (HIV) TAT protein"
XX FT Region 16..35
XX FT /note= "Corresponds to human phospholamban (PLB) amino terminal peptide"

WO200025804-A2.

11-MAY-2000.

02-NOV-1999; 99WO-US025692.

02-NOV-1998; 98US-0106718P.

27-JUL-1999; 99US-0145883P.

(REGC) UNIV CALIFORNIA.

Chien K, Dillman W, Minamisawa S, He H, Hoshijima M, Meyer M;

Scott C, Wang Y, Silverman GJ;

WPI; 2000-365393/31.

Treating cardiac diseases, e.g. heart failure or myocardial dysfunction comprises enhancing cardiac contractility by inhibiting interaction between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine triphosphatase.

Example 5; Page 52; 56pp; English.

The patent discloses a method for the treatment of heart failure, using small peptide complexes and recombinant proteins, that induces phospholamban (PLB) deficiency and inhibits the interaction between PLB and sarcoplasmic reticulum Ca 2+ ATPase (SERCA2a) within cardiomyocytes. The peptide complex comprises of transport peptide like penetratin and cargo peptide selected from mutant PLB, native PLB or antibody against PLB protein (contractilin). Penetratin-PLB peptide functions as a dominant negative inhibitor of PLB-SERCA2a interaction, enhances cardiac contractility and reduces blood pressure. This method is useful for the treatment of cardiac disease e.g. heart failure and myocardial dysfunction. The present sequence is the penetratin-based recombinant peptide TAT-PLB, comprising the amino terminal end of human PLB native protein, attached to the 3' end of denatured human immunodeficiency virus (HIV), TAT protein. Penetratin is a class of peptides, with translocating properties having the ability to carry hydrophilic compounds across the plasma membrane

Sequence 35 AA;

Query Match 100.0%; Score 75; DB 3; Length 35;
Best Local Similarity 100.0%; Pred. No. 2.4e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEKVQYLTRSAIRRAS 16
 |||||
 Db 16 MEKVQYLTRSAIRRAS 31

RESULT 3

AAV71011
 ID AAV71011 standard; peptide; 36 AA.

AC AAV71011;
 XX

DT 29-AUG-2000 (first entry)
 XX

DE Penetratin-based recombinant phospholamban peptide, PLB-ANT.
 XX

KW Phospholamban; PLB; human; sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a;
 KW cationic; cardiomyocyte; transport peptide; penetratin; cargo peptide;
 KW contractilin; cardiac contractility; inhibitor; cardiac disease;
 KW treatment; heart failure; myocardial dysfunction; recombinant peptide;
 KW fruit fly; antennapedia; ANT.
 XX

OS Homo sapiens.
 OS Drosophila sp.
 XX

FH Key Location/Qualifiers
 FT Region 1..20

FT /note= "Corresponds to human phospholamban (PLB) amino
 FT terminal peptide"
 FT Region 21..36

FT /note= "Corresponds to Drosophila antennapedia (ANT)
 FT transport peptide"
 FT

XX WO200025804-A2.
 XX

XX 11-MAY-2000.
 XX

XX 02-NOV-1999; 99WO-US025692.
 PF

XX 02-NOV-1998; 98US-0106718P.
 PR

XX 27-JUL-1999; 99US-0145883P.
 PR

XX (REGC) UNIV CALIFORNIA.
 PA

XX Chien K, Dillman W, Minamisawa S, He H, Hoshijima M, Meyer M;
 PI

PI Scott C, Wang Y, Silverman GJ;
 PI

DR WPI; 2000-365393/31.
 DR

XX Treating cardiac diseases, e.g. heart failure or myocardial dysfunction
 XX comprises enhancing cardiac contractility by inhibiting interaction
 PT between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine
 PT triphosphatase.
 PT

XX Example 5; Page 52; 56pp; English.
 PS

XX The patent discloses a method for the treatment of heart failure, using
 CC small peptide complexes and recombinant proteins, that induces
 CC phospholamban (PLB) deficiency and inhibits the interaction between PLB
 CC and sarcoplasmic reticulum Ca 2+ ATPase (SERCA2a) within cardiomyocytes.
 CC The peptide complex comprises of transport peptide like penetratin and
 CC cargo peptide selected from mutant PLB, native PLB or antibody against
 CC PLB protein (contractilin). Penetratin-PLB peptide functions as a
 CC dominant negative inhibitor of PLB-SERCA2a interaction, enhances cardiac
 CC contractility and reduces blood pressure. This method is useful for the
 CC treatment of cardiac disease e.g. heart failure and myocardial
 CC dysfunction. The present sequence is the penetratin-based recombinant
 CC peptide PLB-ANT, comprising the amino terminal end of human PLB native
 CC protein, attached to the 5' end of the Drosophila antennapedia (ANT)
 CC transport peptide. Penetratin is a class of peptides, with translocating
 CC properties having the ability to carry hydrophilic compounds across the
 CC plasma membrane
 XX

XX Sequence 36 AA;
 SQ

Query Match 100.0%; Score 75; DB 3; Length 36;
 Best Local Similarity 100.0%; Pred. No. 2.5e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEKVQYLTRSAIRRAS 16
 |||||
 Db 1 MEKVQYLTRSAIRRAS 16

RESULT 4

ADE45175
 ID ADE45175 standard; peptide; 36 AA.
 XX

AC ADE45175;
 XX

DT 29-JAN-2004 (first entry)
 DT

XX Human SERCA_2 inhibitor phospholamban, cytosolic domain.
 XX

KW Human; SERCA_2; phospholamban; PLB;
 KW Ca2+ ATPase of the sarco/endoplasmic reticulum; protein co-ordinate data;
 KW cardiant.
 KW

OS Homo sapiens.
 OS

PN US6538022-B1.
 PN

PD 25-MAR-2003.
 PD

XX 18-FEB-1999; 99US-00252063.
 XX

XX 24-SEP-1997; 97US-00937117.
 XX

XX (ORIN) ORION CORP.
 PA

XX Pollseello P, Ovaska M, Tenhunen J, Vidgren J;
 PI

PI Ylberttula-Ikoren M, Tilgmann C, Lotta T, Kaivola J;
 PI

XX WPI; 2004-019625/02.
 XX

XX New compound, useful for relieving inhibitory effects of phospholamban on
 PT cardiac SR Ca2+-ATPase by deactivating phospholamban and stimulating Ca2+
 PT -ATPase.
 PT

XX Disclosure; SEQ ID NO 9; 65pp; English.
 PS

XX The invention relates to a compound which deactivates, and exhibits
 CC affinity for, a phospholamban (PLB) protein (an inhibitor of SERCA 2,
 CC Ca2+ ATPase of the sarco/endoplasmic reticulum) appearing as ADE45167-
 CC ADE45173. The compound has a structure containing three of the four
 CC moieties: an electronegative moiety associating with an S1 binding site
 CC of the phospholamban cytosolic domain when the compound is bound to it,
 CC the binding site comprises Tyr-6, Arg-9 and/or Arg-13; an electronegative
 CC moiety associating with an S2 binding site of the phospholamban cytosolic
 CC domain when the compound is bound to it, the S2 binding site comprises
 CC Arg-14; a hydrophobic moiety associating with an S3 binding site of the
 CC phospholamban cytosolic domain when the compound is bound, the binding
 CC site comprises Met-20, Lys-27 and/or Leu-28; and a hydrophobic moiety
 CC associating with an S4 binding site of the phospholamban cytosolic domain
 CC when the compound is bound, the binding site comprises Phe-32 and/or Phe-
 CC 35. The compound is not 3-benzyl-5,7-bis ((1H-tetrazol-5-yl)-methoxy)-4-
 CC -methyl-2H-methyl-2H-1-benzopyran-2-one. Also included are deactivating
 CC phospholamban, comprising administering the novel compound to stimulate
 CC the Ca 2+ -ATPase. The compound is useful for relieving the inhibitory
 CC effects of phospholamban on cardiac SERCA_2. The present sequence is the
 CC cytosolic domain of human phospholamban.
 XX

XX Sequence 36 AA;
 SQ

Query Match 100.0%; Score 75; DB 8; Length 36;
 Best Local Similarity 100.0%; Pred. No. 2.5e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy		1 MEKQYLTRSAIRRAS 16	
Dd		1 MEKQYLTRSAIRRAS 16	
RESULT 5			
AAV71003			
ID	AAV71003 standard; protein; 52 AA.		
AC	AAV71003;		
XX			
DT	29-AUG-2000 (first entry)		
DE	Human mutant phospholamban (PLB) V49A protein.		
KW	Phospholamban; PLB; human; sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a;		
KW	cadiant; cardiomyocyte; transport peptide; penetratin; cargo peptide;		
KW	contractilin; cardiac contractility; inhibitor; cardiac disease;		
KW	treatment; heart failure; myocardial dysfunction; mutant.		
OS	Homo sapiens.		
XX	Synthetic.		
FT			
Key	Location/Qualifiers		
Misc-difference 49	/note= "Wild type Val replaced with Ala"		
FT			
FT			
FN	WO200025804-A2.		
PD	11-MAY-2000.		
XX			
PF	02-NOV-1999; 99WO-US025692.		
XX			
PR	02-NOV-1998; 98US-0106718P.		
XX	27-JUL-1999; 99US-0145883P.		
PA	(REGC) UNIV CALIFORNIA.		
XX			
PFI	Chien K, Dillman W, Minamisawa S, He H, Hoshijima M, Meyer M;		
PI	Scott C, Wang Y, Silverman GJ;		
XX			
DR	WPI; 2000-365393/31.		
XX	Treating cardiac diseases, e.g. heart failure or myocardial dysfunction		
XX	comprises enhancing cardiac contractility by inhibiting interaction		
XX	between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine		
XX	triphosphatase.		
XX			
XX	Disclosure; Page 48; 56pp; English.		
XX	The patent discloses a method for the treatment of heart failure, using		
CC	small peptide complexes and recombinant proteins, that induces		
CC	phospholamban (PLB) deficiency and inhibits the interaction between PLB		
CC	and sarcoplasmic reticulum Ca 2+ ATPase (SERCA2a) within cardiomyocytes.		
CC	The peptide complex comprises of transport peptide like penetratin and		
CC	cargo peptide selected from mutant PLB, native PLB or antibody against		
CC	PLB protein (contractilin). Penetratin-PLB peptide functions as a		
CC	dominant negative inhibitor of PLB-SERCA2a interaction, enhances cardiac		
CC	contractility and reduces blood pressure. This method is useful for the		
CC	treatment of cardiac disease e.g. heart failure and myocardial		
CC	dysfunction. The present amino acid sequence is the human mutant PLB		
CC	protein, comprising a sense mutation Val49Ala. This mutant sequence when		
CC	overexpressed in the transformed cardiomyocytes, shows increased		
CC	contractility than the wild type PLB sequence		
XX			
XX	Sequence 52 AA;		
Query Match	100.0%; Score 75; DB 3; Length 52;		
Best Local Similarity	100.0%; Pred. NO. 3.7e-06;		
Matches 16; Conservative	0; Mismatches 0; Indels 0; Gaps 0;		
Qy		1 MEKQYLTRSAIRRAS 16	

Query Match 100.0%; Score 75; DB 3; Length 52;
Best Local Similarity 100.0%; Pred. No. 3.7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVOYLTRSAIRAS 16
DB 1 MEKVOYLTRSAIRAS 16

RESULT 7
ID ABP06592 standard; protein; 52 AA.
AC ABP06592;
DT 25-JUN-2002 (first entry)
DE Human ORFX protein sequence SEQ ID NO:13166.
XX Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;
XX hyperproliferative disorder; psoriasis; benign tumour; haemorrhage;
XX degenerative disorder; osteoarthritis; neurodegenerative disorder;
XX cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;
XX hypertension; hypothyroidism; cholesterol ester storage disease;
XX immune deficiency; immune disorder; infectious disease;
XX autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
XX myasthenia gravis.
XX Homo sapiens.
XX WO200192523-A2.
XX 06-DEC-2001.
XX 29-MAY-2001; 2001WO-US010836.
XX 30-MAY-2000; 2000US-0206132P.
XX 29-AUG-2000; 2000US-0228716P.
XX (CURA-) CURAGEN CORP.
XX Shimkets RA, Leach MD;
XX WPI; 2002-106308/14.
XX N-PSDB; ABN22344.
XX Novel human polypeptides and polynucleotides useful for diagnosing,
XX preventing and treating cardiovascular disease, neurodegenerative,
XX hyperproliferative disorders and autoimmune disorders.
XX Disclosure; SEQ ID NO 13166; 1037pp; English.

The present invention describes substantially purified human proteins
(referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1
in the specification). ABN15762 to ABN27252 encode the human ORFX
proteins given in ABP00010 to ABP11500. ORFX proteins are useful for
treating or preventing a pathology associated with an ORFX-associated
disorder in humans, and in the manufacture of a medicament for treating a
syndrome associated with ORFX-associated disorder. ORFX polynucleotide
sequences can be used in gene therapy. ORFX sequences can be used in the
treatment of cancer, hyperproliferative disorders, cirrhosis of liver,
psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage,
osteoarthritis, neurodegenerative disorders, disorders related to organ
transplantation, cardiovascular diseases, diabetes mellitus, systemic
lupus erythematosus, hypertension, hypothyroidism, cholesterol ester
storage disease, various immune deficiencies and disorders, infectious
diseases, autoimmune disorders such as multiple sclerosis, rheumatoid
arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host
disease and autoimmune inflammatory eye disease. ORFX proteins are also
useful for treating burns, incisions, ulcers, for treating osteoporosis,
bone degenerative disorders, periodontal disease, and for gut
protection or regeneration and treatment of lung or liver fibrosis.

reperfusion injury in various tissues and conditions resulting from
systemic cytokine damage. N.B. The sequence data for this patent did not
form part of the printed specification, but was obtained in electronic
format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

QY 1 MEKVOYLTRSAIRAS 16
DB 1 MEKVOYLTRSAIRAS 16

Query Match 100.0%; Score 75; DB 5; Length 52;
Best Local Similarity 100.0%; Pred. No. 3.7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVOYLTRSAIRAS 16
DB 1 MEKVOYLTRSAIRAS 16

RESULT 8
ID ADE45172 standard; protein; 52 AA.
AC ADE45172;
DT 29-JAN-2004 (first entry)
DE Mouse SERCA_2 inhibitor phospholamban.
XX Mouse; SERCA_2; phospholamban; PLB;
XX Ca2+ ATPase Of the sarco/endoplasmic reticulum; protein co-ordinate data;
XX cardiant.
XX Mus sp.
XX US6538022-B1.
XX 25-MAR-2003.
XX 18-FEB-1999; 99US-00252063.
XX 24-SEP-1997; 97US-00937117.
XX (ORIN) ORION CORP.
XX Pollesello P, Ovaska M, Tenhunen J, Vidgren J;
XX Yliperttula-Ikonen M, Tilmann C, Letta T, Kaivola J;
XX WPI; 2004-019625/02.
XX New compound, useful for relieving inhibitory effects of phospholamban on
XX cardiac SR Ca2+-ATPase by deactivating phospholamban and stimulating Ca2+
XX -ATPase.
XX Claim 1; SEQ ID NO 6; 65pp; English.

The invention relates to a compound which deactivates, and exhibits
affinity for, a phospholamban (pLB) protein (an inhibitor of SERCA_2,
Ca2+ ATPase of the sarco/endoplasmic reticulum) appearing as ADE45167-
ADE45173. The compound has a structure containing three of the four
moieties: an electronegative moiety associating with an S1 binding site
of the phospholamban cytosolic domain when the compound is bound to it,
the binding site comprises Tyr-6, Arg-9 and/or Arg-13; an electronegative
moiety associating with an S2 binding site of the phospholamban cytosolic
domain when the compound is bound to it, the S2 binding site comprises
Arg-14; a hydrophobic moiety associating with an S3 binding site of the
phospholamban cytosolic domain when the compound is bound, the binding
site comprises Met-20, Lys-27 and/or Leu-28; and a hydrophobic moiety
associating with an S4 binding site of the phospholamban cytosolic domain
when the compound is bound, the binding site comprises Phe-32 and/or Phe-
35. The compound is not 3-benzyl-5,7-bis ((1H-tetrazol-5-yl)-methoxy)-4-
methyl-2H-methyl-2H-1-benzopyran-2-one. Also included are deactivating
phospholamban, comprising administering the novel compound to stimulate
the Ca2+ -ATPase. The compound is useful for relieving the inhibitory
effects of phospholamban on cardiac SERCA_2. The present sequence is a
phospholamban.

[illegible]

CC	associating with an S4 binding site of the phospholamban cytosolic domain.
CC	when the compound is bound, the binding site comprises Phe-32 and/or Phe-
CC	35. The compound is not 3-benzyl-5,7-bis ((1H-tetrazol-5-yl)-methoxy)-4-
CC	-methyl-2H-methyl-2H-1-benzopyran-2-one. Also included are deactivating
CC	phospholamban, comprising administering the novel compound to stimulate
CC	the Ca ²⁺ + -ATPase. The compound is useful for relieving the inhibitory
CC	effects of phospholamban on cardiac SERCA_2. The present sequence is
CC	human phospholamban.
XX	
XX	Sequence 52 AA;
SQ	
	Query Match 100.0%; Score 75; DB 8; Length 52;
	Best Local Similarity 100.0%; Pred. No. 3.7e-06;
	Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 MEKVQYLTRSAIRRAS 16
Db	1 MEKVQYLTRSAIRRAS 16
RESULT 12	
AAAY71019	
ID ID	AAAY71019 standard; protein; 79 AA.
AC AC	AAAY71019;
XX XX	
DT DT	29-AUG-2000 (first entry)
DE DE	
XX XX	H6 tagged penetratin-based recombinant protein, H6- (V49A)mutantPLB-ANT.
KW KW	Phospholamban; PLB; human; sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a;
KM KM	cardiant; cardiomyocyte; transport peptide; penetratin; cargo peptide;
KW KW	contractilin; cardiac contractility; inhibitor; cardiac disease; mutant;
KW KW	treatment; heart failure; myocardial dysfunction; recombinant protein;
KM KM	fruit fly; ANT; antennapedia; H6 tag; hexahistidine.
XX XX	
OS OS	Homo sapiens.
OS OS	Drosophila sp.
OS OS	Synthetic.
XX XX	
FH FH	Key Location/Qualifiers
FT FT	1..52
FT FT	Region
FT FT	protein
FT FT	/note= "Corresponds to mutant human phospholamban (PLB)
FT FT	Misc-difference 49
FT FT	/note= "Wild type Val replaced with Ala"
FT FT	Region 53..58
FT FT	/note= "Corresponds to hexahistidine tag (H6)"
FT FT	Region 63..78
FT FT	/note= "Corresponds to Drosophila antennapedia (ANT)
FT FT	transport peptide"
PX PX	WO200025804-A2.
FN FN	
XX XX	
PD PD	11-MAY-2000.
XX XX	
XX XX	02-NOV-1999; 99WO-US025692.
PR PR	02-NOV-1998; 98US-0106718P.
PR PR	27-JUL-1999; 99US-0145833P.
XX XX	
XX XX	(REGC) UNIV CALIFORNIA.
PA PA	
XX XX	Chien K, Dillman W, Minamisawa S, He H, Hoshijima M, Meyer M;
PI PI	Scott C, Wang Y, Silverman GJ;
PI PI	WPI; 2000-365393/31.
DR DR	
XX XX	Treating cardiac diseases, e.g. heart failure or myocardial dysfunction
PT PT	comprises enhancing cardiac contractility by inhibiting interaction
PT PT	between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine
PT PT	triphosphatase.
XX XX	

PS Example 6; Page 56; 56pp; English.

XX The patent discloses a method for the treatment of heart failure, using
 CC small peptide complexes and recombinant proteins, that induces
 CC phospholamban (PLB) deficiency and inhibits the interaction between PLB
 CC and sarcoplasmic reticulum Ca²⁺ ATPase (SERCA2a) within cardiomyocytes.
 CC The peptide complex comprises of transport peptide like penetratin and
 CC cargo peptide selected from mutant PLB, native PLB or antibody against
 CC PLB protein (contractilin). Penetratin-PLB peptide functions as a
 CC dominant negative inhibitor of PLB-SERCA2a interaction, enhances cardiac
 CC contractility and reduces blood pressure. This method is useful for the
 CC treatment of cardiac disease e.g. heart failure and myocardial
 CC dysfunction. The present sequence is the hexahistidine (H6) tagged
 CC penetratin-based recombinant protein H6-mutant-PLB-ANT, comprising the
 CC human mutant (Val49Ala) PLB protein and Drosophila antennapedia (ANT)
 CC transport peptide attached by a hexahistidine tag. This sequence is
 CC expressed in Escherichia coli cells

XX Sequence 79 AA;

Query Match 100.0%; Score 75; DB 3; Length 79;
 Best Local Similarity 100.0%; Pred. No. 5.8e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MEKVQYLTRSAIRRAS 16
 Db 1 MEKVQYLTRSAIRRAS 16
 |||||

RESULT 13

AAV71017
 ID AAV71017 standard; protein; 79 AA.

XX AAV71017;

XX 29-AUG-2000 (first entry)

XX Hexahistidine tagged penetratin-based recombinant protein, H6-wtPLB-ANT.
 XX Phospholamban; PLB; human; sarcoplasmic reticulum Ca²⁺ ATPase; SERCA2a;
 XX cardiant; cardiomyocyte; transport peptide; penetratin; cargo peptide;
 XX contractilin; cardiac contractility; inhibitor; cardiac disease;
 XX treatment; heart failure; myocardial dysfunction; recombinant protein;
 XX fruit fly; ANT; antennapedia; H6 tag; hexahistidine.

OS Homo sapiens.
 OS Drosophila sp.
 OS Synthetic.

XX Key Location/Qualifiers
 FT Region 1..52
 FT /notes "Corresponds to Human phospholamban (PLB) protein"
 FT Region 53..58
 FT /notes "Corresponds to hexahistidine tag (H6)"
 FT Region 53..78
 FT /notes "Corresponds to Drosophila antennapedia (ANT)
 FT transport peptide"

XX WO200025804-A2.

XX 11-MAY-2000.

XX 02-NOV-1999; 99WO-US025692.

XX 02-NOV-1998; 98US-0106718P.

XX 27-JUL-1999; 99US-0145883P.

XX (REGC) UNIV CALIFORNIA.

XX Chien K, Dillman W, Minamisawa S, He H, Hoshijima M, Meyer M;
 PI Scott C, Wang Y, Silverman GU;

XX WPI; 2000-365393/31.

XX

PT Treating cardiac diseases, e.g. heart failure or myocardial dysfunction
 CC comprises enhancing cardiac contractility by inhibiting interaction
 PT between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine
 CC triphosphatase.

XX Example 6; Page 54-55; 56pp; English.

XX The patent discloses a method for the treatment of heart failure, using
 CC small peptide complexes and recombinant proteins, that induces
 CC phospholamban (PLB) deficiency and inhibits the interaction between PLB
 CC and sarcoplasmic reticulum Ca²⁺ ATPase (SERCA2a) within cardiomyocytes.
 CC The peptide complex comprises of transport peptide like penetratin and
 CC cargo peptide selected from mutant PLB, native PLB or antibody against
 CC PLB protein (contractilin). Penetratin-PLB peptide functions as a
 CC dominant negative inhibitor of PLB-SERCA2a interaction, enhances cardiac
 CC contractility and reduces blood pressure. This method is useful for the
 CC treatment of cardiac disease e.g. heart failure and myocardial
 CC dysfunction. The present sequence is the hexahistidine (H6) tagged
 CC penetratin-based recombinant protein H6-wtPLB-ANT, comprising the wild
 CC type human PLB protein and Drosophila antennapedia (ANT) transport
 CC peptide attached by a hexahistidine tag. This sequence is expressed in
 CC Escherichia coli cells

XX Sequence 79 AA;

Query Match 100.0%; Score 75; DB 3; Length 79;
 Best Local Similarity 100.0%; Pred. No. 5.8e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MEKVQYLTRSAIRRAS 16
 Db 1 MEKVQYLTRSAIRRAS 16
 |||||

RESULT 14

AAV71006

ID AAV71006 standard; protein; 52 AA.

XX AAV71006;

XX 29-AUG-2000 (first entry)

XX Human mutant phospholamban (PLB) S16N protein.

XX Phospholamban; PLB; human; sarcoplasmic reticulum Ca²⁺ ATPase; SERCA2a;
 KW cardiant; cardiomyocyte; transport peptide; penetratin; cargo peptide;
 KW contractilin; cardiac contractility; inhibitor; cardiac disease;
 KW treatment; heart failure; myocardial dysfunction; mutant.

OS Homo sapiens.
 OS Synthetic.

XX Key Location/Qualifiers
 FT Misc-difference 16
 FT /note= "Wild type Ser replaced with Asn"

XX WO200025804-A2.

XX 11-MAY-2000.

XX 02-NOV-1999; 99WO-US025692.

XX 02-NOV-1998; 98US-0106718P.

XX 27-JUL-1999; 99US-0145883P.

XX (REGC) UNIV CALIFORNIA.

XX Chien K, Dillman W, Minamisawa S, He H, Hoshijima M, Meyer M;
 PI Scott C, Wang Y, Silverman GU;

XX WPI; 2000-365393/31.

PT Treating cardiac diseases, e.g. heart failure or myocardial dysfunction
 PT comprises enhancing cardiac contractility by inhibiting interaction
 PT between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine
 PT triphosphatase.

PS Disclosure; Page 49; 56pp; English.

XX The patent discloses a method for the treatment of heart failure, using
 CC small peptide complexes and recombinant proteins, that induces
 CC phospholamban (PLB) deficiency and inhibits the interaction between PLB
 CC and sarcoplasmic reticulum Ca 2+ ATPase (SERCA2a) within cardiomyocytes.
 CC The peptide complex comprises of transport peptide like penetratin and
 CC cargo peptide selected from mutant PLB, native PLB or antibody against
 CC PLB protein (concratitin). Penetratin-PLB peptide functions as a
 CC dominant negative inhibitor of PLB-SERCA2a interaction, enhances cardiac
 CC contractility and reduces blood pressure. This method is useful for the
 CC treatment of cardiac disease e.g. heart failure and myocardial
 CC dysfunction. The present amino acid sequence is the human mutant PLB
 CC protein, comprising the mutation Ser16Asn. This mutant sequence when
 CC overexpressed in the transformed cardiomyocytes, shows increased
 CC contractility than the wild type PLB sequence

XX Sequence 52 AA;

Query Match 96.0%; Score 72; DB 3; Length 52;

Best Local Similarity 93.8%; Pred. NO. 1.3e-05; Indels 0; Gaps 0;
 Matches 15; Conservative 1; Mismatches 0;

Qy 1 MEKVQYLTRSAIRRAS 16
 Db 1 MEKVQYLTRSAIRRAAN 16
 |||||

RESULT 15

ID ADE45168 standard; protein; 52 AA.

AC ADE45168;

DT 29-JAN-2004 (first entry)

DE Pig SERCA_2 inhibitor phospholamban.

XX Pig; SERCA_2; phospholamban; PLB;
 KW Ca2+ ATPase of the sarco/endoplasmic reticulum; protein co-ordinate data;
 KW cardiant.

XX Sus sp.

PN US6538022-B1.

PD 25-MAR-2003.

PF 18-FEB-1999; 99US-00252063.

PP 24-SEP-1997; 97US-00937117.

PR (ORIN) ORION CORP.

XX Pollesello P, Ovaska M, Tenhunen J, Vidgren J;
 PI Yliperttula-Ikonen M, Tilgmann C, Lotta T, Kaivola J;

XX WPI; 2004-019625/02.

XX New compound, useful for relieving inhibitory effects of phospholamban on
 PT cardiac SR Ca2+-ATPase by deactivating phospholamban and stimulating Ca2+
 PT -ATPase.

XX Claim 1; SEQ ID NO 2; 65pp; English.

XX The invention relates to a compound which deactivates, and exhibits
 CC affinity for, a phospholamban (PLB) protein (an inhibitor of SERCA_2,
 CC Ca2+ ATPase of the sarco/endoplasmic reticulum) appearing as ADE45167-

CC ADE45173. The compound has a structure containing three of the four
 CC moieties: an electronegative moiety associating with an S1 binding site
 CC of the phospholamban cytosolic domain when the compound is bound to it,
 CC the binding site comprises Tyr-6, Arg-9 and/or Arg-13; an electronegative
 CC moiety associating with an S2 binding site of the phospholamban cytosolic
 CC domain when the compound is bound to it, the S2 binding site comprises
 CC Arg-14; a hydrophobic moiety associating with an S3 binding site of the
 CC phospholamban cytosolic domain when the compound is bound, the binding
 CC site comprises Met-20, Lys-27 and/or Leu-28; and a hydrophobic moiety
 CC associating with an S4 binding site of the phospholamban cytosolic domain
 CC when the compound is bound, the binding site comprises Phe-32 and/or Phe-
 CC 35. The compound is not 3-benzyl-5,7-bis ((1H-tetrazol-5-yl)-methoxy)-4
 CC -methyl-2H-1-benzopyran-2-one. Also included are deactivating
 CC phospholamban, comprising administering the novel compound to stimulate
 CC the Ca 2+ -ATPase. The compound is useful for relieving the inhibitory
 CC effects of phospholamban on cardiac SERCA_2. The present sequence is a
 CC phospholamban.

XX Sequence 52 AA;

Query Match 96.0%; Score 72; DB 8; Length 52;

Best Local Similarity 93.8%; Pred. NO. 1.3e-05;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEKVQYLTRSAIRRAS 16

Db 1 MDKVQYLTRSAIRRAS 16
 |||||

RESULT 16

ID ADE45169 standard; protein; 52 AA.

AC ADE45169;

DT 29-JAN-2004 (first entry)

DE Dog SERCA_2 inhibitor phospholamban.

XX Dog; SERCA_2; phospholamban; PLB;
 KW Ca2+ ATPase of the sarco/endoplasmic reticulum; protein co-ordinate data;
 KW cardiant.

XX Canis sp.

PN US6538022-B1.

PD 25-MAR-2003.

PF 18-FEB-1999; 99US-00252063.

PP 24-SEP-1997; 97US-00937117.

PR (ORIN) ORION CORP.

XX Pollesello P, Ovaska M, Tenhunen J, Vidgren J;
 PI Yliperttula-Ikonen M, Tilgmann C, Lotta T, Kaivola J;

XX WPI; 2004-019625/02.

XX New compound, useful for relieving inhibitory effects of phospholamban on
 PT cardiac SR Ca2+-ATPase by deactivating phospholamban and stimulating Ca2+
 PT -ATPase.

XX Claim 1; SEQ ID NO 3; 65pp; English.

XX The invention relates to a compound which deactivates, and exhibits
 CC affinity for, a phospholamban (PLB) protein (an inhibitor of SERCA_2,
 CC Ca2+ ATPase of the sarco/endoplasmic reticulum) appearing as ADE45167-
 CC ADE45173. The compound has a structure containing three of the four
 CC moieties: an electronegative moiety associating with an S1 binding site
 CC of the phospholamban cytosolic domain when the compound is bound to it,
 CC the binding site comprises Tyr-6, Arg-9 and/or Arg-13; an electronegative

CC moiety associating with an S2 binding site of the phospholamban cytosolic
 CC domain when the compound is bound to it, the S2 binding site comprises
 CC Arg-14; a hydrophobic moiety associating with an S3 binding site of the
 CC phospholamban cytosolic domain when the compound is bound, the binding
 CC site comprises Met-20, Lys-27 and/or Leu-28; and a hydrophobic moiety
 CC associating with an S4 binding site of the phospholamban cytosolic domain
 CC when the compound is bound, the binding site comprises Phe-32 and/or Phe-
 CC 35. The compound is not 3-benzyl-5,7-bis ((1H-tetrazol-5-yl)-methoxy)-4-
 CC -methyl-2H-methyl-2H-1-benzopyran-2-one. Also included are deactivating
 CC phospholamban, comprising administering the novel compound to stimulate
 CC the Ca²⁺-ATPase. The compound is useful for relieving the inhibitory
 CC effects of phospholamban on cardiac SERCA₂. The present sequence is a
 CC phospholamban.
 CC
 XX Sequence 52 AA;

Query Match 96.0%; Score 72; DB 8; Length 52;
 Best Local Similarity 93.8%; Pred. No. 1.3e-05;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEKVQLTRSAIRRAS 16
 Db 1 MEKVQLTRSAIRRAS 16

RESULT 17
 AAY71014
 ID AAY71014 standard; peptide; 35 AA.

XX AAY71014;

XX 29-AUG-2000 (first entry)

XX Penetratin-based recombinant phospholamban peptide, TAT-mutant PLB.

XX Phospholamban; PLB; human; sarcoplasmic reticulum Ca²⁺ ATPase; SERCA2a;
 KW cardiant; cardiomyocyte; transport peptide; penetratin; cargo peptide;
 KW contractilin; cardiac contractility; inhibitor; cardiac disease; mutant;
 KW treatment; heart failure; myocardial dysfunction; recombinant protein;
 KW HIV; TAT protein.

XX Homo sapiens.
 OS Human immunodeficiency virus.

XX Key Location/Qualifiers

FT Region 5..15

FT /note= "Corresponds to denatured human immunodeficiency
 virus (HIV) TAT protein"

FT Region 16..35

FT /note= "Corresponds to mutant human phospholamban (PLB)

FT amino terminal peptide"

FT Misc-difference 31

FT /note= "Wild type Ser replaced with Glu"

XX WO200025804-A2.

XX 11-MAY-2000.

XX 02-NOV-1999; 99WO-US025692.

XX 02-NOV-1998; 98US-0106718P.

XX 27-JUL-1999; 99US-0145883P.

XX (REGC) UNIV CALIFORNIA.

XX Chien K, Dillman W, Minamisawa S, He H, Hoshijima M, Meyer M;

XX Scott C, Wang Y, Silverman GJ;

XX WPI; 2000-365393/31.

XX Treating cardiac diseases, e.g. heart failure or myocardial dysfunction
 FT comprises enhancing cardiac contractility by inhibiting interaction
 FT between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine

PT triphosphatase.

XX Example 5; Page 53; 56pp; English.

XX The patent discloses a method for the treatment of heart failure, using
 CC small peptide complexes and recombinant proteins, that induces
 CC phospholamban (PLB) deficiency and inhibits the interaction between PLB
 CC and sarcoplasmic reticulum Ca²⁺ ATPase (SERCA2a) within cardiomyocytes.
 CC The peptide complex comprises of transport peptide like penetratin and
 CC cargo peptide selected from mutant PLB, native PLB or antibody against
 CC PLB protein (contractilin). Penetratin-PLB peptide functions as a
 CC dominant negative inhibitor of PLB-SERCA2a interaction, enhances cardiac
 CC contractility and reduces blood pressure. This method is useful for the
 CC treatment of cardiac disease e.g. heart failure and myocardial
 CC dysfunction. The present sequence is the penetratin-based recombinant
 CC peptide TAT-mutant PLB, comprising the amino terminal end of human PLB
 CC immunodeficiency virus (HIV), TAT protein. Penetratin is a class of
 CC peptides, with translocating properties having the ability to carry
 CC hydrophilic compounds across the plasma membrane

XX Sequence 35 AA;

Query Match 94.7%; Score 71; DB 3; Length 35;

Best Local Similarity 100.0%; Pred. No. 1.3e-05;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEKVQLTRSAIRRA 15

Db 16 MEKVQLTRSAIRRA 30

RESULT 18

AAY71013

ID AAY71013 standard; peptide; 36 AA.

XX AAY71013;

XX 29-AUG-2000 (first entry)

XX Penetratin-based recombinant phospholamban peptide, mutant PLB-ANT.

XX Phospholamban; PLB; human; sarcoplasmic reticulum Ca²⁺ ATPase; SERCA2a;
 KW cardiant; cardiomyocyte; transport peptide; penetratin; cargo peptide;
 KW contractilin; cardiac contractility; inhibitor; cardiac disease; mutant;
 KW treatment; heart failure; myocardial dysfunction; recombinant protein;
 KW fruit fly; ANT; antennapedia.

XX Homo sapiens.

OS Drosophila sp.

XX Key Location/Qualifiers

FT Region 1..20

FT /note= "Corresponds to mutant human phospholamban (PLB)
 amino terminal peptide"

FT Misc-difference 16

FT /note= "Wild type Ser replaced with Glu"

FT Region 21..36

FT /note= "Corresponds to Drosophila antennapedia (ANT)
 transport peptide"

XX WO200025804-A2.

XX 11-MAY-2000.

XX 02-NOV-1999; 99WO-US025692.

XX 02-NOV-1998; 98US-0106718P.

XX 27-JUL-1999; 99US-0145883P.

XX (REGC) UNIV CALIFORNIA.

XX Chien K, Dillman W, Minamisawa S, He H, Hoshijima M, Meyer M;

PI Scott C, Wang Y, Silverman GJ;
 DR WPI; 2000-365393/31.
 XX
 PT Treating cardiac diseases, e.g. heart failure or myocardial dysfunction
 PT comprises enhancing cardiac contractility by inhibiting interaction
 PT between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine
 PT triphosphatase.
 XX
 PS Example 5; Page 53; 56pp; English.
 XX
 CC The patent discloses a method for the treatment of heart failure, using
 CC small peptide complexes and recombinant proteins, that induces
 CC phospholamban (PLB) deficiency and inhibits the interaction between PLB
 CC and sarcoplasmic reticulum Ca 2+ ATPase (SERCA2a) within cardiomyocytes.
 CC The peptide complex comprises of transport peptide like penetratin and
 CC cargo peptide selected from mutant PLB, native PLB or antibody against
 CC PLB protein (contractilin). Penetratin-PLB peptide functions as a
 CC dominant negative inhibitor of PLB-SERCA2a interaction, enhances cardiac
 CC contractility and reduces blood pressure. This method is useful for the
 CC treatment of cardiac disease e.g. heart failure and myocardial
 CC dysfunction. The present sequence is the penetratin-based recombinant
 CC peptide, mutant PLB-ANT, comprising the amino terminal end of human PLB
 CC mutant (Ser16Glu) protein, attached to the 5' end of the Drosophila
 CC antennapedia (ANT) transport peptide. Penetratin is a class of peptides,
 CC with translocating properties having the ability to carry hydrophilic
 CC compounds across the plasma membrane
 XX
 SQ Sequence 36 AA;
 Query Match 94.7%; Score 71; DB 3; Length 36;
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MEKVQVLTSAIRRA 15
 DB 1 MEKVQVLTSAIRRA 15
 RESULT 19
 ABB79404
 ID ABB79404 standard; peptide; 52 AA.
 AC ABB79404;
 XX
 DT 24-JUN-2002 (first entry)
 XX
 DE Human phospholamban pseudophosphorylation mutant S16E PLB.
 XX
 KW Human; phospholamban; PLB; cardiact; heart disease; gene therapy;
 KW cardiac function; mutant; mutain.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 16 /note= "Wildtype Ser substituted by Glu"
 XX
 PN US2002032167-A1.
 XX
 PD 14-MAR-2002.
 XX
 PF 11-SEP-2001; 2001US-00954571.
 XX
 PR 11-SEP-2000; 2000US-0231821P.
 XX
 PA (CHIE//) CHIEN K R.
 PA (HOSH//) HOSHIMA M.
 PA (ROSS//) ROSS J.
 PA (IKED//) IKEDA Y.
 XX
 PI Chien KR, Hoshijma M, Ross J, Ikeda Y;
 XX

DR WPI; 2002-361185/39.
 XX
 PT Delivering a dose of a gene expression cassette in a fluid selectively to
 PT heart for sustained expression, useful for improving or enhancing cardiac
 PT function, by employing a viral vector together with a vascular
 PT permeabilizing agent.
 XX
 PS Example 6; Fig 1; 12pp; English.
 XX
 CC The invention relates to delivering a therapeutic dose of a gene
 CC expression cassette in a fluid selectively to heart for sustained
 CC expression, comprising employing a viral vector together with a vascular
 CC permeabilising agent. The method is useful for gene therapy delivering
 CC genes for improving or enhancing cardiac function, particularly in
 CC hamster models of heart disease. The present sequence is that of a
 CC pseudophosphorylation mutant of phospholamban (S16EPLEB). This point
 CC mutant is among a number of dominant negative mutants identified and
 CC characterised in WO00/25804 and used in the method of the present
 CC invention
 XX
 SQ Sequence 52 AA;
 Query Match 94.7%; Score 71; DB 5; Length 52;
 Best Local Similarity 100.0%; Pred. No. 2e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MEKVQVLTSAIRRA 15
 DB 1 MEKVQVLTSAIRRA 15
 RESULT 20
 ADE45173
 ID ADE45173 standard; protein; 52 AA.
 AC ADE45173;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Chicken SERCA_2 inhibitor phospholamban.
 XX
 KW Chicken; SERCA_2; phospholamban; PLB;
 KW Ca2+ ATPase of the sarco/endoplasmic reticulum; protein co-ordinate data;
 KW cardiant.
 XX
 OS Gallus sp.
 XX
 PN US6538022-B1.
 XX
 PD 25-MAR-2003.
 XX
 PF 18-FEB-1999; 99US-00252063.
 XX
 PR 24-SEP-1997; 97US-00937117.
 XX
 PA (ORIN) ORION CORP.
 XX
 PI Pollesello P, Ovaska M, Tenhunen J, Völgren J;
 PI Yliperttula-Ikonen M, Tilgmann C, Lotta T, Kaivola J;
 XX
 DR WPI; 2004-019625/02.
 XX
 PT New compound, useful for relieving inhibitory effects of phospholamban on
 PT cardiac SR Ca2+-ATPase by deactivating phospholamban and stimulating Ca2+
 PT -ATPase.
 XX
 FS Claim 1; SEQ ID NO 7; 65pp; English.
 XX
 CC The invention relates to a compound which deactivates, and exhibits
 CC affinity for, a phospholamban (PLB) protein (an inhibitor of SERCA 2,
 CC Ca2+ ATPase of the sarco/endoplasmic reticulum) appearing as ADE45167-
 CC ADE45173. The compound has a structure containing three of the four
 CC moieties: an electronegative moiety associating with an SI binding site

CC of the phospholamban cytosolic domain when the compound is bound to it,
 CC the binding site comprises Tyr-6, Arg-9 and/or Arg-13; an electronegative
 CC moiety associating with an S2 binding site of the phospholamban cytosolic
 CC domain when the compound is bound to it, the S2 binding site comprises
 CC Arg-14; a hydrophobic moiety associating with an S3 binding site of the
 CC phospholamban cytosolic domain when the compound is bound, the binding
 CC site comprises Met-20, Lys-27 and/or Leu-28; and a hydrophobic moiety
 CC associating with an S4 binding site of the phospholamban cytosolic domain
 CC when the compound is bound, the binding site comprises Phe-32 and/or Phe-
 CC 35. The compound is not 3-benzyl-5,7-bis ((1H-tetrazol-5-yl)-methoxy)-4-
 CC -methyl-2H-methyl-2H-1-benzopyran-2-one. Also included are deactivating
 CC phospholamban, comprising administering the novel compound to stimulate
 CC the Ca²⁺ - ATPase. The compound is useful for relieving the inhibitory
 CC effects of phospholamban on cardiac SERCA₂. The present sequence is a
 CC phospholamban.
 CC
 SQ Sequence 52 AA;

Query Match 94.7%; Score 71; DB 8; Length 52;
 Best Local Similarity 87.5%; Pred. No. 28-05;
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MEKVQYLTRSAIRRAS 16
 |||||:||||:
 Db 1 MEKVQYLTRSAIRRAS 16

RESULT 21
 AAY71018
 ID AAY71018 standard; protein; 79 AA.

XX AC AAY71018;
 XX DT 29-AUG-2000 (first entry)
 XX DE H6 tagged penetratin-based recombinant protein, H6-(S16E)mutantPLB-ANT.
 XX KW Phospholamban; PLB; human; sarcoplasmic reticulum Ca²⁺ ATPase; SERCA2a;
 KW cardiant; cardiomyocyte; transport peptide; penetratin; cargo peptide;
 KW contractilin; cardiac contractility; inhibitor; cardiac disease; mutant;
 KW treatment; heart failure; myocardial dysfunction; recombinant protein;
 KW fruit fly; ANT; antennapedia; H6 tag; hexahistidine.
 XX OS Homo sapiens.
 OS Drosophila sp.
 OS Synthetic.

XX FH Key Location/Qualifiers
 FT Region 1..52
 FT /notes= "Corresponds to mutant human phospholamban (PLB)
 protein"
 FT Misc-difference 16
 FT /notes= "Wild type Ser replaced with Glu"
 FT Region 53..58
 FT /notes= "Corresponds to hexahistidine tag (H6)"
 FT Region 63..78
 FT /notes= "Corresponds to Drosophila antennapedia (ANT)
 transport peptide"

XX PN WC2000025804-A2.
 XX PD 11-MAY-2000.
 XX PF 02-NOV-1999; 99WO-US025692.
 XX PR 02-NOV-1998; 98US-0106718P.
 XX PR 27-JUL-1999; 99US-0145883P.
 XX PA (REGC) UNIV CALIFORNIA.
 XX PI Chien K, Dillman W, Minamisawa S, He H, Hoshijima M, Meyer M;
 PI Scott C, Wang Y, Silverman GJ;
 XX WPI; 2000-365393/31.

DR WPI; 2000-365393/31.
 XX Treating cardiac diseases, e.g. heart failure or myocardial dysfunction
 PT comprises enhancing cardiac contractility by inhibiting interaction
 PT between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine
 PT triphosphatase.
 XX Example 6; Page 55; 56pp; English.
 PS
 CC The patent discloses a method for the treatment of heart failure, using
 CC small peptide complexes and recombinant proteins, that induces
 CC phospholamban (PLB) deficiency and inhibits the interaction between PLB
 CC and sarcoplasmic reticulum Ca²⁺ ATPase (SERCA2a) within cardiomyocytes.
 CC The peptide complex comprises of transport peptide like penetratin and
 CC cargo peptide selected from mutant PLB, native PLB or antibody against
 CC PLB protein (contractilin). Penetratin-PLB peptide functions as a
 CC dominant negative inhibitor of PLB-SERCA2a interaction, enhances cardiac
 CC contractility and reduces blood pressure. This method is useful for the
 CC treatment of cardiac disease e.g. heart failure and myocardial
 CC dysfunction. The present sequence is the hexahistidine (H6) tagged
 CC penetratin-based recombinant protein H6-mutantPLB-ANT, comprising the
 CC human mutant (Ser16Glu) PLB protein and Drosophila antennapedia (ANT)
 CC transport peptide attached by a hexahistidine tag. This sequence is
 CC expressed in Escherichia coli cells
 XX
 SQ Sequence 79 AA;

Query Match 94.7%; Score 71; DB 3; Length 79;
 Best Local Similarity 100.0%; Pred. No. 3.1e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MEKVQYLTRSAIRRA 15
 |||||:||||:
 Db 1 MEKVQYLTRSAIRRA 15

RESULT 22
 AAY71005
 ID AAY71005 standard; protein; 52 AA.

XX AC AAY71005;
 XX DT 29-AUG-2000 (first entry)
 XX DE Human mutant phospholamban (PLB) R14E protein.
 XX KW Phospholamban; PLB; human; sarcoplasmic reticulum Ca²⁺ ATPase; SERCA2a;
 KW cardiant; cardiomyocyte; transport peptide; penetratin; cargo peptide;
 KW contractilin; cardiac contractility; inhibitor; cardiac disease;
 KW treatment; heart failure; myocardial dysfunction; mutant.
 XX OS Homo sapiens.
 OS Synthetic.
 XX FH Key Location/Qualifiers
 FT Misc-difference 14
 FT /note= "Wild type Arg replaced with Glu"
 XX PN WO2000025804-A2.
 XX PD 11-MAY-2000.
 XX PF 02-NOV-1999; 99WO-US025692.
 XX PR 02-NOV-1998; 98US-0106718P.
 XX PR 27-JUL-1999; 99US-0145883P.
 XX PA (REGC) UNIV CALIFORNIA.
 XX PI Chien K, Dillman W, Minamisawa S, He H, Hoshijima M, Meyer M;
 PI Scott C, Wang Y, Silverman GJ;
 XX WPI; 2000-365393/31.

XX Treating cardiac diseases, e.g. heart failure or myocardial dysfunction
 PT comprises enhancing cardiac contractility by inhibiting interaction
 PT between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine
 PT triphosphatase.

XX Disclosure; Page 48-49; 56pp; English.

XX The patent discloses a method for the treatment of heart failure, using
 CC small peptide complexes and recombinant proteins, that induces
 CC phospholamban (PLB) deficiency and inhibits the interaction between PLB
 CC and sarcoplasmic reticulum Ca 2+ ATPase (SERCA2a) within cardiomyocytes.
 CC The peptide complex comprises of transport peptide like penetratin and
 CC cargo peptide selected from mutant PLB, native PLB or antibody against
 CC PLB protein (contractilin). Penetratin-PLB peptide functions as a
 CC dominant negative inhibitor of PLB-SERCA2a interaction, enhances cardiac
 CC contractility and reduces blood pressure. This method is useful for the
 CC treatment of cardiac disease e.g. heart failure and myocardial
 CC dysfunction. The present amino acid sequence is the human mutant PLB
 CC protein, comprising a sense mutation Arg14Glu. This mutant sequence when
 CC overexpressed in the transformed cardiomyocytes, shows increased
 CC contractility than the wild type PLB sequence

XX Sequence 52 AA;

Query Match 93.3%; Score 70; DB 3; Length 52;
 Best Local Similarity 93.8%; Pred. No. 3e-05;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MEKVQVLTSAIRRAS 16
 |||||
 Db 1 MEKVQVLTSAIRRAS 16

RESULT 23

AAAY71004
 ID AAY71004 standard; protein; 52 AA.

XX AC AAY71004;

XX DT 29-AUG-2000 (first entry)

XX DE Human mutant phospholamban (PLB) E2A protein.

XX Phospholamban; PLB; human; sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a;
 KW cardiant; cardiomyocyte; transport peptide; penetratin; cargo peptide;
 KW contractilin; cardiac contractility; inhibitor; cardiac disease;
 KW treatment; heart failure; myocardial dysfunction; mutant.

XX Homo sapiens.
 OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 2 /note= "Wild type Glu replaced with Ala"

XX WO200025804-A2.

XX PD 11-MAY-2000.

XX PF 02-NOV-1999; 99WO-US025692.

XX PR 02-NOV-1998; 98US-0106718P.

XX PR 27-JUL-1999; 99US-0145883P.

XX (REGC) UNIV CALIFORNIA.

XX Chien K, Dillman W, Minamisawa S, He H, Hoshijima M, Meyer M;

PI Scott C, Wang Y, Silverman GJ;

XX WPI; 2000-365393/31.

XX Treating cardiac diseases, e.g. heart failure or myocardial dysfunction

PT comprises enhancing cardiac contractility by inhibiting interaction
 PT between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine
 PT triphosphatase.

XX Disclosure; Page 48; 56pp; English.

XX The patent discloses a method for the treatment of heart failure, using
 CC small peptide complexes and recombinant proteins, that induces
 CC phospholamban (PLB) deficiency and inhibits the interaction between PLB
 CC and sarcoplasmic reticulum Ca 2+ ATPase (SERCA2a) within cardiomyocytes.
 CC The peptide complex comprises of transport peptide like penetratin and
 CC cargo peptide selected from mutant PLB, native PLB or antibody against
 CC PLB protein (contractilin). Penetratin-PLB peptide functions as a
 CC dominant negative inhibitor of PLB-SERCA2a interaction, enhances cardiac
 CC contractility and reduces blood pressure. This method is useful for the
 CC treatment of cardiac disease e.g. heart failure and myocardial
 CC dysfunction. The present amino acid sequence is the human mutant PLB
 CC protein, comprising the mutation Glu2Ala. This mutant sequence when
 CC overexpressed in the transformed cardiomyocytes, shows increased
 CC contractility than the wild type PLB sequence

XX Sequence 52 AA;

Query Match 92.0%; Score 69; DB 3; Length 52;
 Best Local Similarity 93.8%; Pred. No. 4.6e-05;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MEKVQVLTSAIRRAS 16

Db 1 MAKVQVLTSAIRRAS 16

RESULT 24

AAAY71007

ID AAY71007 standard; protein; 52 AA.

XX AC AAY71007;

XX DT 29-AUG-2000 (first entry)

XX DE Human mutant phospholamban (PLB) K3E/R14E protein.

XX Phospholamban; PLB; human; sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a;
 KW cardiant; cardiomyocyte; transport peptide; penetratin; cargo peptide;
 KW contractilin; cardiac contractility; inhibitor; cardiac disease;
 KW treatment; heart failure; myocardial dysfunction; mutant.

XX Homo sapiens.
 OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 3 /note= "Wild type Lys replaced with Glu"

FT Misc-difference 14 /note= "Wild type Arg replaced with Glu"

XX WO200025804-A2.

XX PD 11-MAY-2000.

XX PF 02-NOV-1999; 99WO-US025692.

XX PR 02-NOV-1998; 98US-0106718P.

XX PR 27-JUL-1999; 99US-0145883P.

XX (REGC) UNIV CALIFORNIA.

XX Chien K, Dillman W, Minamisawa S, He H, Hoshijima M, Meyer M;

PI Scott C, Wang Y, Silverman GJ;

XX WPI; 2000-365393/31.

XX Treating cardiac diseases, e.g. heart failure or myocardial dysfunction

PT comprises enhancing cardiac contractility by inhibiting interaction
PT between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine
PT triphosphatase.
XX
PS Disclosure; Page 49; 56pp; English.
XX
XX The patent discloses a method for the treatment of heart failure, using
CC small peptide complexes and recombinant proteins, that induces
CC phospholamban (PLB) deficiency and inhibits the interaction between PLB
CC and sarcoplasmic reticulum Ca 2+ ATPase (SERCA2a) within cardiomyocytes.
CC The peptide complex comprises of transport peptide like penetratin and
CC cargo peptide selected from mutant PLB, native PLB or antibody against
CC PLB protein (constrictin). Penetratin-PLB peptide functions as a
CC dominant negative inhibitor of PLB-SERCA2a interaction, enhances cardiac
CC contractility and reduces blood pressure. This method is useful for the
CC treatment of cardiac disease e.g. heart failure and myocardial
CC dysfunction. The present amino acid sequence is the human mutant PLB
CC protein, comprising the double mutation Lys3Glu and Arg15Glu. This mutant
CC sequence, when overexpressed in the transformed cardiomyocytes, shows
CC increased contractility than the wild type PLB sequence
XX
SQ Sequence 52 AA;
Query Match 88.0%; Score 66; DB 3; Length 52;
Best Local Similarity 87.5%; Pred. No. 0.00016;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MEKVQYLTSAIRRAS 16
DB 1 MEKVQYLTSAIRRAS 16
RESULT 25
ADC87928
ID ADC87928 standard; protein; 116 AA.
XX
AC ADC87928;
XX
DT 01-JAN-2004 (first entry)
XX
DE Ribosomal protein similar to FCWP1 #144.
XX
KW Antifungal protein; ribosomal protein; FCWP1; ALVAFP;
KW plant fungal infection; Alternaria; Ascochyta; Botrytis; Cercospora;
KW Colletotrichum; Diplodia; Fusarium; Gaemanomyces; Helminthosporium;
KW Macrophomina; Mycosphaerella; Nectria; Peronospora; Phoma;
KW Phymatotrichum; Phytophthora; Plasmodia; Podosphaera; Puccinia; Puthium;
KW Pyrenophora; Pyricularia; Pythium; Rhizoctonia; Sclerotinia; Sclerotium;
KW Septoria; Thielaviopsis; Venturia; Verticillium.
XX
OS Unidentified.
XX
PN US6573361-B1.
XX
PD 03-JUN-2003.
XX
PF 07-DEC-2000; 2000US-00732210.
XX
PR 07-DEC-1999; 99US-0169340F.
PR 07-DEC-1999; 99US-0169513P.
XX
PA (MONS) MONSANTO TECHNOLOGY LLC.
XX
PI Bunkers GJ, Liang J, Mittanck CA, Seale JW, Wu YS;
XX
DR WPI; 2003-754558/71.
XX
PT Novel antifungal protein FCWP1, isolated from Fusarium culmorum, useful
PT for controlling fungal infections in plants.
XX
PS Example 21; SEQ ID NO 181; 27pp; English.
XX
XX The invention relates to an isolated antifungal ribosomal protein from

CC fusarium culmorum, FCWP1. Also included is a fusion protein between the
CC signal peptide of the antifungal protein ALVAFP from Alysum and FCWP1,
CC encoded by the nucleic acid appearing as ADC87759. The FCWP1 proteins are
CC useful for controlling fungal infections in plants, such as those caused
CC by Alternaria (e.g. Alternaria brassicola, Alternaria solani),
CC Ascochyta (e.g. Ascochyta pisi); Botrytis (e.g. Botrytis cinerea),
CC Cercospora (e.g. Cercospora kikuchii, Cercospora zea-maydis),
CC Colletotrichum (e.g. Colletotrichum lindemuthianum), Diplodia (e.g.
CC Diplodia maydis), Fusarium (e.g. Fusarium nivale, Fusarium oxysporum,
CC Fusarium graminearum, Fusarium culmorum, Fusarium solani, Fusarium
CC moniliforme, Fusarium roseum), Gaemanomyces (e.g. Gaemanomyces
CC graminis f.sp. tritici), Helminthosporium (e.g. Helminthosporium turicum
CC (e.g. Macrophomina phaseolina, Maganaporthe grisea), Mycosphaerella
CC (e.g. Mycosphaerella figiensis), Nectria (Nectria reamotococca),
CC Peronospora (e.g. Peronospora manshurica, Peronospora tabacina), Phoma
CC (e.g. Phoma betae), Phymatotrichum (e.g. Phymatotrichum omnivorum),
CC Phytophthora (e.g. Phytophthora cinnamomi, Phytophthora cactorum,
CC Phytophthora phaseoli, Phytophthora parasitica, Phytophthora
CC citrophthora), Phytophthora megasperma f.sp. sojae, Phytophthora
CC infestans), Plasmodia (e.g. Plasmodia viticola), Podosphaera (e.g.
CC striformis, Puccinia graminis f.sp. tritici, Puccinia asparagi,
CC Puccinia recondita, Puccinia arachidis), Puthium (e.g. Puthium
CC aphanidermatum), Pyrenophora (e.g. Pyrenophora tritici-repentens),
CC Pyricularia (e.g. Pyricularia oryzae), Pythium (e.g. Pythium ultimum),
CC Rhizoctonia (e.g. Rhizoctonia solani, Rhizoctonia cerealis), Sclerotium
CC (e.g. Sclerotium rolfsii), Sclerotinia (e.g. Sclerotinia sclerotiorum),
CC Septoria (e.g. Septoria lycopersici, Septoria tritici), Stagonospora
CC nodorum / Phaeosphaeria nodorum, Septoria tritici, Thielaviopsis (e.g.
CC Thielaviopsis basicola), Uncinula (e.g. Uncinula necator), Venturia
CC (e.g. Venturia inaequalis) or Verticillium (e.g. Verticillium dahliae,
CC Verticillium albo-atrum). Mutations in the proteolytic consensus
CC sequences contained within FCWP1 provides improved stability of its
CC antifungal activity. Also disclosed are ribosomal proteins with similar
CC PI (>7) and molecular weight (<20kDa) to FCWP1, which may act as
CC antifungal proteins. The present sequence represents one of the ribosomal
CC proteins similar to FCWP1. Note: the sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=6573361B1.
XX
SQ Sequence 116 AA;

Query Match 54.7%; Score 41; DB 7; Length 116;
Best Local Similarity 45.7%; Pred. No. 14;
Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 MEKVQYLTSAIRRA 15
DB 81 VEXIELVTRGDVRA 95

Search completed: October 1, 2004, 12:13:15
Job time : 71.2 secs

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OM protein - protein search, using sw model

Run on: October 1, 2004, 12:07:51 ; Search time 17 Seconds
(without alignments)
48.589 Million cell updates/sec

Title: US-09-830-779-8

Perfect score: 75

Sequence: 1 MEKVQLRESAIRRAS 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

Issued Patents AA.*
1: /cgn2_6/ptodata/2/aa/5A.COMB.pdp.*
2: /cgn2_6/ptodata/2/aa/5B.COMB.pdp.*
3: /cgn2_6/ptodata/2/aa/6A.COMB.pdp.*
4: /cgn2_6/ptodata/2/aa/6B.COMB.pdp.*
5: /cgn2_6/ptodata/2/aa/PCITUS.COMB.pdp.*
6: /cgn2_6/ptodata/2/aa/backfiles1.pdp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	75	100.0	36	4	US-09-252-063-9
2	75	100.0	52	4	US-09-252-063-1
3	75	100.0	52	4	US-09-252-063-4
4	75	100.0	52	4	US-09-252-063-5
5	75	100.0	52	4	US-09-252-063-6
6	75	100.0	52	4	US-09-549-872B-15
7	72	96.0	52	4	US-09-252-063-2
8	72	96.0	52	4	US-09-252-063-3
9	72	96.0	52	4	US-09-549-872B-14
10	71	94.7	52	4	US-09-252-063-7
11	41	54.7	116	4	US-09-732-210-181
12	37	49.3	631	4	US-09-252-991A-18000
13	36	48.0	98	4	US-09-489-039A-7319
14	36	48.0	194	4	US-09-489-039A-11071
15	36	48.0	686	4	US-09-252-991A-19332
16	36	48.0	765	4	US-09-252-991A-24791
17	36	48.0	924	2	US-08-588-983-18
18	36	48.0	924	2	US-08-588-976-18
19	35	46.7	210	4	US-09-252-991A-28362
20	35	46.7	211	4	US-09-134-001C-5136
21	35	46.7	216	4	US-09-134-001C-6395
22	35	46.7	357	4	US-09-910-174B-14
23	35	46.7	357	4	US-09-620-461-14
24	35	46.7	437	4	US-09-277-262-4
25	35	46.7	516	4	US-09-277-262-2
26	34.5	46.0	835	2	US-08-968-751-4
27	34.5	46.0	864	4	US-09-323-872A-28
28	34.5	46.0	864	4	US-09-323-872A-28
29	34	45.3	230	4	US-09-540-236-2466
30	34	45.3	238	4	US-09-107-532A-5165
31	34	45.3	310	4	US-09-107-532A-5580
32	34	45.3	331	4	US-09-328-352-5369
33	33.5	44.7	53	4	US-09-673-355A-511
34	33	44.0	24	4	US-08-561-450E-3
35	33	44.0	50	6	5169933-31
36	33	44.0	71	4	US-09-489-039A-9691
37	33	44.0	104	4	US-09-134-001C-4945
38	33	44.0	172	4	US-09-252-991A-24148
39	33	44.0	180	4	US-09-252-991A-18799
40	33	44.0	235	4	US-09-198-452A-752
41	33	44.0	276	2	US-08-713-072C-4
42	33	44.0	297	4	US-09-252-991A-16808
43	33	44.0	313	3	US-09-413-814-9
44	33	44.0	320	4	US-09-543-681A-6146
45	33	44.0	327	6	5171684-6
46	33	44.0	350	4	US-08-637-670-39
47	33	44.0	373	4	US-09-328-352-5753
48	33	44.0	374	4	US-09-679-279-6
49	33	44.0	409	4	US-09-533-029-104
50	33	44.0	495	4	US-09-107-532A-3679
51	33	44.0	573	4	US-09-328-352-6420
52	33	44.0	612	4	US-09-489-039A-10702
53	33	44.0	787	4	US-09-489-039A-7628
54	33	44.0	804	4	US-09-107-532A-6348
55	33	44.0	807	4	US-09-252-991A-18831
56	33	44.0	972	3	US-08-335-844A-24
57	33	44.0	972	4	US-09-129-366-24
58	33	44.0	1124	4	US-09-191-786-1
59	32	42.7	100	4	US-09-732-210-1175
60	32	42.7	113	4	US-09-732-210-681
61	32	42.7	139	4	US-08-065-844A-8
62	32	42.7	169	4	US-09-252-991A-32083
63	32	42.7	213	4	US-09-328-352-6122
64	32	42.7	390	1	US-07-669-171-2
65	32	42.7	390	1	US-08-132-405-1
66	32	42.7	390	1	US-08-395-939A-1
67	32	42.7	390	5	PCT-US91-01861-1
68	32	42.7	390	5	5168051-2
69	32	42.7	394	5	PCT-US94-03705-5
70	32	42.7	412	4	US-09-252-991A-28034
71	32	42.7	420	4	US-09-134-001C-3805
72	32	42.7	443	4	US-09-328-352-7207
73	32	42.7	457	3	US-09-416-213-2
74	32	42.7	457	4	US-09-416-214-2
75	32	42.7	457	4	US-09-035-676-2
76	32	42.7	483	4	US-09-252-991A-31365
77	32	42.7	571	4	US-09-489-039A-14334
78	32	42.7	589	4	US-09-328-352-7592
79	32	42.7	604	4	US-09-391-104-30
80	32	42.7	604	3	US-09-000-041A-2
81	32	42.7	607	3	US-09-211-704A-10
82	32	42.7	622	4	US-09-252-991A-19802
83	32	42.7	664	2	US-08-426-125-7
84	32	42.7	664	2	US-08-455-355-7
85	32	42.7	664	4	US-09-367-512-6
86	32	42.7	667	2	US-08-426-125-6
87	32	42.7	667	2	US-08-455-355-6
88	32	42.7	667	4	US-09-367-512-5
89	32	42.7	682	4	US-09-252-991A-31275
90	32	42.7	784	4	US-09-252-991A-20416
91	32	42.7	812	4	US-09-198-452A-978
92	32	42.7	978	2	US-08-415-593-43
93	32	42.7	1044	4	US-09-252-991A-22493
94	32	42.7	1154	4	US-09-489-039A-7724
95	32	42.7	1799	4	US-09-134-000C-5178
96	32	42.7	2568	4	US-09-866-108A-3
97	31.5	42.0	343	4	US-09-489-039A-10330
98	31.5	42.0	1729	4	US-09-553-690-2
99	31	41.3	36	1	US-08-487-890A-29
100	31	41.3	36	2	US-08-478-435-29

Sequence 16, Appl
Sequence 2466, Ap
Sequence 5165, Ap
Sequence 5580, Ap
Sequence 5369, Ap
Sequence 511, Appl
Sequence 3, Appl
Patent No. 5169933
Sequence 9691, Ap
Sequence 4945, Ap
Sequence 24148, A
Sequence 18799, A
Sequence 752, Appl
Sequence 4, Appl
Sequence 16808, A
Sequence 9, Appl
Sequence 6146, Ap
Patent No. 5171684
Sequence 39, Appl
Sequence 5753, Ap
Sequence 6, Appl
Sequence 104, Appl
Sequence 3679, Ap
Sequence 6420, Ap
Sequence 10702, A
Sequence 7628, Ap
Sequence 6348, Ap
Sequence 18831, A
Sequence 24, Appl
Sequence 24, Appl
Sequence 1, Appl
Sequence 1175, Ap
Sequence 681, Appl
Sequence 8, Appl
Sequence 32083, A
Sequence 6122, Ap
Sequence 2, Appl
Sequence 1, Appl
Sequence 1, Appl
Patent No. 5168051
Sequence 5, Appl
Sequence 28034, A
Sequence 3805, Ap
Sequence 7207, Ap
Sequence 2, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 14334, A
Sequence 7592, Ap
Sequence 30, Appl
Sequence 2, Appl
Sequence 10, Appl
Sequence 18802, A
Sequence 7, Appl
Sequence 7, Appl
Sequence 6, Appl
Sequence 6, Appl
Sequence 5, Appl
Sequence 31275, A
Sequence 20416, A
Sequence 43, Appl
Sequence 22493, A
Sequence 7724, Ap
Sequence 5178, Ap
Sequence 10330, A
Sequence 2, Appl
Sequence 29, Appl
Sequence 29, Appl

ALIGNMENTS

RESULT 1
 US-09-252-063-9
 ; Sequence 9, Application US/09252063
 ; Patent No. 6538022
 ; GENERAL INFORMATION:
 ; APPLICANT: Pollesello, Piero
 ; APPLICANT: Ovaska, Martti
 ; APPLICANT: Tenhunen, Jukka
 ; APPLICANT: Vidgren, Jukka
 ; APPLICANT: Yliperttula-Ikonen, Marjo
 ; APPLICANT: Tilgmann, Carola
 ; APPLICANT: Lotta, Timo
 ; APPLICANT: Kaivola, Juha
 ; TITLE OF INVENTION: Compounds for Deactivating Phospholamban Function on
 ; FILE REFERENCE: 1102.0250001
 ; CURRENT APPLICATION NUMBER: US/09/252,063
 ; EARLIER FILING DATE: 1999-02-18
 ; EARLIER FILING DATE: 08/937,117
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 9
 ; LENGTH: 36
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: cystolic part
 ; OTHER INFORMATION: of phospholamban peptide
 US-09-252-063-9

Query Match 100.0%; Score 75; DB 4; Length 36;
 Best Local Similarity 100.0%; Pred. No. 2e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRAS 16
 |||||
 Db 1 MEKVQYLTRSAIRRAS 16
 |||||
 RESULT 2
 US-09-252-063-1
 ; Sequence 1, Application US/09252063
 ; Patent No. 6538022
 ; GENERAL INFORMATION:
 ; APPLICANT: Pollesello, Piero
 ; APPLICANT: Ovaska, Martti
 ; APPLICANT: Tenhunen, Jukka
 ; APPLICANT: Vidgren, Jukka
 ; APPLICANT: Yliperttula-Ikonen, Marjo
 ; APPLICANT: Tilgmann, Carola
 ; APPLICANT: Lotta, Timo
 ; APPLICANT: Kaivola, Juha
 ; TITLE OF INVENTION: Compounds for Deactivating Phospholamban Function on
 ; FILE REFERENCE: 1102.0250001
 ; CURRENT APPLICATION NUMBER: US/09/252,063
 ; EARLIER FILING DATE: 1999-02-18
 ; EARLIER FILING DATE: 08/937,117
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 1
 ; LENGTH: 52
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-252-063-1

Query Match 100.0%; Score 75; DB 4; Length 52;
 Best Local Similarity 100.0%; Pred. No. 3e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRAS 16
 |||||
 Db 1 MEKVQYLTRSAIRRAS 16
 |||||
 RESULT 3
 US-09-252-063-4
 ; Sequence 4, Application US/09252063
 ; Patent No. 6538022
 ; GENERAL INFORMATION:
 ; APPLICANT: Pollesello, Piero
 ; APPLICANT: Ovaska, Martti
 ; APPLICANT: Tenhunen, Jukka
 ; APPLICANT: Vidgren, Jukka
 ; APPLICANT: Yliperttula-Ikonen, Marjo
 ; APPLICANT: Tilgmann, Carola
 ; APPLICANT: Lotta, Timo
 ; APPLICANT: Kaivola, Juha
 ; TITLE OF INVENTION: Compounds for Deactivating Phospholamban Function on
 ; FILE REFERENCE: 1102.0250001
 ; CURRENT APPLICATION NUMBER: US/09/252,063
 ; EARLIER FILING DATE: 1999-02-18
 ; EARLIER FILING DATE: 08/937,117
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 4
 ; LENGTH: 52
 ; TYPE: PRT
 ; ORGANISM: Oryctolagus cuniculus
 US-09-252-063-4

Query Match 100.0%; Score 75; DB 4; Length 52;
 Best Local Similarity 100.0%; Pred. No. 3e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRAS 16
 |||||
 Db 1 MEKVQYLTRSAIRRAS 16
 |||||
 RESULT 4
 US-09-252-063-5
 ; Sequence 5, Application US/09252063
 ; Patent No. 6538022
 ; GENERAL INFORMATION:
 ; APPLICANT: Pollesello, Piero
 ; APPLICANT: Ovaska, Martti
 ; APPLICANT: Tenhunen, Jukka
 ; APPLICANT: Vidgren, Jukka
 ; APPLICANT: Yliperttula-Ikonen, Marjo
 ; APPLICANT: Tilgmann, Carola
 ; APPLICANT: Lotta, Timo
 ; APPLICANT: Kaivola, Juha
 ; TITLE OF INVENTION: Compounds for Deactivating Phospholamban Function on
 ; FILE REFERENCE: 1102.0250001
 ; CURRENT APPLICATION NUMBER: US/09/252,063
 ; EARLIER FILING DATE: 1999-02-18
 ; EARLIER FILING DATE: 08/937,117
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 5
 ; LENGTH: 52
 ; TYPE: PRT
 ; ORGANISM: Rattus sp.
 US-09-252-063-5

Query Match 100.0%; Score 75; DB 4; Length 52;
Best Local Similarity 100.0%; Pred. No. 3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVOYLTRSAIRRAS 16
| | | | | | | | | | | | | | | |
DB 1 MEKVOYLTRSAIRRAS 16

RESULT 5
US-09-252-063-6
; Sequence 6, Application US/09252063
; Patent No. 6538022
; GENERAL INFORMATION:
; APPLICANT: Pollesello, Piero
; APPLICANT: Ovaska, Martti
; APPLICANT: Tenhunen, Jukka
; APPLICANT: Vidgren, Jukka
; APPLICANT: Yliperttula-Ikonen, Marjo
; APPLICANT: Tilgmann, Carola
; APPLICANT: Lotta, Timo
; APPLICANT: Kaivola, Juha
; TITLE OF INVENTION: Compounds for Deactivating Phospholamban Function on
; FILE REFERENCE: 1102.0250001
; CURRENT APPLICATION NUMBER: US/09/252,063
; PRIOR FILING DATE: 1999-02-18
; EARLIER FILING DATE: 1997-09-24
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-252-063-6

Query Match 100.0%; Score 75; DB 4; Length 52;
Best Local Similarity 100.0%; Pred. No. 3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVOYLTRSAIRRAS 16
| | | | | | | | | | | | | | | |
DB 1 MEKVOYLTRSAIRRAS 16

RESULT 6
US-09-549-872B-15
; Sequence 15, Application US/09549872B
; Patent No. 6540996
; GENERAL INFORMATION:
; APPLICANT: Zwaal, Richard
; APPLICANT: Groenen, Jose
; APPLICANT: Bogaert, Thierry
; TITLE OF INVENTION: COMPOUND SCREENING METHODS
; FILE REFERENCE: D00590/70008 (JRV/RE)
; CURRENT APPLICATION NUMBER: US/09/549,872B
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: GB 9908670.4
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: US 60/129,596
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: GB 9912736.7
; PRIOR FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-549-872B-15

Query Match 100.0%; Score 75; DB 4; Length 52;
Best Local Similarity 100.0%; Pred. No. 3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVOYLTRSAIRRAS 16
| | | | | | | | | | | | | | | |
DB 1 MEKVOYLTRSAIRRAS 16

RESULT 7
US-09-252-063-2
; Sequence 2, Application US/09252063
; Patent No. 6538022
; GENERAL INFORMATION:
; APPLICANT: Pollesello, Piero
; APPLICANT: Ovaska, Martti
; APPLICANT: Tenhunen, Jukka
; APPLICANT: Vidgren, Jukka
; APPLICANT: Yliperttula-Ikonen, Marjo
; APPLICANT: Tilgmann, Carola
; APPLICANT: Lotta, Timo
; APPLICANT: Kaivola, Juha
; TITLE OF INVENTION: Compounds for Deactivating Phospholamban Function on
; FILE REFERENCE: 1102.0250001
; CURRENT APPLICATION NUMBER: US/09/252,063
; PRIOR FILING DATE: 1999-02-18
; EARLIER FILING DATE: 1997-09-24
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Sus sp.
US-09-252-063-2

Query Match 96.0%; Score 72; DB 4; Length 52;
Best Local Similarity 93.8%; Pred. No. 1.1e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVOYLTRSAIRRAS 16
| : | | | | | | | | | | | | | |
DB 1 MDKVOYLTRSAIRRAS 16

RESULT 8
US-09-252-063-3
; Sequence 3, Application US/09252063
; Patent No. 6538022
; GENERAL INFORMATION:
; APPLICANT: Pollesello, Piero
; APPLICANT: Ovaska, Martti
; APPLICANT: Tenhunen, Jukka
; APPLICANT: Vidgren, Jukka
; APPLICANT: Yliperttula-Ikonen, Marjo
; APPLICANT: Tilgmann, Carola
; APPLICANT: Lotta, Timo
; APPLICANT: Kaivola, Juha
; TITLE OF INVENTION: Compounds for Deactivating Phospholamban Function on
; FILE REFERENCE: 1102.0250001
; CURRENT APPLICATION NUMBER: US/09/252,063
; PRIOR FILING DATE: 1999-02-18
; EARLIER FILING DATE: 1997-09-24
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Canis sp.
US-09-252-063-3

Query Match 96.0%; Score 72; DB 4; Length 52;
 Best Local Similarity 93.8%; Pred. No. 1.1e-06;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRAS 16
 :|||||:|||||:
 Db 1 MDKVQYLTRSAIRRAS 16

RESULT 9
 US-09-549-872B-14
 ; Sequence 14, Application US/03549872B
 ; Patent No. 6540996
 ; GENERAL INFORMATION:
 ; APPLICANT: Zwaal, Richard
 ; APPLICANT: Groener, Jose
 ; APPLICANT: Bogardt, Thierry
 ; TITLE OF INVENTION: COMPOUND SCREENING METHODS
 ; FILE REFERENCE: D00590/70008 (GRV/RE)
 ; CURRENT APPLICATION NUMBER: US/09/549,872B
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: GB 9908670.4
 ; PRIOR FILING DATE: 1999-04-15
 ; PRIOR APPLICATION NUMBER: US 60/129,596
 ; PRIOR FILING DATE: 1999-04-15
 ; PRIOR APPLICATION NUMBER: GB 9912736.7
 ; PRIOR FILING DATE: 1999-06-01
 ; NUMBER OF SEQ ID NOS: 39
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 14
 ; LENGTH: 52
 ; TYPE: PRT
 ; ORGANISM: Sus sp.
 US-09-549-872B-14

Query Match 96.0%; Score 72; DB 4; Length 52;
 Best Local Similarity 93.8%; Pred. No. 1.1e-06;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRAS 16
 :|||||:|||||:
 Db 1 MDKVQYLTRSAIRRAS 16

RESULT 10
 US-09-252-063-7
 ; Sequence 7, Application US/09252063
 ; Patent No. 6538022
 ; GENERAL INFORMATION:
 ; APPLICANT: Pollesello, Piero
 ; APPLICANT: Ovaeka, Martti
 ; APPLICANT: Tenhunen, Jukka
 ; APPLICANT: Viidgren, Jukka
 ; APPLICANT: Vlierttula-Ikonen, Marjo
 ; APPLICANT: Tilgmann, Carola
 ; APPLICANT: Lotte, Timo
 ; APPLICANT: Kaivola, Juna
 ; TITLE OF INVENTION: Compounds for Deactivating Phospholamban Function on
 ; FILE REFERENCE: 1102.0250001
 ; CURRENT APPLICATION NUMBER: US/09/252,063
 ; CURRENT FILING DATE: 1999-02-18
 ; EARLIER APPLICATION NUMBER: 08/937,117
 ; EARLIER FILING DATE: 1997-09-24
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 7
 ; LENGTH: 52
 ; TYPE: PRT
 ; ORGANISM: Gallus sp.
 US-09-252-063-7

Query Match 94.7%; Score 71; DB 4; Length 52;
 Best Local Similarity 87.5%; Pred. No. 1.7e-06;
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRAS 16
 :|||||:|||||:
 Db 1 MEKVQYLTRSAIRRAS 16

RESULT 11
 US-09-732-210-181
 ; Sequence 181, Application US/09732210
 ; Patent No. 6573361
 ; GENERAL INFORMATION:
 ; APPLICANT: Bunkers, Greg J.
 ; APPLICANT: Liang, Jihong
 ; APPLICANT: Mittanck, Cindy A.
 ; APPLICANT: Seale, Jeffrey W.
 ; APPLICANT: Wu, Yonnie S.
 ; TITLE OF INVENTION: Anti-fungal Proteins and Methods for Their Use
 ; FILE REFERENCE: 38-21(15036)B
 ; CURRENT APPLICATION NUMBER: US/09/732,210
 ; CURRENT FILING DATE: 2000-12-07
 ; PRIOR APPLICATION NUMBER: US 60/169,513
 ; PRIOR FILING DATE: 1999-12-07
 ; PRIOR APPLICATION NUMBER: US 60/169,340
 ; PRIOR FILING DATE: 1999-12-07
 ; NUMBER OF SEQ ID NOS: 1753
 ; SEQ ID NO 181
 ; LENGTH: 116
 ; TYPE: PRT
 ; ORGANISM: Streptomyces coelicolor
 US-09-732-210-181

Query Match 54.7%; Score 41; DB 4; Length 116;
 Best Local Similarity 46.7%; Pred. No. 2;
 Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRA 15
 :|||:|||||:
 Db 81 VEKIELVTRGDYRRA 95

RESULT 12
 US-09-252-991A-18000
 ; Sequence 18000, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 18000
 ; LENGTH: 631
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-18000

Query Match 49.3%; Score 37; DB 4; Length 631;
 Best Local Similarity 50.0%; Pred. No. 76;
 Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRR 14
 :|||:|||||:
 Db 430 VELLQFLPRSRVRR 443

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RESULT 13
US-09-489-039A-7319
; Sequence 7319, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 7319
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-7319

Query Match      48.0%; Score 36; DB 4; Length 98;
Best Local Similarity 58.3%; Pred. No. 15;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      3 KVOYLTRSAIRR 14
      ||:||:||:||:
Db      51 KPCHLTRSGWRK 62

RESULT 14
US-09-489-039A-11071
; Sequence 11071, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 11071
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11071

Query Match      48.0%; Score 36; DB 4; Length 194;
Best Local Similarity 58.3%; Pred. No. 32;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      1 MEKVQYLTRSAI 12
      ||:||:||:||:
Db      111 MERVYLLQSQI 122

RESULT 15
US-09-252-991A-19332
; Sequence 19332, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US/08/588,983
; FILING DATE: Concurrently herewith
; CLASSIFICATION: 424
```

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; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 19332
; LENGTH: 886
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19332

Query Match      48.0%; Score 36; DB 4; Length 686;
Best Local Similarity 77.8%; Pred. No. 1.3e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      4 VQYLTRSAI 12
      ||:||:||:||:
Db      522 VQYLTRSGSL 530

RESULT 16
US-09-252-991A-24791
; Sequence 24791, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 24791
; LENGTH: 765
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24791

Query Match      48.0%; Score 36; DB 4; Length 765;
Best Local Similarity 50.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY      2 EKQVYLTRSAIRRA 15
      ||:||:||:||:
Db      502 EQVRLDREELRRA 515

RESULT 17
US-08-588-983-18
; Sequence 18, Application US/08588983
; Patent No. 5854067
; GENERAL INFORMATION:
; APPLICANT: Christopher B. Newgard, et al.
; TITLE OF INVENTION: Methods and Compositions
; TITLE OF INVENTION: for Inhibiting Hexokinase
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: US
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/588,983
; FILING DATE: Concurrently herewith
; CLASSIFICATION: 424
```

```
ATTORNEY/AGENT INFORMATION:
NAME: Fussey, Shelley P.M.
REGISTRATION NUMBER: 39,458
REFERENCE/DOCKET NUMBER: UTSD:424/FUS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
TELEX: n/a
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 924 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-588-983-18

Query Match      48.0%; Score 36; DB 2; Length 924;
Best Local Similarity 61.5%; Pred. No. 1.8e+02;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      2 EKVOYLTRSAIRR 14
Db      638 QDVYLLREAIRR 650

RESULT 18
US-08-588-976-18
Sequence 18, Application US/08589976
Patent No. 5891717
GENERAL INFORMATION:
APPLICANT: Christopher B. Newgard, et al.
TITLE OF INVENTION: Methods and Compositions for
TITLE OF INVENTION: Inhibiting Hexokinase
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: US
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/588,976
FILING DATE: Concurrently herewith
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fussey, Shelley P.M.
REGISTRATION NUMBER: 39,458
REFERENCE/DOCKET NUMBER: UTSD:481/FUS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
TELEX: n/a
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 924 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-588-976-18

Query Match      48.0%; Score 36; DB 2; Length 924;
Best Local Similarity 61.5%; Pred. No. 1.8e+02;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      2 EKVOYLTRSAIRR 14
Db      638 QDVYLLREAIRR 650
```

```
RESULT 19
US-09-252-991A-28362
Sequence 28362, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 28362
LENGTH: 210
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28362

Query Match      46.7%; Score 35; DB 4; Length 210;
Best Local Similarity 53.8%; Pred. No. 54;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY      2 EKVOYLTRSAIRR 14
Db      180 EAHQYLSREAMKR 192

RESULT 20
US-09-134-001C-5136
Sequence 5136, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GFC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 5136
LENGTH: 211
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5136

Query Match      46.7%; Score 35; DB 4; Length 211;
Best Local Similarity 46.7%; Pred. No. 54;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY      2 EKVOYLTRSAIRAS 16
Db      182 EKVDLTKETERTT 196

RESULT 21
US-09-134-000C-6395
Sequence 6395, Application US/09134000C
Patent No. 6617156
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FACALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
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; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6395
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-6395

Query Match 46.7%; Score 35; DB 4; Length 216;
Best Local Similarity 50.0%; Pred. No. 56;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 5 QYLTRSAIRRAS 16
Db 161 QYINRETLRRVS 172

RESULT 22

US-09-910-174B-14
; Sequence 14, Application US/09910174B
; Patent No. 6630575
; GENERAL INFORMATION:
; APPLICANT: Coyle, Anthony J.
; APPLICANT: Fraser, Christopher C.
; APPLICANT: Manning, Stephen
; TITLE OF INVENTION: B7-H2 Molecules, No. 6630575el Members of the B7
; TITLE OF INVENTION: Family and Uses Thereof
; FILE REFERENCE: 5800/236924
; CURRENT APPLICATION NUMBER: US/09/910,174B
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 09/620,461
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 357
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-910-174B-14

Query Match 46.7%; Score 35; DB 4; Length 357;
Best Local Similarity 75.0%; Pred. No. 97;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EKQYQLTR 9
Db 313 KKIQLYLR 320

RESULT 23

US-09-620-461-14
; Sequence 14, Application US/09620461
; Patent No. 6635750
; GENERAL INFORMATION:
; APPLICANT: Coyle, Anthony J.
; APPLICANT: Fraser, Christopher C.
; APPLICANT: Manning, Stephen
; TITLE OF INVENTION: B7-H2 Molecules, No. 6635750el Members of the B7
; TITLE OF INVENTION: Family and Uses Thereof
; FILE REFERENCE: 5800-149
; CURRENT APPLICATION NUMBER: US/09/620,461
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 357
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-620-461-14

Query Match 46.7%; Score 35; DB 4; Length 357;
Best Local Similarity 75.0%; Pred. No. 97;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EKQYQLTR 9
Db 313 KKIQLYLR 320

RESULT 24

US-09-277-262-4
; Sequence 4, Application US/09277262
; Patent No. 6395482
; GENERAL INFORMATION:
; APPLICANT: Karayicigou, Maria
; APPLICANT: Gogos, Joseph A
; TITLE OF INVENTION: METHODS OF DETERMINING A SUSCEPTIBILITY TO OR PRESENCE
; TITLE OF INVENTION: OF SCHIZOPHRENIA, OR A DISEASE OR DISORDER RELATED
; TITLE OF INVENTION: THEREO
; FILE REFERENCE: 600-1-223 CIP
; CURRENT APPLICATION NUMBER: US/09/277,262
; CURRENT FILING DATE: 1999-03-26
; EARLIER APPLICATION NUMBER: 09/229,530
; EARLIER FILING DATE: 1999-01-13
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-277-262-4

Query Match 46.7%; Score 35; DB 4; Length 497;
Best Local Similarity 43.8%; Pred. No. 1,4e+02;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MEKVQYLTRSAIRRAS 16
Db 452 MEVLPYLSRRALSENS 467

RESULT 25

US-09-277-262-2
; Sequence 2, Application US/09277262
; Patent No. 6395482
; GENERAL INFORMATION:
; APPLICANT: Karayicigou, Maria
; APPLICANT: Gogos, Joseph A
; TITLE OF INVENTION: METHODS OF DETERMINING A SUSCEPTIBILITY TO OR PRESENCE
; TITLE OF INVENTION: OF SCHIZOPHRENIA, OR A DISEASE OR DISORDER RELATED
; TITLE OF INVENTION: THEREO
; FILE REFERENCE: 600-1-223 CIP
; CURRENT APPLICATION NUMBER: US/09/277,262
; CURRENT FILING DATE: 1999-03-26
; EARLIER APPLICATION NUMBER: 09/229,530
; EARLIER FILING DATE: 1999-01-13
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 516
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-277-262-2

Query Match 46.7%; Score 35; DB 4; Length 516;
Best Local Similarity 43.8%; Pred. No. 1,5e+02;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MEKVQYLTRSAIRRAS 16
Db 471 MEVLPYLSRRALSENS 486

Fri Oct 1 16:13:12 2004

us-09-830-779-8.ra1

Page 8

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Job time : 19 secs

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OM protein - protein search, using sw model

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Title: US-09-830-779-8

Perfect score: 75

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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18: /cgn2_6/prodata/2/pubpaa/US10F_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	75	100.0	36	16	US-10-705-791-10
4	75	100.0	52	12	US-09-954-571-2
5	75	100.0	52	12	US-09-954-571-4
6	75	100.0	52	12	US-09-954-571-5
7	75	100.0	52	14	US-10-371-101-15
8	75	100.0	52	16	US-10-408-765A-478
9	75	100.0	52	16	US-10-705-791-1
10	75	100.0	52	16	US-10-705-791-2
11	75	100.0	79	16	US-10-705-791-17
12	75	100.0	79	16	US-10-705-791-19
13	72	96.0	52	12	US-09-954-571-3
14	72	96.0	52	14	US-10-371-101-14
15	72	96.0	52	16	US-10-705-791-5

16	71	94.7	35	16	US-10-705-791-13	Sequence 13, Appl
17	71	94.7	36	16	US-10-705-791-12	Sequence 12, Appl
18	71	94.7	52	12	US-09-954-571-1	Sequence 1, Appl
19	71	94.7	79	16	US-10-705-791-18	Sequence 18, Appl
20	70	93.3	52	16	US-10-705-791-4	Sequence 4, Appl
21	69	92.0	52	16	US-10-705-791-3	Sequence 3, Appl
22	66	88.0	52	16	US-10-705-791-6	Sequence 6, Appl
23	41	54.7	44	12	US-10-424-599-238702	Sequence 238702, A
24	41	54.7	68	12	US-10-425-114-46161	Sequence 46161, A
25	41	54.7	116	14	US-10-156-761-10177	Sequence 10177, A
26	41	54.7	451	15	US-10-369-493-21630	Sequence 21630, A
27	40	53.3	121	12	US-10-282-122A-47242	Sequence 47242, A
28	40	53.3	1108	15	US-10-369-493-1247	Sequence 1247, Ap
29	40	53.3	1108	15	US-10-369-493-20314	Sequence 20314, A
30	39	52.0	452	16	US-10-437-963-201301	Sequence 201301, A
31	38	50.7	113	12	US-10-282-122A-53984	Sequence 53984, A
32	38	50.7	790	16	US-10-437-963-139951	Sequence 139951, A
33	38	50.7	931	16	US-10-437-963-188757	Sequence 188757, A
34	37	49.3	112	12	US-10-424-599-175485	Sequence 175485, A
35	36.5	48.7	331	14	US-10-197-844-2	Sequence 2, Appl
36	36	48.0	75	16	US-10-437-963-202409	Sequence 202409, A
37	36	48.0	111	12	US-10-424-599-170920	Sequence 170920, A
38	36	48.0	111	12	US-10-424-599-195561	Sequence 195561, A
39	36	48.0	113	9	US-09-738-626-5733	Sequence 5733, Ap
40	36	48.0	114	12	US-10-282-122A-52593	Sequence 52593, A
41	36	48.0	119	16	US-10-767-701-55916	Sequence 55916, A
42	36	48.0	207	12	US-10-282-122A-71415	Sequence 71415, A
43	36	48.0	297	16	US-10-437-963-195227	Sequence 195227, A
44	36	48.0	344	15	US-10-131-410-177	Sequence 177, App
45	36	48.0	401	14	US-10-156-761-7673	Sequence 7673, Ap
46	36	48.0	409	12	US-10-282-122A-66259	Sequence 66259, A
47	36	48.0	417	12	US-10-389-647-494	Sequence 494, App
48	36	48.0	434	14	US-10-171-404A-46	Sequence 46, Appl
49	36	48.0	465	12	US-10-282-122A-48867	Sequence 48867, A
50	36	48.0	556	15	US-10-369-493-4879	Sequence 4879, Ap
51	36	48.0	629	16	US-10-437-963-153082	Sequence 153082, A
52	36	48.0	690	16	US-10-437-963-195233	Sequence 195233, A
53	36	48.0	720	16	US-10-433-794-20	Sequence 20, Appl
54	36	48.0	765	12	US-10-182-243-56	Sequence 56, Appl
55	36	48.0	765	14	US-10-128-174-3	Sequence 3, Appl
56	36	48.0	765	14	US-10-128-174-34	Sequence 34, Appl
57	36	48.0	765	14	US-10-128-174-35	Sequence 35, Appl
58	36	48.0	765	14	US-10-128-174-36	Sequence 36, Appl
59	36	48.0	765	14	US-10-128-174-37	Sequence 37, Appl
60	36	48.0	765	14	US-10-128-174-38	Sequence 38, Appl
61	36	48.0	765	14	US-10-128-174-39	Sequence 39, Appl
62	36	48.0	765	14	US-10-128-174-40	Sequence 40, Appl
63	36	48.0	765	14	US-10-128-174-41	Sequence 41, Appl
64	36	48.0	765	14	US-10-128-174-44	Sequence 44, Appl
65	36	48.0	808	16	US-10-437-963-195225	Sequence 195225, A
66	36	48.0	861	14	US-10-156-761-11000	Sequence 11000, A
67	36	48.0	867	15	US-10-369-493-10043	Sequence 10043, A
68	36	48.0	1138	16	US-10-437-963-128342	Sequence 128342, A
69	36	48.0	1465	16	US-10-437-963-128382	Sequence 128382, A
70	36	48.0	1489	16	US-10-437-963-128335	Sequence 128335, A
71	36	48.0	1572	16	US-10-437-963-128334	Sequence 128334, A
72	36	48.0	1639	16	US-10-437-963-128336	Sequence 128336, A
73	36	48.0	1806	16	US-10-437-963-128590	Sequence 128590, A
74	36	48.0	1841	16	US-10-437-963-128482	Sequence 128482, A
75	36	48.0	1859	16	US-10-437-963-128415	Sequence 128415, A
76	36	48.0	1875	16	US-10-437-963-128379	Sequence 128379, A
77	36	48.0	1908	16	US-10-437-963-128442	Sequence 128442, A
78	36	48.0	1936	16	US-10-437-963-128450	Sequence 128450, A
79	36	48.0	1966	16	US-10-437-963-128339	Sequence 128339, A
80	36	48.0	1987	16	US-10-437-963-128617	Sequence 128617, A
81	36	48.0	2093	16	US-10-437-963-128540	Sequence 128540, A
82	35	46.7	24	12	US-10-372-876-453	Sequence 453, App
83	35	46.7	24	14	US-10-097-065-453	Sequence 453, App
84	35	46.7	61	9	US-09-864-761-40542	Sequence 40542, A
85	35	46.7	61	9	US-09-864-761-41598	Sequence 41598, A
86	35	46.7	62	10	US-09-764-891-3012	Sequence 3012, Ap
87	35	46.7	90	16	US-10-437-963-144511	Sequence 144511, A
88	35	46.7	96	11	US-09-864-408A-4858	Sequence 4858, Ap

Sequence 152503, 99 12 US-10-424-599-152503
 Sequence 147002, 35 46.7 106 16 US-10-437-963-147002
 Sequence 61911, A 90 46.7 106 16 US-10-282-122A-61911
 Sequence 103091, 91 46.7 113 12 US-10-437-963-103091
 Sequence 442, App 92 46.7 114 16 US-10-372-876-442
 Sequence 442, App 93 46.7 131 12 US-10-097-065-442
 Sequence 454, App 94 46.7 131 14 US-10-112-944-454
 Sequence 71171, A 95 46.7 132 12 US-10-282-122A-71171
 Sequence 57201, A 96 46.7 207 12 US-10-282-122A-57201
 Sequence 164, App 97 46.7 234 12 US-10-093-463-164
 Sequence 2255, App 98 46.7 240 15 US-10-104-047-2255
 Sequence 52269, A 99 46.7 248 15 US-10-104-047-2255
 Sequence 52269, A 100 46.7 296 12 US-10-425-114-52269

ALIGNMENTS

RESULT 1
 US-10-705-791-8
 ; Sequence 8, Application US/10705791
 ; Publication No. US20040121942A1
 ; GENERAL INFORMATION:
 ; APPLICANT: The Regents of the University of California
 ; APPLICANT: Chien, Kenneth
 ; APPLICANT: Dillmann, Wolfgang
 ; APPLICANT: Minamisawa, Susanne
 ; APPLICANT: He, Huaping
 ; APPLICANT: Hoshijima, Masahiko
 ; APPLICANT: Meyer, Markus
 ; APPLICANT: Scott, Christopher
 ; APPLICANT: Wang, Yibin
 ; APPLICANT: Silverman, Gregg J.
 ; TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
 ; FILE REFERENCE: 6627-PA9025
 ; CURRENT FILING DATE: 2003-11-10
 ; PRIOR APPLICATION NUMBER: 60/106,718
 ; PRIOR FILING DATE: 1998-11-02
 ; PRIOR APPLICATION NUMBER: PCT/US99/25692
 ; PRIOR FILING DATE: 1999-11-02
 ; NUMBER OF SEQ ID NOS: 19
 ; SOFTWARE: Patent in version 3.2
 ; SEQ ID NO 8
 ; LENGTH: 16
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-705-791-8

Query Match 100.0%; Score 75; DB 16; Length 16;
 Best Local Similarity 100.0%; Pred. No. 5.3e-07; Mismatches 0; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRAS 16
 Db 1 MEKVQYLTRSAIRRAS 16

RESULT 2
 US-10-705-791-11
 ; Sequence 11, Application US/10705791
 ; Publication No. US20040121942A1
 ; GENERAL INFORMATION:
 ; APPLICANT: The Regents of the University of California
 ; APPLICANT: Chien, Kenneth
 ; APPLICANT: Dillmann, Wolfgang
 ; APPLICANT: Minamisawa, Susanne
 ; APPLICANT: He, Huaping
 ; APPLICANT: Hoshijima, Masahiko
 ; APPLICANT: Meyer, Markus
 ; APPLICANT: Scott, Christopher
 ; APPLICANT: Wang, Yibin
 ; APPLICANT: Silverman, Gregg J.

; TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
 ; FILE REFERENCE: 6627-PA9025
 ; CURRENT FILING DATE: 2003-11-10
 ; PRIOR APPLICATION NUMBER: 60/106,718
 ; PRIOR FILING DATE: 1998-11-02
 ; PRIOR APPLICATION NUMBER: PCT/US99/25692
 ; PRIOR FILING DATE: 1999-11-02
 ; NUMBER OF SEQ ID NOS: 19
 ; SOFTWARE: Patent in version 3.2
 ; SEQ ID NO 11
 ; LENGTH: 35
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-705-791-11

Query Match 100.0%; Score 75; DB 16; Length 35;
 Best Local Similarity 100.0%; Pred. No. 1.2e-06; Mismatches 0; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRAS 16
 Db 16 MEKVQYLTRSAIRRAS 31

RESULT 3
 US-10-705-791-10
 ; Sequence 10, Application US/10705791
 ; Publication No. US20040121942A1
 ; GENERAL INFORMATION:
 ; APPLICANT: The Regents of the University of California
 ; APPLICANT: Chien, Kenneth
 ; APPLICANT: Dillmann, Wolfgang
 ; APPLICANT: Minamisawa, Susanne
 ; APPLICANT: He, Huaping
 ; APPLICANT: Hoshijima, Masahiko
 ; APPLICANT: Meyer, Markus
 ; APPLICANT: Scott, Christopher
 ; APPLICANT: Wang, Yibin
 ; APPLICANT: Silverman, Gregg J.
 ; TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
 ; FILE REFERENCE: 6627-PA9025
 ; CURRENT FILING DATE: 2003-11-10
 ; PRIOR APPLICATION NUMBER: 60/106,718
 ; PRIOR FILING DATE: 1998-11-02
 ; PRIOR APPLICATION NUMBER: PCT/US99/25692
 ; PRIOR FILING DATE: 1999-11-02
 ; NUMBER OF SEQ ID NOS: 19
 ; SOFTWARE: Patent in version 3.2
 ; SEQ ID NO 10
 ; LENGTH: 36
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 ; ORGANISM: Homo sapiens
 US-10-705-791-10

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 Best Local Similarity 100.0%; Pred. No. 1.3e-06; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MEKVQYLTRSAIRRAS 16
 Db 1 MEKVQYLTRSAIRRAS 16

RESULT 4
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 ; Sequence 2, Application US/09954571
 ; Publication No. US20020032167A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Chien, Kenneth R

; APPLICANT: Hoshijima, Masahiko
; APPLICANT: Ross, John
; APPLICANT: Ikeda, Yasuhiro
; TITLE OF INVENTION: HIGH EFFICIENCY CARDIAC GENE TRANSFER
; FILE REFERENCE: 6627-PA0123
; CURRENT APPLICATION NUMBER: US/09/954,571
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: 60/231,821
; PRIOR FILING DATE: 2000-11-09
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-954-571-2

Query Match 100.0%; Score 75; DB 12; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEKVQYLTRSAIRRAS 16
Db 1 MEKVQYLTRSAIRRAS 16

RESULT 5
US-09-954-571-4
; Sequence 4, Application US/09954571
; Publication No. US20020032167A1
; GENERAL INFORMATION:
; APPLICANT: Chien, Kenneth R
; APPLICANT: Hoshijima, Masahiko
; APPLICANT: Ross, John
; TITLE OF INVENTION: HIGH EFFICIENCY CARDIAC GENE TRANSFER
; FILE REFERENCE: 6627-PA0123
; CURRENT APPLICATION NUMBER: US/09/954,571
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: 60/231,821
; PRIOR FILING DATE: 2000-11-09
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-954-571-4

Query Match 100.0%; Score 75; DB 12; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEKVQYLTRSAIRRAS 16
Db 1 MEKVQYLTRSAIRRAS 16

RESULT 6
US-09-954-571-5
; Sequence 5, Application US/09954571
; Publication No. US20020032167A1
; GENERAL INFORMATION:
; APPLICANT: Chien, Kenneth R
; APPLICANT: Hoshijima, Masahiko
; APPLICANT: Ross, John
; TITLE OF INVENTION: HIGH EFFICIENCY CARDIAC GENE TRANSFER
; FILE REFERENCE: 6627-PA0123
; CURRENT APPLICATION NUMBER: US/09/954,571
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: 60/231,821
; PRIOR FILING DATE: 2000-11-09

; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Oryctolagus cuniculus
US-09-954-571-5

Query Match 100.0%; Score 75; DB 12; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEKVQYLTRSAIRRAS 16
Db 1 MEKVQYLTRSAIRRAS 16

RESULT 7
US-10-371-101-15
; Sequence 15, Application US/10371101
; Publication No. US20030149995A1
; GENERAL INFORMATION:
; APPLICANT: Zwaal, Richard
; APPLICANT: Groenen, Jose
; APPLICANT: Bogardt, Thierry
; TITLE OF INVENTION: COMPOUND SCREENING METHODS
; FILE REFERENCE: D00590.70035.US
; CURRENT APPLICATION NUMBER: US/10/371,101
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: GB 9908670.4
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: US 60/129,596
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: GB 9912736.7
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: 09/549,872
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-371-101-15

Query Match 100.0%; Score 75; DB 14; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEKVQYLTRSAIRRAS 16
Db 1 MEKVQYLTRSAIRRAS 16

RESULT 8
US-10-408-765A-478
; Sequence 478, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 478
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-478

Query Match 100.0%; Score 75; DB 16; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRAS 16
Db 1 MEKVQYLTRSAIRRAS 16

RESULT 9
US-10-705-791-1
; Sequence 1, Application US/10705791
; Publication No. US20040121942A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; APPLICANT: Chien, Kenneth
; APPLICANT: Dillmann, Wolfgang
; APPLICANT: Minamisawa, Susanne
; APPLICANT: He, Huaping
; APPLICANT: Hoshijima, Masahiko
; APPLICANT: Meyer, Markus
; APPLICANT: Scott, Christopher
; APPLICANT: Wang, Yibin
; APPLICANT: Silverman, Gregg J.
; TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBEAN ACTIVITY FOR THE TREATMENT
; FILE REFERENCE: 6627-PA9025
; CURRENT APPLICATION NUMBER: US/10/705,791
; CURRENT FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: 60/106,718
; PRIOR FILING DATE: 1998-11-02
; PRIOR APPLICATION NUMBER: PCT/US99/25692
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-705-791-1

Query Match 100.0%; Score 75; DB 16; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRAS 16
Db 1 MEKVQYLTRSAIRRAS 16

RESULT 10
US-10-705-791-2
; Sequence 2, Application US/10705791
; Publication No. US20040121942A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; APPLICANT: Chien, Kenneth
; APPLICANT: Dillmann, Wolfgang
; APPLICANT: Minamisawa, Susanne
; APPLICANT: He, Huaping
; APPLICANT: Hoshijima, Masahiko
; APPLICANT: Meyer, Markus
; APPLICANT: Scott, Christopher
; APPLICANT: Wang, Yibin
; APPLICANT: Silverman, Gregg J.
; TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBEAN ACTIVITY FOR THE TREATMENT
; FILE REFERENCE: 6627-PA9025
; CURRENT APPLICATION NUMBER: US/10/705,791
; CURRENT FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: 60/106,718
; PRIOR FILING DATE: 1998-11-02
; PRIOR APPLICATION NUMBER: PCT/US99/25692
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-705-791-2

; FILE REFERENCE: 6627-PA9025
; CURRENT APPLICATION NUMBER: US/10/705,791
; CURRENT FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: 60/106,718
; PRIOR FILING DATE: 1998-11-02
; PRIOR APPLICATION NUMBER: PCT/US99/25692
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-705-791-2

Query Match 100.0%; Score 75; DB 16; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRAS 16
Db 1 MEKVQYLTRSAIRRAS 16

RESULT 11
US-10-705-791-17
; Sequence 17, Application US/10705791
; Publication No. US20040121942A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; APPLICANT: Chien, Kenneth
; APPLICANT: Dillmann, Wolfgang
; APPLICANT: Minamisawa, Susanne
; APPLICANT: He, Huaping
; APPLICANT: Hoshijima, Masahiko
; APPLICANT: Meyer, Markus
; APPLICANT: Scott, Christopher
; APPLICANT: Wang, Yibin
; APPLICANT: Silverman, Gregg J.
; TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBEAN ACTIVITY FOR THE TREATMENT
; FILE REFERENCE: 6627-PA9025
; CURRENT APPLICATION NUMBER: US/10/705,791
; CURRENT FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: 60/106,718
; PRIOR FILING DATE: 1998-11-02
; PRIOR APPLICATION NUMBER: PCT/US99/25692
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 79
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-705-791-17

Query Match 100.0%; Score 75; DB 16; Length 79;
Best Local Similarity 100.0%; Pred. No. 3e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRAS 16
Db 1 MEKVQYLTRSAIRRAS 16

RESULT 12
US-10-705-791-19
; Sequence 19, Application US/10705791
; Publication No. US20040121942A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; APPLICANT: Chien, Kenneth
; APPLICANT: Dillmann, Wolfgang
; APPLICANT: Minamisawa, Susanne
; APPLICANT: He, Huaping
; APPLICANT: Hoshijima, Masahiko
; APPLICANT: Meyer, Markus
; APPLICANT: Scott, Christopher
; APPLICANT: Wang, Yibin
; APPLICANT: Silverman, Gregg J.
; TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBEAN ACTIVITY FOR THE TREATMENT
; FILE REFERENCE: 6627-PA9025
; CURRENT APPLICATION NUMBER: US/10/705,791
; CURRENT FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: 60/106,718
; PRIOR FILING DATE: 1998-11-02
; PRIOR APPLICATION NUMBER: PCT/US99/25692
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19
; LENGTH: 79
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-705-791-19

; APPLICANT: Minamisawa, Susanne
; APPLICANT: He, Huaping
; APPLICANT: Hoshijima, Masahiko
; APPLICANT: Meyer, Markus
; APPLICANT: Scott, Christopher
; APPLICANT: Wang, Yibin
; APPLICANT: Silverman, Gregg J.
; TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
; FILE REFERENCE: 6627-PA9025
; CURRENT APPLICATION NUMBER: US/10/705,791
; PRIOR FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: 60/106,718
; PRIOR FILING DATE: 1998-11-02
; PRIOR APPLICATION NUMBER: PCT/US99/25692
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 19
; LENGTH: 79
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-705-791-19

Query Match 100.0%; Score 75; DB 16; Length 79;
Best Local Similarity 100.0%; Pred. No. 3e-06; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 0;

Qy 1 MEKVQYLTSAIRRAS 16
|:|||||
Db 1 MEKVQYLTSAIRRAS 16

RESULT 13

US-09-954-571-3
; Sequence 3, Application US/09954571
; Publication No. US20020032167A1
; GENERAL INFORMATION:
; APPLICANT: Chien, Kenneth R
; APPLICANT: Hoshijima, Masahiko
; APPLICANT: Ross, John
; APPLICANT: Ikeda, Yasuhiro
; TITLE OF INVENTION: HIGH EFFICIENCY CARDIAC GENE TRANSFER
; FILE REFERENCE: 6627-PA0123
; CURRENT APPLICATION NUMBER: US/09/954,571
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: 60/231,821
; PRIOR FILING DATE: 2000-11-09
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 3
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-954-571-3

Query Match 96.0%; Score 72; DB 12; Length 52;
Best Local Similarity 93.8%; Pred. No. 6.9e-06; Indels 0; Gaps 0;
Matches 15; Conservative 1; Mismatches 0;

Qy 1 MEKVQYLTSAIRRAS 16
|:|||||
Db 1 MEKVQYLTSAIRRAS 16

RESULT 14

US-10-371-101-14
; Sequence 14, Application US/10371101
; Publication No. US20030149995A1
; GENERAL INFORMATION:
; APPLICANT: Zwaal, Richard
; APPLICANT: Groenen, Jose
; APPLICANT: Bogaert, Thierry

; TITLE OF INVENTION: COMPOUND SCREENING METHODS
; FILE REFERENCE: D00590.70035.US
; CURRENT APPLICATION NUMBER: US/10/371,101
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: GB 9908670.4
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: US 60/129,596
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: GB 9912736.7
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: 09/549,872
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 14
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Sus. sp.
US-10-371-101-14

Query Match 96.0%; Score 72; DB 14; Length 52;
Best Local Similarity 93.8%; Pred. No. 6.9e-06; Indels 0; Gaps 0;
Matches 15; Conservative 1; Mismatches 0;

Qy 1 MEKVQYLTSAIRRAS 16
|:|||||
Db 1 MEKVQYLTSAIRRAS 16

RESULT 15

US-10-705-791-5
; Sequence 5, Application US/10705791
; Publication No. US20040121942A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; APPLICANT: Chien, Kenneth
; APPLICANT: Dillmann, Wolfgang
; APPLICANT: Minamisawa, Susanne
; APPLICANT: He, Huaping
; APPLICANT: Hoshijima, Masahiko
; APPLICANT: Meyer, Markus
; APPLICANT: Scott, Christopher
; APPLICANT: Wang, Yibin
; APPLICANT: Silverman, Gregg J.
; TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
; FILE REFERENCE: 6627-PA9025
; CURRENT APPLICATION NUMBER: US/10/705,791
; CURRENT FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: 60/106,718
; PRIOR FILING DATE: 1998-11-02
; PRIOR APPLICATION NUMBER: PCT/US99/25692
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 5
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-705-791-5

Query Match 96.0%; Score 72; DB 16; Length 52;
Best Local Similarity 93.8%; Pred. No. 6.9e-06; Indels 0; Gaps 0;
Matches 15; Conservative 1; Mismatches 0;

Qy 1 MEKVQYLTSAIRRAS 16
|:|||||
Db 1 MEKVQYLTSAIRRAS 16

RESULT 16

US-10-705-791-13
; Sequence 13, Application US/10705791

Publication No. US20040121942A1
 GENERAL INFORMATION:
 APPLICANT: The Regents of the University of California
 APPLICANT: Chien, Kenneth
 APPLICANT: Dillmann, Wolfgang
 APPLICANT: Minamisawa, Susanne
 APPLICANT: He, Huaping
 APPLICANT: Hoshijima, Masahiko
 APPLICANT: Meyer, Markus
 APPLICANT: Scott, Christopher
 APPLICANT: Wang, Yibin
 APPLICANT: Silverman, Gregg J.
 TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
 TITLE OF INVENTION: METHOD FOR CARDIAC DISEASE
 FILE REFERENCE: 6627-PA9025
 CURRENT APPLICATION NUMBER: US/10/705,791
 CURRENT FILING DATE: 2003-11-10
 PRIOR FILING DATE: 1998-11-02
 PRIOR APPLICATION NUMBER: PCT/US99/25692
 PRIOR FILING DATE: 1999-11-02
 NUMBER OF SEQ ID NOS: 19
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO 13
 LENGTH: 35
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-705-791-13

Query Match 94.7%; Score 71; DB 16; Length 35;
 Best Local Similarity 100.0%; Pred. No. 6.9e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRA 15
 DB 16 MEKVQYLTRSAIRRA 30

RESULT 17
 US-10-705-791-12
 Sequence 12, Application US/10705791
 Publication No. US20040121942A1
 GENERAL INFORMATION:
 APPLICANT: The Regents of the University of California
 APPLICANT: Chien, Kenneth
 APPLICANT: Dillmann, Wolfgang
 APPLICANT: Minamisawa, Susanne
 APPLICANT: He, Huaping
 APPLICANT: Hoshijima, Masahiko
 APPLICANT: Meyer, Markus
 APPLICANT: Scott, Christopher
 APPLICANT: Wang, Yibin
 APPLICANT: Silverman, Gregg J.
 TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
 TITLE OF INVENTION: METHOD FOR CARDIAC DISEASE
 FILE REFERENCE: 6627-PA9025
 CURRENT APPLICATION NUMBER: US/10/705,791
 CURRENT FILING DATE: 2003-11-10
 PRIOR FILING DATE: 1998-11-02
 PRIOR APPLICATION NUMBER: PCT/US99/25692
 PRIOR FILING DATE: 1999-11-02
 NUMBER OF SEQ ID NOS: 19
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO 12
 LENGTH: 36
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-705-791-12

Query Match 94.7%; Score 71; DB 16; Length 36;
 Best Local Similarity 100.0%; Pred. No. 7.2e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRA 15
 DB 1 MEKVQYLTRSAIRRA 15

RESULT 18
 US-09-954-571-1
 Sequence 1, Application US/09954571
 Publication No. US20020032167A1
 GENERAL INFORMATION:
 APPLICANT: Chien, Kenneth R
 APPLICANT: Hoshijima, Masahiko
 APPLICANT: Ross, John
 APPLICANT: Ikeda, Yasuhiro
 TITLE OF INVENTION: HIGH EFFICIENCY CARDIAC GENE TRANSFER
 FILE REFERENCE: 6627-PA0123
 CURRENT APPLICATION NUMBER: US/09/954,571
 CURRENT FILING DATE: 2001-09-11
 PRIOR APPLICATION NUMBER: 60/231,821
 PRIOR FILING DATE: 2000-11-09
 NUMBER OF SEQ ID NOS: 5
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO 1
 LENGTH: 52
 TYPE: PRT
 ORGANISM: Artificial
 FEATURE:
 OTHER INFORMATION: Mutant form of human protein sequence
 US-09-954-571-1

Query Match 94.7%; Score 71; DB 12; Length 52;
 Best Local Similarity 100.0%; Pred. No. 1.1e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRA 15
 DB 1 MEKVQYLTRSAIRRA 15

RESULT 19
 US-10-705-791-18
 Sequence 18, Application US/10705791
 Publication No. US20040121942A1
 GENERAL INFORMATION:
 APPLICANT: The Regents of the University of California
 APPLICANT: Chien, Kenneth
 APPLICANT: Dillmann, Wolfgang
 APPLICANT: Minamisawa, Susanne
 APPLICANT: He, Huaping
 APPLICANT: Hoshijima, Masahiko
 APPLICANT: Meyer, Markus
 APPLICANT: Scott, Christopher
 APPLICANT: Wang, Yibin
 APPLICANT: Silverman, Gregg J.
 TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
 TITLE OF INVENTION: OF CARDIAC DISEASE
 FILE REFERENCE: 6627-PA9025
 CURRENT APPLICATION NUMBER: US/10/705,791
 CURRENT FILING DATE: 2003-11-10
 PRIOR FILING DATE: 1998-11-02
 PRIOR APPLICATION NUMBER: PCT/US99/25692
 PRIOR FILING DATE: 1999-11-02
 NUMBER OF SEQ ID NOS: 19
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO 18
 LENGTH: 79
 TYPE: PRT
 ORGANISM: Escherichia coli
 US-10-705-791-18

Query Match 94.7%; Score 71; DB 16; Length 79;

```
Best Local Similarity 100.0%; Pred. No. 1.7e-05; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0;

Qy 1 MEKVQYLTRSAIRRA 15
Db 1 MEKVQYLTRSAIRRA 15

RESULT 20
US-10-705-791-4
; Sequence 4, Application US/10705791
; Publication No. US20040121942A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; APPLICANT: Chien, Kenneth
; APPLICANT: Dillmann, Wolfgang
; APPLICANT: Minamisawa, Susanne
; APPLICANT: He, Huaping
; APPLICANT: Hoshijima, Masahiko
; APPLICANT: Meyer, Markus
; APPLICANT: Scott, Christopher
; APPLICANT: Wang, Yibin
; APPLICANT: Silverman, Gregg J.
; TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
; FILE REFERENCE: 6827-PA9025
; CURRENT APPLICATION NUMBER: US/10/705,791
; PRIOR FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: 60/106,718
; PRIOR FILING DATE: 1998-11-02
; PRIOR APPLICATION NUMBER: PCT/US99/25692
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-705-791-4

Query Match 93.3%; Score 70; DB 16; Length 52;
Best Local Similarity 93.8%; Pred. No. 1.6e-05; Indels 1; Gaps 0;
Matches 15; Conservative 0; Mismatches 0;

Qy 1 MEKVQYLTRSAIRRA 16
Db 1 MEKVQYLTRSAIRRA 16

RESULT 21
US-10-705-791-3
; Sequence 3, Application US/10705791
; Publication No. US20040121942A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; APPLICANT: Chien, Kenneth
; APPLICANT: Dillmann, Wolfgang
; APPLICANT: Minamisawa, Susanne
; APPLICANT: He, Huaping
; APPLICANT: Hoshijima, Masahiko
; APPLICANT: Meyer, Markus
; APPLICANT: Scott, Christopher
; APPLICANT: Wang, Yibin
; APPLICANT: Silverman, Gregg J.
; TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
; FILE REFERENCE: 6827-PA9025
; CURRENT APPLICATION NUMBER: US/10/705,791
; PRIOR FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: 60/106,718
; PRIOR FILING DATE: 1998-11-02
; PRIOR APPLICATION NUMBER: PCT/US99/25692
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-705-791-3

Query Match 93.3%; Score 70; DB 16; Length 52;
Best Local Similarity 93.8%; Pred. No. 1.6e-05; Indels 1; Gaps 0;
Matches 15; Conservative 0; Mismatches 0;

Qy 1 MEKVQYLTRSAIRRA 16
Db 1 MEKVQYLTRSAIRRA 16

RESULT 22
US-10-705-791-6
; Sequence 6, Application US/10705791
; Publication No. US20040121942A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; APPLICANT: Chien, Kenneth
; APPLICANT: Dillmann, Wolfgang
; APPLICANT: Minamisawa, Susanne
; APPLICANT: He, Huaping
; APPLICANT: Hoshijima, Masahiko
; APPLICANT: Meyer, Markus
; APPLICANT: Scott, Christopher
; APPLICANT: Wang, Yibin
; APPLICANT: Silverman, Gregg J.
; TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
; FILE REFERENCE: 6827-PA9025
; CURRENT APPLICATION NUMBER: US/10/705,791
; PRIOR FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: 60/106,718
; PRIOR FILING DATE: 1998-11-02
; PRIOR APPLICATION NUMBER: PCT/US99/25692
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-705-791-6

Query Match 88.0%; Score 66; DB 16; Length 52;
Best Local Similarity 87.5%; Pred. No. 9.1e-05; Indels 1; Gaps 0;
Matches 14; Conservative 1; Mismatches 1;

Qy 1 MEKVQYLTRSAIRRA 16
Db 1 MEKVQYLTRSAIRRA 16

RESULT 23
US-10-424-599-238702
; Sequence 238702, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
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; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-705-791-3

Query Match 92.0%; Score 69; DB 16; Length 52;
Best Local Similarity 93.8%; Pred. No. 2.5e-05; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 1;

Qy 1 MEKVQYLTRSAIRRA 16
Db 1 MEKVQYLTRSAIRRA 16

RESULT 22
US-10-705-791-6
; Sequence 6, Application US/10705791
; Publication No. US20040121942A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; APPLICANT: Chien, Kenneth
; APPLICANT: Dillmann, Wolfgang
; APPLICANT: Minamisawa, Susanne
; APPLICANT: He, Huaping
; APPLICANT: Hoshijima, Masahiko
; APPLICANT: Meyer, Markus
; APPLICANT: Scott, Christopher
; APPLICANT: Wang, Yibin
; APPLICANT: Silverman, Gregg J.
; TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
; FILE REFERENCE: 6827-PA9025
; CURRENT APPLICATION NUMBER: US/10/705,791
; PRIOR FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: 60/106,718
; PRIOR FILING DATE: 1998-11-02
; PRIOR APPLICATION NUMBER: PCT/US99/25692
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-705-791-6

Query Match 88.0%; Score 66; DB 16; Length 52;
Best Local Similarity 87.5%; Pred. No. 9.1e-05; Indels 1; Gaps 0;
Matches 14; Conservative 1; Mismatches 1;

Qy 1 MEKVQYLTRSAIRRA 16
Db 1 MEKVQYLTRSAIRRA 16

RESULT 23
US-10-424-599-238702
; Sequence 238702, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 1, 2004, 12:05:26 ; Search time 15.6 Seconds

(without alignments)
98.658 Million cell updates/sec

Title: US-09-830-779-8

Perfect score: 75

Sequence: 1 MEKVQLTRSAIRAS 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

PIR 78:**

1: PIR1:**

2: PIR2:**

3: PIR3:**

4: PIR4:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	75	100.0	52	A40424	phospholamban - hu
2	75	100.0	52	S37638	phospholamban - ra
3	75	100.0	52	A49057	phospholamban - mo
4	75	100.0	52	B40424	phospholamban - ra
5	72	96.0	52	A28002	phospholamban - do
6	72	96.0	52	S05540	phospholamban - ch
7	71	94.7	52	A39535	phospholamban - pi
8	41	54.7	116	T34780	ribosomal protein
9	41	54.7	451	F75083	phospho-sugar muta
10	40	53.3	121	B70187	ribosomal protein
11	40	53.3	1108	E71104	probable cell divi
12	39	52.0	481	B71104	hypothetical prote
13	38	50.7	119	D6155	hypothetical prote
14	37	49.3	283	H69179	conserved hypotet
15	37	49.3	296	F70879	hypothetical prote
16	37	49.3	308	AC1867	hypothetical prote
17	37	49.3	2712	T05113	hypothetical prote
18	36	48.0	236	D69048	conserved hypotet
19	36	48.0	294	T00104	probable dTTP-4-de
20	36	48.0	335	A24785	hypothetical prote
21	36	48.0	409	F83493	probable MFS trans
22	36	48.0	410	T12833	hypothetical prote
23	36	48.0	417	H83370	hypothetical prote
24	36	48.0	434	T04263	phosphoprotein pho
25	36	48.0	462	AH1053	probable exported
26	36	48.0	486	I55449	gene P22A protein
27	36	48.0	549	A90253	hypothetical prote
28	36	48.0	622	JC5425	transcription init
29	36	48.0	736	I51691	disvelled homolo

30	48.0	924	1	S13913	hexokinase (EC 2.7
31	48.0	1148	2	D90815	transcription-repa
32	48.0	1148	2	H85674	hypothetical prote
33	46.7	185	2	AG2026	hypothetical prote
34	46.7	196	2	B83226	aliphatic amidase
35	46.7	283	2	G83754	transcription regu
36	46.7	307	2	T21879	hypothetical prote
37	46.7	390	2	T05000	cysteine synthase
38	46.7	390	2	S53487	porphobilinogen sy
39	46.7	403	2	B69338	conserved hypotet
40	46.7	444	2	S68122	tubulin beta-4 cha
41	46.7	455	2	H71028	hypothetical prote
42	46.7	515	2	S02194	DNA-directed RNA p
43	46.7	535	2	T37189	hypothetical prote
44	46.7	561	2	G90303	hypothetical prote
45	46.7	561	1	S34120	DNA-directed DNA p
46	46.7	781	2	T50055	C2H2 zinc finger p
47	46.7	1013	2	T31211	trwC protein homol
48	46.7	1102	2	S65235	probable membrane
49	46.7	1710	2	T14005	phospholipase D (E
50	46.0	452	2	T34542	hypothetical prote
51	46.0	813	2	C97292	ATPases with chape
52	46.0	1027	2	T46296	hypothetical prote
53	46.0	1120	2	JC7765	mitotic spindle as
54	45.3	101	2	T39075	hypothetical prote
55	45.3	108	2	D85482	hypothetical prote
56	45.3	108	2	E90631	hypothetical prote
57	45.3	134	1	LNCH16	16k galactose-bind
58	45.3	170	2	T36571	hypothetical prote
59	45.3	172	2	S62166	NADH2 dehydrogenas
60	45.3	172	2	S62167	NADH2 dehydrogenas
61	45.3	173	2	S44396	NADH2 dehydrogenas
62	45.3	173	2	S44397	NADH2 dehydrogenas
63	45.3	185	1	R52X6M	ribosomal protein
64	45.3	185	2	T03233	probable ribosomal
65	45.3	191	2	A65137	hypothetical 21.0
66	45.3	191	2	H91160	hypothetical prote
67	45.3	191	2	G86006	hypothetical prote
68	45.3	200	2	AE0788	cytochrome c-type
69	45.3	214	2	B81270	probable outer mem
70	45.3	239	2	T06603	hypothetical prote
71	45.3	292	2	G95926	probable saccharid
72	45.3	321	2	T44336	hypothetical prote
73	45.3	328	2	S70885	UDP-galactose 4-ep
74	45.3	367	2	AF2494	hypothetical prote
75	45.3	395	2	T00574	probable protein x
76	45.3	409	2	H81831	probable phospholip
77	45.3	431	2	H84392	O-acetyl homoserin
78	45.3	433	2	D75632	probable hemolysin
79	45.3	434	2	A69082	coenzyme F390 synt
80	45.3	525	2	AD2022	hypothetical prote
81	45.3	542	2	T46464	hypothetical prote
82	45.3	548	2	S56152	H+-transporting tw
83	45.3	576	2	AC3038	biotin carboxylase
84	45.3	576	2	H98247	biotin carboxylase
85	45.3	586	1	JC4219	pyruvate kinase (E
86	45.3	604	2	T45627	replication factor
87	45.3	604	2	T15091	hypothetical prote
88	45.3	662	2	T41512	u5 snrnp-like RNA
89	45.3	676	2	S74635	protoporphyrin IX
90	45.3	676	2	T46870	protoporphyrin IX
91	45.3	821	2	T19705	hypothetical prote
92	45.3	833	2	A50448	probable insectici
93	45.3	839	2	A38172	adenylate cyclase
94	45.3	991	2	T25412	hypothetical prote
95	45.3	1857	1	S01787	fatty-acid synthas
96	45.3	3339	2	T49799	related to TOM1 pr
97	44.0	55	2	S33915	hypothetical prote
98	44.0	62	2	S37135	Class II histocomp
99	44.0	102	1	H8504	histone H4 - bovin
100	44.0	102	1	H8504	histone H4 - pig

R/Fujii, J.; Lytton, J.; Tada, M.; MacLennan, D.H.
 FEBS Lett. 227, 51-55, 1988
 A:Title: Rabbit cardiac and slow-twitch muscle express the same phospholamban gene.
 A:Reference number: S00249; MUID:8811222; PMID:2562883
 A:Accession: S00249
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-52 <F02>
 A:Cross-references: GB:Y00761; NID:g1661; PIDN:CAA68730.1; PID:g1662
 C:Comment: Phospholamban is expressed in cardiac muscle, slow twitch skeletal muscle, and after phosphorylation, the Ca++ pump is activated and the rate of muscle relaxation is increased.
 C:Genetics:
 A:Note: only one gene was detected
 A:Note: the single intron is upstream of the coding region
 A:Superfamily: phospholamban
 C:Keywords: acetylated amino end; ATPase inhibitor; muscle; pentamer; phosphoprotein; transmembrane #status predicted <TMM>
 F:31-52/Domain: transmembrane #status predicted <TMM>
 F:1/Modified site: acetylated amino end (Met) #status predicted
 F:16/Binding site: phosphate (Ser) (covalent) (by calmodulin-dependent kinase) #status predicted
 F:17/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase) #status predicted

Query Match 100.0%; Score 75; DB 1; Length 52;
 Best Local Similarity 100.0%; Pred. No. 5.4e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEKVQYLTRSAIRRAS 16
 Db 1 MEKVQYLTRSAIRRAS 16

RESULT 5
 phospholamban - dog
 C:Species: Canis lupus familiaris (dog)
 C:Date: 23-Aug-1987 #sequence revision 27-Jun-1994 #text_change 18-Jun-1999
 C:Accession: A29002; A26805; A25307; A24818; I46227
 R/Fujii, J.; Ueno, A.; Kitano, K.; Tanaka, S.; Kadoma, M.; Tada, M.
 J. Clin. Invest. 79, 301-304, 1987
 A:Title: Complete complementary DNA-derived amino acid sequence of canine cardiac phospholamban.
 A:Reference number: A29002; MUID:87083954; PMID:3793929
 A:Accession: A29002
 A:Molecule type: mRNA
 A:Residues: 1-52 <F02>
 A:Cross-references: GB:M16012; NID:g164043; PIDN:AA330884.1; PID:g164044
 R/Uyeda, A.; Kitano, K.; Fujii, J.; Kadoma, M.; Tada, M.; Tanaka, S.
 Nucleic Acids Res. 15, 6738, 1987
 A:Title: The cDNA sequence of the major phospholamban mRNA in canine cardiac ventricular muscle.
 A:Reference number: A26805; MUID:87316936; PMID:3628007
 A:Accession: A26805
 A:Molecule type: mRNA
 A:Residues: 1-52 <F02>
 A:Cross-references: GB:Y00399; NID:g911; PIDN:CAA68461.1; PID:g912
 R/Simmerman, H.K.B.; Collins, J.H.; Rheibert, J.L.; Wegener, A.D.; Jones, L.R.
 J. Biol. Chem. 261, 13333-13341, 1986
 A:Title: Sequence analysis of phospholamban. Identification of phosphorylation sites and A:Reference number: A25307; MUID:87088549; PMID:3759968
 A:Contents: partial sequence and phosphorylation sites
 A:Accession: A25307
 A:Molecule type: protein
 A:Residues: 10-45 <SIM>
 R/Fujii, J.; Kadoma, M.; Tada, M.; Toda, H.; Sakiyama, F.
 Biochem. Biophys. Res. Commun. 138, 1044-1050, 1986
 A:Title: Characterization of structural unit of phospholamban by amino acid sequencing and A:Reference number: A24818; MUID:86323152; PMID:3753485
 A:Contents: partial sequence and acetylation site
 A:Accession: A24818
 A:Molecule type: protein
 A:Residues: 1-35, 'X', 37-40, 'X', 42-45 <F02>
 R/Uyeda, A.; Kitano, K.; Fujii, J.; Kadoma, M.; Tada, M.; Tanaka, S.
 Nucleic Acids Symp. Ser. 17, 121-124, 1986
 A:Title: Characterization of recombinant cDNA clones for canine cardiac phospholamban.
 A:Reference number: I46227; MUID:87174860; PMID:3562256

A:Accession: I46227
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-52 <F02>
 A:Cross-references: GB:M35393; NID:g164045; PIDN:AA341618.1; PID:g164046
 C:Comment: Phospholamban is expressed in cardiac muscle, slow twitch skeletal muscle, and after phosphorylation, the Ca++ pump is activated and the rate of muscle relaxation is increased.
 C:Superfamily: phospholamban
 C:Keywords: acetylated amino end; ATPase inhibitor; muscle; pentamer; phosphoprotein; transmembrane #status predicted <TMM>
 F:31-52/Domain: transmembrane #status predicted <TMM>
 F:1/Modified site: acetylated amino end (Met) #status predicted
 F:16/Binding site: phosphate (Ser) (covalent) (by calmodulin-dependent kinase) #status predicted
 F:17/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase) #status predicted

Query Match 96.0%; Score 72; DB 1; Length 52;
 Best Local Similarity 93.8%; Pred. No. 2e-06;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEKVQYLTRSAIRRAS 16
 Db 1 MDXVQLTRSAIRRAS 16

RESULT 6
 S05540
 phospholamban - pig
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 21-Nov-1993 #sequence_revision 27-Jun-1994 #text_change 18-Jun-1999
 C:Accession: S05540
 R/Verboomen, H.; Wuytack, F.; Eggermont, J.A.; de Jaegere, S.; Missiaen, L.; Raeymaekers Biochem. J. 262, 353-356, 1989
 A:Title: cDNA cloning and sequencing of phospholamban from pig stomach smooth muscle.
 A:Reference number: S05540; MUID:90856437; PMID:2530978
 A:Accession: S05540
 A:Molecule type: mRNA
 A:Residues: 1-52 <F02>
 A:Cross-references: EMBL:X15075; NID:g2055; PIDN:CAA33171.1; PID:g2056
 C:Comment: Phospholamban is expressed in cardiac muscle, slow twitch skeletal muscle, and after phosphorylation, the Ca++ pump is activated and the rate of muscle relaxation is increased.
 C:Superfamily: phospholamban
 C:Keywords: acetylated amino end; ATPase inhibitor; muscle; pentamer; phosphoprotein; transmembrane #status predicted <TMM>
 F:31-52/Domain: transmembrane #status predicted <TMM>
 F:1/Modified site: acetylated amino end (Met) #status predicted
 F:16/Binding site: phosphate (Ser) (covalent) (by calmodulin-dependent kinase) #status predicted
 F:17/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase) #status predicted

Query Match 96.0%; Score 72; DB 1; Length 52;
 Best Local Similarity 93.8%; Pred. No. 2e-06;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEKVQYLTRSAIRRAS 16
 Db 1 MDXVQLTRSAIRRAS 16

RESULT 7
 A39535
 phospholamban - chicken
 C:Species: Gallus gallus (chicken)
 C:Date: 06-Mar-1992 #sequence_revision 27-Jun-1994 #text_change 18-Jun-1999
 C:Accession: A39535; B39535; A44531
 R/Toyofuku, T.; Zak, R.
 J. Biol. Chem. 266, 5375-5383, 1991
 A:Title: Characterization of cDNA and genomic sequences encoding a chicken phospholamban.
 A:Reference number: A39535; MUID:91170195; PMID:1825996
 A:Accession: A39535
 A:Molecule type: mRNA
 A:Residues: 1-17, 'L', 19-52 <F02>
 A:Cross-references: GB:M59039; NID:g212575; PIDN:AAA62738.1; PID:g212576
 A:Note: the authors translated the codon CTT for residue 18 as Ile
 A:Accession: B39535

A:Molecule type: DNA
A:Residues: 1-52 <T02>
A:Cross-references: GB:M59038
A:Note: the sequence of residues 33-52 and the corresponding nucleotide sequence are not
R:Toyotoku, T.; Zak, R.
A:Reference number: A44531
A:Accession: A44531
A:Molecule type: DNA
A:Residues: 1-52 <T03>
A:Cross-references: GB:M59038
C:Comment: Phospholamban is expressed in cardiac muscle, slow twitch skeletal muscle, and
C:Comment: Phospholamban is the major phosphorylated protein in cardiac muscle sarcoplasm
e; after phosphorylation, the Ca²⁺ pump is activated and the rate of muscle relaxation i
C:Genetics:
A:Note: only one gene was detected
A:Note: the single intron is upstream of the coding region
C:Superfamily: phospholamban
C:Keywords: acetylated amino end; ATPase inhibitor; muscle; pentamer; phosphoprotein; tr
F:31-52/Domain: transmembrane #status predicted <TM>
F:1/Modified site: acetylated amino end (Met) #status predicted
F:16/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predict
F:17/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase) #status p
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Best Local Similarity 87.5%; Pred. No. 3e-06;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MEKVQYLTRSAIRRAS 16
Db 1 MEKVQYLTRSAIRRAS 16
RESULT 8
T34780
ribosomal protein L19 - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 21-Jan-2000
C:Accession: T34780
R:Murphy, L.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
Submitted to the EMBL Data Library, June 1998
A:Reference number: Z21557
A:Accession: T34780
A:Status: Preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-116 <MUR>
A:Cross-references: EMBL:AL023797; PIDN:CAA19387.1; GSPDB:GN00070; SCQEDB:SC2E1.12
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: rplS; SCQEDB:SC2E1.12
C:Superfamily: Escherichia coli ribosomal protein L19
Query Match 54.7%; Score 41; DB 2; Length 116;
Best Local Similarity 46.9%; Pred. No. 2.8;
Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
Qy 1 MEKVQYLTRSAIRRA 15
Db 81 VEKIELVTRGCVRA 95
RESULT 9
F75083
phospho-sugar mutase PAB1666 - Pyrococcus abyssi (strain Orsay)
C:Species: Pyrococcus abyssi
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C:Accession: F75083
R:anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
A:Reference number: A75001
A:Accession: F75083
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-451 <KAW>
A:Cross-references: GB:AJ248286; GB:AL096836; NID:G5458366; PIDN:CAB49971.1; PID:G545848;
A:Experimental source: strain Orsay
C:Genetics:
A:Gene: PAB1666
C:Superfamily: phosphomannomutase
Query Match 54.7%; Score 41; DB 2; Length 451;
Best Local Similarity 50.0%; Pred. No. 12;
Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
Qy 1 MEKVQYLTRSAIRRAS 16
Db 435 MEKAEKLVKDAIKKAS 450
RESULT 10
B70187
ribosomal protein L19 (rplS) - Lyme disease spirochete
C:Species: Borrelia burgdorferi (Lyme disease spirochete)
C:Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 13-Aug-1999
C:Accession: B70187
R:Praser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White,
son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,
; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
Nature 350, 580-585, 1997
A:Authors: Smith, H.O.; Venter, J.C.
A:Title: Genomic sequence of a Lyme disease spirochete, Borrelia burgdorferi.
A:Reference number: A70100; MUID:98065943; PMID:9403855
A:Accession: B70187
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-121 <KLE>
A:Cross-references: GB:AF001170; GB:AE000783; NID:G2688623; PIDN:AAC67044.1; PID:G268862;
A:Experimental source: strain B31
C:Superfamily: Escherichia coli ribosomal protein L19
Query Match 53.3%; Score 40; DB 2; Length 121;
Best Local Similarity 53.3%; Pred. No. 4.5;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
Qy 1 MEKVQYLTRSAIRRA 15
Db 80 TEKVEVLRRGKVRRA 94
RESULT 11
E71104
probable cell division control protein - Pyrococcus horikoshii
C:Species: Pyrococcus horikoshii
C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 05-Nov-1999
C:Accession: E71104
R:Kawarayashi, Y.; Sawada, M.; Horikawa, H.; Hailkawa, Y.; Hino, Y.; Yamamoto, S.; Sekine,
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudo, T.; Yamazaki, J.; Kushida, N.; Oguchi,
DNA Res. 5, 55-76, 1998
A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
A:Reference number: A71000; MUID:98344137; PMID:9679194
A:Accession: E71104
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-1108 <KAW>
A:Cross-references: GB:AF000003; NID:G3236130; PIDN:BAA29695.1; PID:dl030638; PID:G325701
A:Experimental source: strain OT3
A:Note: this accession replaces an interim accession for a sequence replaced by GenBank
C:Genetics:
A:Gene: PH0606
Query Match 53.3%; Score 40; DB 2; Length 1108;
Best Local Similarity 53.3%; Pred. No. 47;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
Qy 1 MEKVQYLTRSAIRRA 15

Db 668 MEVKDYLTRBVRKA 682
||||| :|:

RESULT 12

B75167

hypothetical protein PAB0334 - Pyrococcus abyssi (strain Orsay)

C:Species: Pyrococcus abyssi

C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000

C:Accession: B75167

R:anonymous, Genoscope

submitted to the EMBL Data Library, July 1999

A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru

A:Reference number: A75001

A:Accession: B75167

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-481 <KAW>

A:Cross-references: GB:AJ248284; GB:AL096836; NID:G5457730; PIDN:CAB49417.1; PID:G545792

A:Experimental source: strain Orsay

C:Genetics:

A:Gene: PAB0334

Query Match 52.0%; Score 39; DB 2; Length 481;

Best Local Similarity 50.0%; Pred. No. 30;

Matches 7; Conservative 3; Mismatches 3; Indels 4; Gaps 0;

Qy

2 EKVOYLTRSAIRRA 15

||||| :|:

38 EKIKYIRAFERA 51

||||| :|:

RESULT 13

D69155

hypothetical protein MTH425 - Methanobacterium thermoautotrophicum (strain Delta H)

C:Species: Methanobacterium thermoautotrophicum

C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 24-Nov-1999

C:Accession: D69155

R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;

Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.;

ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.

J. Bacteriol. 179, 7135-7155, 1997

A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct

A:Reference number: A69000; MUID:98037514; PMID:9371463

A:Accession: D69155

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-119 <MTH>

A:Cross-references: GB:AE000827; GB:AE000666; NID:G2621489; PIDN:AAB84931.1; PID:G262149

A:Experimental source: strain Delta H

C:Genetics:

A:Gene: MTH425

A:Start codon: TTG

C:Superfamily: Methanobacterium thermoautotrophicum hypothetical protein MTH425

Query Match

Best Local Similarity 50.7%; Score 38; DB 2; Length 119;

Matches 6; Conservative 6; Mismatches 6; Indels 4; Gaps 0;

Qy

1 MEKVQYLTRSAIRRAS 16

||||| :|:

35 MDNIMYLTQSTVYQSS 50

RESULT 14

H69179

conserved hypothetical protein MTH601 - Methanobacterium thermoautotrophicum (strain Del

C:Species: Methanobacterium thermoautotrophicum

C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 17-Mar-2000

C:Accession: H69179

R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;

Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.;

ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.

J. Bacteriol. 179, 7135-7155, 1997

A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct

A:Reference number: A69000; MUID:98037514; PMID:9371463

A:Accession: H69179

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-283 <MTH>

A:Cross-references: GB:AE000842; GB:AE000666; NID:G2621676; PIDN:AAB85107.1; PID:G262168

A:Experimental source: strain Delta H

C:Genetics:

A:Gene: MTH601

C:Superfamily: hypothetical protein AF1307

Query Match

Best Local Similarity 49.3%; Score 37; DB 2; Length 283;

Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy

6 YLTRSAIRRAS 16

||||| :|:

209 YLTREAFKRAA 219

||||| :|:

RESULT 15

F70879

hypothetical protein Rv2751 - Mycobacterium tuberculosis (strain H37RV)

C:Species: Mycobacterium tuberculosis

C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999

C:Accession: F70879

R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.;

Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.;

Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.;

Nature 393, 537-544, 1998

A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome

A:Reference number: A70500; MUID:98295987; PMID:9634230

A:Accession: F70879

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-296 <COL>

A:Cross-references: GB:AL008967; GB:AL123456; NID:G3261491; PIDN:CAA15547.1; PID:G117388

A:Experimental source: strain H37RV

C:Genetics:

A:Gene: Rv2751

Query Match

Best Local Similarity 49.3%; Score 37; DB 2; Length 296;

Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy

5 QYLTRSAIRR 14

||||| :|:

180 QYLTERAVRR 189

RESULT 16

AC1867

hypothetical protein alr0484 [imported] - Nostoc sp. (strain PCC 7120)

C:Species: Nostoc sp. PCC 7120

A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002

C:Accession: AC1867

R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi

Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S

DNA Res. 8, 205-213, 2001

A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana

A:Reference number: AB1807; MUID:21595285; PMID:11759840

A:Accession: AC1867

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-308 <KUR>

A:Cross-references: GB:BA000019; PIDN:BAV72442.1; PID:G1129829; GSPDB:GN00179

A:Experimental source: strain PCC 7120

C:Genetics:

A:Gene: alr0484

```

Query Match      49.3%; Score 37; DB 2; Length 308;
Best Local Similarity 53.3%; Pred.No. 44;
Matches      8; Conservative      3; Mismatches      4; Indels      0; Gaps      0;

QY      1 MKVQYLTRSAIRRA 15
      :|:|:|:|:|:|:|:|
DB      212 LEEVQLVRSVMTRA 226

RESULT 17
T05113
Hypothetical protein F28M20.240 - Arabidopsis thaliana
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 23-Jul-1999
C.Accession: T05113
R.C.R:R,Bevan, M.; Riegar, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Hoheisel, J.; Mewes,
Submitted to the Protein Sequence Database, November 1998
A.Reference number: 215398
A.Accession: T05113
A.Molecule type: DNA
A.Residues: 1-2712 <BEV>
A.Cross-references: EMBL:AL031004
A.Experimental source: cultivar Columbia; BAC clone F28M20
C.Genetics:
A.Map position: 4
A.Introns: 17/3; 240/1; 1950/1; 2118/3; 2381/1; 2599/3; 2645/1; 2679/2
A.Note: F28M20.240

```

```

Query Match      49.3%; Score 37; DB 2; Length 2712;
Best Local Similarity 63.6%; Pred. No. 4.3e+02;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      1 MERQYLTRSA 11
      :|:|:|:|
Db      1473 LERVENIARSA 1483

```

RESULT 18
 D5048
 conserved hypothetical protein MTH1364 - Methanobacterium thermoautotrophicum (strain Delta H)
 C:Species: Methanobacterium thermoautotrophicum
 C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
 C:Accession: D69048
 R:Smith, D.R.; Doucette-Stamm, L.A.; Delonghery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
 Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jwani, N.;
 Chu, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
 J. Bacteriol. 179, 7135-7155, 1997
 A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
 A:Reference numbers: A69000; MUID:98037514; PMID:9371463
 A:Accession: D69048
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-236 <MTH>
 A:Cross-references: GB:AE000899; GB:AE000666; NID:G2622468; PID:G262247
 A:Experimental source: strain Delta H
 C:Genetics:
 A:Gene: MTH1364

```

Query March      48.0%; Score 36; DS 2; Length 236;
Best Local Similarity 45.7%; Pred. NO. 51;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Oy      1 MEKVQYLTRSAIRRA 15
      :||:|||||
Db      210 VEXLEYLNERAIRPS 224

```

RESULT 19
 T00104
 probable gdp-4-dehydrothamose reductase (EC 1.1.1.133) - Actinobacillus actinomycetemcomitans
 Alternate names: dtdp-4-keto-L-rhamnose reductase
 Species: Actinobacillus actinomycetemcomitans

C.Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 21-Jul-2000
C.Accession: T00104
R.Nakano, Y.; Yoshida, Y.; Yamashita, Y.; Koga, T.
Biochim. Biophys. Acta 1442, 409-414, 1998
A.Title: A gene cluster for 6-deoxy-L-talan synthesis in *Actinobacillus actinomycetescomi*
A.Reference number: Z1411; MUID:99023768; PMID:9805002
A.Accession: T00104
A.Status: translated from GB/EMBL/DBJ
A.Molecule type: DNA
A.Residues: 1-294 <NAK>
A.Cross-references: EMBL:AB010415; NID:G3132248; PID:N3132256
A.Experimental source: strain NCTC 9710
C.Function:
A.Description: probably catalyzes the reaction of dTDP-6-deoxy-L-mannose + NADP(+) to dTl
A.Pathway: dTDP-ribose biosynthesis
C:Superfamily: dTDP-dihydroxyacetone synthase
C:Keywords: oxidoreductase

```
Query Match      48.0%; Score 36; DB 2; Length 294;
Best Local Similarity 61.5%; Pred. No. 65;
Matches B; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
```

RESULT 20
A24785
hypothetical protein 335 - slime mold (Dictyostelium discoideum) transposon DIRS-1
C:Species: Dictyostelium discoideum
C:Date: 23-Aug-1987 #sequence_revision 23-Aug-1987 #text_change 18-Jun-1993
C:Accession: A24785
R:Cappello, J.; Handelsman, K.; Lodish, H.F.
Cell 43, 105-115, 1985
A:Title: Sequence of Dictyostelium DIRS-1: an apparent retrotransposon with inverted term
A:Reference numbers: A94654; MUID:96079481; PMID:2416457
A:Accession: A24785
A:Molecule type: DNA
A:Residues: 1-335 <CAP>

```

Query Match      48.0%; Score 36; DB 2; Length 335;
Best Local Similarity 58.3%; Pred. Nismat. 74;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      1 MEKVQYLTRSAI 12
          : | | | | |
Db      188 VELISYLTQSAI 199

```

RESULT 21
F83493
Probable MFS transporter PA1212 [imported] - *Pseudomonas aeruginosa* (strain PA01)
C:Species: *Pseudomonas aeruginosa*
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: F83493
C:Reviewer: C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warener, P.; Hickey, M.J.; Bri-
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic patho-
A:Reference number: A82950; MUID:20437337; PMID:10384843
A:Accession: F83493
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-409 <STO>
A:Cross-references: GB:AE004551; GB:AE004091; NID:G9947135; PIDN:AAG04601.1; GSPDB:GN001;
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA1212

Query Match 48.0%; Score 36; DB 2; Length 409;
Best Local Similarity 77.8%; Pred. No. 91;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 VOYLTRSAI 12
| | | | |
Db 245 VOYLTRSL 253

RESULT 22
TI2833
hypothetical protein yonV - Bacillus subtilis phage SPBc2
C:Species: Bacillus subtilis phage SPBc2
C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 15-Oct-1999
C:Accession: TI2833; E69315
R:Lazarevic, V.; Dueserhoef, A.; Soldo, B.; Hilbert, H.; Maue, C.; Karamata, D.
submitted to the EMBL Data Library, August 1997
A:Description: The complete nucleotide sequence of the Bacillus subtilis SPBc2 prophage
A:Reference number: Z17583
A:Accession: TI2833
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-410 <LAZ>
A:Cross-references: EMBL:AF020713; NID:G3025478; PID:G3025547; PIDN:AAC13042.1
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Allioni, G.; Azevedo, V.; Brette
C.; Bron, S.; Broutin, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrati, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galle
Tech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koeter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois
Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekowska, A.; Seron
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.
A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69560; MUID:98044033; PMID:9384377
A:Accession: E69915
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-410 <KUN>
A:Cross-references: GB:Z99115; GB:AL009126; NID:G2634478; PIDN:CAB14016.1; PID:el183545;
A:Experimental source: strain 168
C:Genetics:
A:Gene: yonV

Query Match 48.0%; Score 36; DB 2; Length 410;
Best Local Similarity 58.3%; Pred. No. 92;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 EKVOYLTRSAIR 13
| | | | |
Db 373 EMQWLRSAIR 384

RESULT 23
H83370
hydrogen cyanide synthase HcnC PA2195 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: H83370
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: H83370
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-417 <STO>
A:Cross-references: GB:AE004646; GB:AE004091; NID:G9948213; PIDN:AAG05583.1; GSPDB:GN001

A:Experimental source: strain PA01
C:Genetics:
A:Gene: hcnC; PA2195

Query Match 48.0%; Score 36; DB 2; Length 417;
Best Local Similarity 50.0%; Pred. No. 93;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 EKVOYLTRSAIRRA 15
| | | | |
Db 154 EQVWLDREELRA 167

RESULT 24
T04263
phosphoprotein phosphatase (EC 3.1.3.16) AB11 - Arabidopsis thaliana
N:Alternate names: protein F20B18.190
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 08-Oct-1999
C:Accession: T04263; A54588
R:Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Hoheisel, J.; Mewes, H.W.; Mayer, K.F.X
submitted to the Protein Sequence Database, March 1999
A:Reference number: Z15263
A:Accession: T04263
A:Molecule type: DNA
A:Residues: 1-434 <BEV>
A:Cross-references: EMBL:AL049483
A:Experimental source: cultivar Columbia; BAC clone F20B18
R:Meyer, K.; Leube, M.P.; Grill, E.
Science 264, 1452-1455, 1994
A:Title: A protein phosphatase 2C involved in ABA signal transduction in Arabidopsis tha
A:Reference number: A54588; MUID:94255767; PMID:8197457
A:Accession: A54588
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-104, 'V', 106-434 <MEY>
A:Cross-references: GB:X78886; NID:G509418; PIDN:CAA55484.1; PID:G509419
C:Genetics:
A:Gene: AB11
A:Map position: 4
A:Introns: 183/3; 280/3; 316/1
A:Note: F20B18.190
C:Keywords: phosphoric monoester hydrolase

Query Match 48.0%; Score 36; DB 2; Length 434;
Best Local Similarity 43.8%; Pred. No. 97;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRAS 16
| | | | |
Db 396 MSAEVLKLAIRGS 411

RESULT 25
AH1053
probable exported protein STY4756 [imported] - Salmonella enterica subsp. enterica serov
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A:Note: This species has also been called Salmonella typhi
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C:Accession: AH1053
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Conington, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AH1053
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-462 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD06877.1; PID:gi6505525; GSPDB:GN00176
C:Genetics:

A:Gene: STY4756

Query Match 48.0%; Score 36; DB 2; Length 462;
 Best Local Similarity 53.8%; Pred. No. 1e+02;
 Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 EKQVLTSAIR 14

Db :|||:| |
 294 DKVTWIREASRR 306

Search completed: October 1, 2004, 12:19:41
 Job time : 20.6 secs

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 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Cardiac phospholamban (PLB)
 GN PLN.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 [1]
 RN R1 MEDLINE=91268032; PubMed=1828805;
 RA Fujii J., Zaran-Herzberg A., Willard H.F., Tada M., MacLennan D.H.;
 RT "Structure of the rabbit phospholamban gene, cloning of the human
 cDNA, and assignment of the gene to human chromosome 6";
 RL J. Biol. Chem. 266:11669-11675(1991).
 [2]
 RN R2 SEQUENCE FROM N.A.
 RA Salvatore C.A., Jacobson M.A.;
 RL Submitted (XXX-1992) to the EMBL/GenBank/DBJ databases.
 [3]
 RN R3 SEQUENCE FROM N.A.
 RA MEDLINE=99222499; PubMed=10198197;
 RA McTiernan C.F., Frye C.S., Lemster B.H., Kinder E.A.,
 RA Ogletree-Hughes M.L., Moravec C.S., Feldman A.M.;
 RT "The human phospholamban gene: structure and expression";
 RL J. Mol. Cell. Cardiol. 31:679-692(1999).
 [4]
 RN R4 SEQUENCE FROM N.A.
 RA TISSUE=Liver;
 RC MEDLINE=22398257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zerborg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
 RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
 RA Sapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin P.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.N.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [5]
 RN R5 STRUCTURE BY NMR OF 1-25
 RA MEDLINE=95298769; PubMed=7779806;
 RA Mortishire-Smith R.J., Pittenberger S.M., Burke C.J., Middaugh C.R.,
 RA Garsky V.M., Johnson R.G.;
 RT "Solution structure of the cytoplasmic domain of phospholamban:
 RT phosphorylation leads to a local perturbation in secondary
 RT structure";
 RL Biochemistry 34:7603-7613(1995).
 [6]
 RN R6 3D-STRUCTURE MODELING.
 RA MEDLINE=95269058; PubMed=7749920;
 RA Adams P.D., Arkin I.T., Engelman D.M., Bruenger A.T.;
 RT "Computational searching and mutagenesis suggest a structure for the
 RT pentameric transmembrane domain of phospholamban";
 RL Nat. Struct. Biol. 2:154-162(1995).
 [7]
 RN R7 3D-STRUCTURE MODELING.
 RA MEDLINE=98170970; PubMed=9512019;

RA Herzyk P., Hubbard R.E.;
 RT "Using experimental information to produce a model of the
 RT transmembrane domain of the ion channel phospholamban.";
 RL Biophys. J. 74:1203-1214(1998).
 CC -!- FUNCTION: Phospholamban has been postulated to regulate the
 CC activity of the calcium pump of cardiac sarcoplasmic reticulum.
 CC -!- SUBUNIT: Homopentamer.
 CC -!- SUBCELLULAR LOCATION: Membrane.
 CC -!- TISSUE SPECIFICITY: Heart.
 CC -!- PTM: Phosphorylated in response to beta-adrenergic stimulation.
 CC -!- SIMILARITY: Belongs to the phospholamban family.
 CC
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 CC
 CC EMBL; M63603; AAA60083.1; -;
 DR EMBL; M60411; AAA60109.1; -;
 DR EMBL; AF177764; AAD55950.1; -;
 DR EMBL; BC005269; AAH05269.1; -;
 DR EIR; A40424; A40424;
 DR PDB; 1K9N; 14-NOV-01.
 DR PDB; 1KCH; 28-NOV-01.
 DR PDB; 1PLN; 29-DEC-99.
 DR PDB; 1PLP; 31-JUL-95.
 DR PDB; 1PSL; 03-JUN-95.
 DR Genew; HGNC:9080; PLN.
 DR MIM; 172405; -;
 DR InterPro; IPR005984; P_lamban.
 DR Pfam; PF04272; Phospholamban; 1.
 DR TIGRFA; TIGR01294; P_lamban; 1.
 KW Transmembrane; Phosphorylation; Acetylation; 3D-structure.
 FT DOMAIN 1 31 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 32 52 POTENTIAL.
 FT MOD_RES 1 1 ACETYLATION (BY SIMILARITY).
 FT MOD_RES 16 16 PHOSPHORYLATION (BY PKA) (BY SIMILARITY).
 FT MOD_RES 17 17 PHOSPHORYLATION (BY CMK) (BY
 FT TURN 2 3 SIMILARITY).
 FT TURN 4 14
 FT TURN 15 15
 FT TURN 15 15
 SQ SEQUENCE 52 AA; 6108 MW; 0766304A76A854D3 CRC64;
 Query Match 100.0%; Score 75; DB 1; Length 52;
 Best Local Similarity 100.0%; Pred. No. 1.3e-07; Mismatches 0; Gaps 0;
 Matches 16; Conservative 0; Indels 0;
 QY 1 MEKQYLTRSAIRPAS 16
 DB 1 MEKQYLTRSAIRPAS 16
 RESULT 2
 PPLA_MOUSE
 ID PPLA_MOUSE STANDARD; PRT; 52 AA.
 AC P20006;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Cardiac phospholamban (PLB)
 GN PLN.
 OS Mus musculus (Mouse),
 OS Rattus norvegicus (Rat), and
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090, 10116, 9986;
 [1]
 RN R1 SEQUENCE FROM N.A.

DR	HSP; P26678; lPLP.
DR	MGD; MGI:97622; Pln.
DR	InterPro; IPR005984; P_lamban.
DR	Pfam; PF04272; Phospholamban; 1.
DR	TIGRFAMs; TIGR01294; P_lamban; 1.
KW	Transmembrane; Phosphorylation; Acetylation.
FT	DOMAIN 1 31 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 32 52 POTENTIAL.
FT	MOD_RES 1 1 ACETYLATION (BY SIMILARITY).
FT	MOD_RES 16 1 PHOSPHORYLATION (BY PKA) (BY SIMILARITY).
FT	MOD_RES 17 17 PHOSPHORYLATION (BY CAMK) (BY SIMILARITY).
SQ	SEQUENCE 52 AA; 6094 MW; 0763601F76A854D3 CRC64;
Query Match 100.0%; Score 75; DB 1; Length 52;	
Best Local Similarity 100.0%; Pred. No. 1.3e-07;	
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps	
QY	1 MEKVQLTSAIRRAS 16
DG	1 MEKVQLTSAIRRAS 16
RESULT 3	
PPLA_PIG	STANDARD; PRT; 52 AA.
ID_PPLA_PIG	
AC	P07473;
CD	01-APR-1988 (Rel. 07, Created)
DT	01-APR-1988 (Rel. 07, Last sequence update)
DI	10-OCT-2003 (Rel. 42, Last annotation update)
DT	Cardiac phospholamban (PLB).
DE	GN PLN.
GN	Sus scrofa (Pig), and
OS	Canis familiaris (Dog).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_Taxid=9823, 9615;	
[1]	
RP	SEQUENCE FROM N.A.
RC	SPECIES=C.familiaris;
RX	MEDLINE=87083954; PubMed=3793929;
RA	Fujii J., Ueno A., Kitano K., Tanaka S., Kadoma M., Tada M.;
RT	"Complete complementary DNA-derived amino acid sequence of canine
RI	cardiac phospholamban.";
RL	J. Clin. Invest. 79:301-304(1987).
[2]	
RP	SEQUENCE FROM N.A.
RC	SPECIES=C.familiaris; TISSUE=Heart ventricle;
RX	MEDLINE=87316936; PubMed=3628007;
RA	Uyeda A., Kitano K., Fujii J., Kadoma M., Tada M., Tanaka S.;
RT	"The cDNA sequence of the major phospholamban mRNA in canine cardiac
RI	ventricular muscle.";
RL	Nucleic Acids Res. 15:6738-6738(1987).
[3]	
RP	SEQUENCE OF 1-45.
RC	SPECIES=C.familiaris;
RX	MEDLINE=86332152; PubMed=3753485;
RA	Fujii J., Kadoma M., Tada M., Toda H., Sakiyama F.;
RT	"Characterization of structural unit of phospholamban by amino acid
RI	sequencing and electrophoretic analysis.";
RL	Biochem. Biophys. Res. Commun. 138:1044-1050(1986).
[4]	
RP	SEQUENCE OF 10-45.
RC	SPECIES=C.familiaris;
RX	MEDLINE=87008549; PubMed=3759968;
RA	Simmernan H.K.B., Collins J.H., Theibert J.L., Wegener A.D.,
RT	Jones L.R.;
RI	"Sequence analysis of phospholamban. Identification of
RL	phosphorylation sites and two major structural domains.";
[5]	
RP	PHOSPHORYLATION.
RC	SPECIES=C.familiaris;


```

SEQUENCE FROM N.A.
RC STRAIN-MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=22608306; PubMed=12092562;
RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
RT Sakaki Y., Hattori M., Omura S.;
RT "Complete genome sequence and comparative analysis of the industrial
RL microorganism Streptomyces avermitilis.";
RL Nat. Biotechnol. 21:526-531(2003).
CC -!- FUNCTION: This protein is located at the 30S-50S ribosomal subunit
CC interface and may play a role in the structure and function of the
CC aminoacyl-tRNA binding site (By similarity).
CC -!- SIMILARITY: Belongs to the L19P family of ribosomal proteins.
CC
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CC
CC EMBL; AL939124; CAA19387.1; -
CC HAMAP; MF_00402; -; 1
CC InterPro; IPR001857; Ribosomal L19.
CC PRINTS; PF01245; Ribosomal L19; 1.
CC PRODOM; PD002979; Ribosomal L19; 1.
CC TIGRFAMs; TIGR01024; rpls bact; 1.
CC PROSITE; PS01015; RIBOSOMAL L19; 1.
CC TIGRFAMs; TIGR01024; rpls bact; 1.
CC PROSITE; PS01015; RIBOSOMAL L19; 1.
CC Ribosomal protein; Complete proteome.
CC Ribosomal protein; Complete proteome.
CC SEQUENCE 116 AA; 13186 MW; 47081773B07F6EB6 CRC64;
Query Match 54.7%; Score 41; DB 1; Length 116;
Best Local Similarity 46.7%; Pred. No. 1;
Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
QY 1 MEKVQYLTRSAIRRA 15
DB 81 VEKIELVTRGDVERA 95
RESULT 6
RL19_STRCO STANDARD; PRT; 116 AA.
AC Q69883;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 50S ribosomal protein L19.
GN RPLS OR SC05595 OR SC2B1.12.
OS Streptomyces coelicolor, and
OS Streptomyces lividans.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902, 1916;
[1]
SEQUENCE FROM N.A.
RC SPECIES=S.coelicolor; STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953;
RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Quail M.A., Kieser H.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieffer H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble L., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RA "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147(2002).
[2]
SEQUENCE FROM N.A.

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SPECIES=S.lividans; STRAIN=TK21;
RC Parro V., Mellado R.P.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: This protein is located at the 30S-50S ribosomal subunit
CC interface and may play a role in the structure and function of the
CC aminoacyl-tRNA binding site (By similarity).
CC -!- SIMILARITY: Belongs to the L19P family of ribosomal proteins.
CC
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CC
CC EMBL; AL939124; CAA19387.1; -
CC EMBL; Z86111; CAB06800.1; -
CC PIR; T34780; T34780.
CC HAMAP; MF_00402; -; 1
CC InterPro; IPR001857; Ribosomal L19.
CC PRINTS; PF01245; Ribosomal L19; 1.
CC PRODOM; PD002979; Ribosomal L19; 1.
CC TIGRFAMs; TIGR01024; rpls bact; 1.
CC PROSITE; PS01015; RIBOSOMAL L19; 1.
CC Ribosomal protein; Complete proteome.
CC Ribosomal protein; Complete proteome.
CC SEQUENCE 116 AA; 13142 MW; 37D782C6763D0A90 CRC64;
Query Match 54.7%; Score 41; DB 1; Length 116;
Best Local Similarity 46.7%; Pred. No. 1;
Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
QY 1 MEKVQYLTRSAIRRA 15
DB 81 VEKIELVTRGDVERA 95
RESULT 7
RL19_BORBU STANDARD; PRT; 121 AA.
AC O51642;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 50S ribosomal protein L19.
GN RPLS OR BR0899.
OS Borrelia burgdorferi (Lyme disease spirochete).
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=139;
[1]
SEQUENCE FROM N.A.
RC STRAIN=ATCC 35210 / B31;
RX MEDLINE=98065943; PubMed=9403685;
RA Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
RA Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
RA Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
RA Peterson J., Kervage A.R., Quackenbush J., Salzberg S., Hanson M.,
RA van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,
RA Ueberback T., Watthey L., McDonald L., Artiach P., Bowman C.,
RA Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
RA Smith H.O., Venter J.C.;
RA "Genomic sequence of a Lyme disease spirochaete, Borrelia
RT burgdorferi.";
RL Nature 390:580-586(1997).
CC -!- FUNCTION: This protein is located at the 30S-50S ribosomal subunit
CC interface and may play a role in the structure and function of the
CC aminoacyl-tRNA binding site (By similarity).
CC -!- SIMILARITY: Belongs to the L19P family of ribosomal proteins.
CC
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DR EMBL; AE001170; AAC67044.1; -;
 DR PIR; B70187; B70187.
 DR TIGR; BB0699; -;
 DR HAMAP; MF_00402; -; 1.
 DR InterPro; IPR001857; Ribosomal L19.
 DR Pfam; PF01245; Ribosomal L19; 1.
 DR PRINTS; PR00061; RIBOSOMAL_L19.
 DR PRODOM; PD002979; Ribosomal L19; 1.
 DR TIGRFAMS; TIGR01024; rplS_bact; 1.
 DR PROSITE; PS01015; RIBOSOMAL_L19; 1.
 DR Ribosomal protein; Complete proteome.
 KW Ribosomal protein; Complete proteome.
 SQ SEQUENCE 121 AA; 14011 MW; A33F7B1E4DF24070 CRC64;

Query Match 53.3%; Score 40; DB 1; Length 121;
 Best Local Similarity 53.3%; Pred. No. 1.7;
 Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MEKVQLTRSAIRRA 15
 :|||:|:|:|:
 DB 80 IERVEVLRGKVRRA 94

RESULT 8
 SYA_THRC STANDARD; PRT; 871 AA.
 ID SYA_THRC
 AC QHJW4;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Alanine-tRNA synthetase (EC 6.1.1.7) (Alanine-tRNA ligase) (AlaRS).
 GN ALAS OR TA0849.
 OS Thermoplasma acidophilum.

CC Archaea; Euryarchaeota; Thermoplasmatia; Thermoplasmatiales;
 CC Thermoplasmataceae; Thermoplasma.
 CC NCBI_TaxID=2303;
 CC [1]
 CC SEQUENCE FROM N.A.
 CC STRAIN=DSM 1728;
 CC MEDLINE=20479972; PubMed=11029001;
 CC Ruepp A., Graml W., Santos-Martinez M.-L., Korstke K.K., Volker C.,
 CC Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.;
 CC "The genome sequence of the thermoacidophilic scavenger Thermoplasma
 CC acidophilum.";
 CC Nature 407:508-513(2000).

CC -|- CATALYTIC ACTIVITY: ATP + L-alanine + tRNA(Ala) = AMP +
 CC diphosphate + L-alanyl-tRNA(Ala).
 CC -|- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -|- SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.

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 CC -----

DR EMBL; AL445065; CAC11978.1; -;
 DR HAMAP; MF_00036; -; 1.
 DR InterPro; IPR002318; tRNA-synt_2c.
 DR InterPro; IPR006193; tRNA synt_Ala.
 DR Pfam; PF01411; tRNA-synt_2c; 1.
 DR PRINTS; PR00980; TRNASYNTHALA.
 DR TIGRFAMS; TIGR00344; alaS; 1.
 DR PROSITE; PS50860; AA_TRNA_LIGASE_II_ALA; 1.
 DR Aminoacyl-tRNA synthetase; Protein Biosynthesis; Ligase; ATP-binding;
 KW Aminoacyl-tRNA synthetase; Protein Biosynthesis; Ligase; ATP-binding;
 Complete proteome.
 SQ SEQUENCE 871 AA; 99907 MW; 6A6B55478463666D CRC64;

Query Match 52.0%; Score 39; DB 1; Length 871;
 Best Local Similarity 69.2%; Pred. No. 22;
 Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 KQVQLTRSAIRRA 15
 :|||:|:|:|:
 DB 353 KGYLARVLIIRRA 365

RESULT 9

RL19_THETN STANDARD; PRT; 115 AA.
 ID RL19_THETN
 AC Q8R3X4;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE 50S ribosomal protein L19.
 GN RPLS OR TTE1457.
 OS Thermoplasma acidophilum.

CC Bacteria; Firmicutes; Clostridia; Thermoplasmatiales;
 CC Thermoplasmataceae; Thermoplasma.
 CC NCBI_TaxID=119072;
 CC [1]
 CC SEQUENCE FROM N.A.
 CC STRAIN=MB4 / JCM 11007;
 CC MEDLINE=21992816; PubMed=11997336;
 CC Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
 CC Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
 CC Tan H., Chen R., Wang J., Yu J., Yang H.;
 CC "A complete sequence of T. tengcongensis genome.";
 CC Genome Res. 12:699-700(2002).

CC -|- FUNCTION: This protein is located at the 30S-50S ribosomal subunit
 CC interface and may play a role in the structure and function of the
 CC aminoacyl-tRNA binding site (By similarity).
 CC -|- SIMILARITY: Belongs to the L19p family of ribosomal proteins.

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 CC -----

DR EMBL; AE013104; AAM24679.1; -;
 DR HAMAP; MF_00402; -; 1.
 DR InterPro; IPR001857; Ribosomal L19.
 DR Pfam; PF01245; Ribosomal L19; 1.
 DR PRINTS; PR00061; RIBOSOMAL_L19.
 DR PRODOM; PD002979; Ribosomal L19; 1.
 DR TIGRFAMS; TIGR01024; rplS_bact; 1.
 DR PROSITE; PS01015; RIBOSOMAL_L19; 1.
 DR Ribosomal protein; Complete proteome.
 KW Ribosomal protein; Complete proteome.
 SQ SEQUENCE 115 AA; 13395 MW; 9EE39A1B89D3122B CRC64;

Query Match 50.7%; Score 38; DB 1; Length 115;
 Best Local Similarity 40.0%; Pred. No. 3.8;
 Matches 6; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 MEKVQLTRSAIRRA 15
 :|||:|:|:|:
 DB 80 LEKIEVLRGKVRRA 94

RESULT 10

PSD_CHLCV STANDARD; PRT; 299 AA.
 ID PSD_CHLCV
 AC Q82IL3;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Phosphatidylserine decarboxylase preenzyme (EC 4.1.1.65) [Contains:
 CC

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DE Phosphatidylserine decarboxylase alpha chain; Phosphatidylserine
DE decarboxylase beta chain).
DN PSD OR CCA00927.
OS Chlamydomonas reinhardtii.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydiales.
OX NCBI TaxID=83557;
[1] _TaxID=83557;
RN SEQUENCE FROM N.A.
RP STRAIN=GPIC;
RC MEDLINE=22569155; PubMed=12682364;
RX Read T.D., Myers G.S.A., Brunham R.C., Nelson W.C., Paulsen I.T.,
RA Heidelberg J., Holtzapfel E., Khouri H., Federova N.B., Carty H.A.,
RA Umayang L.A., Haft D.H., Peterson J., Beaman M.J., White O.,
RA Salzberg S.L., Hsia R.-C., McClarty G., Rank R.G., Bavovil P.M.,
RA Fraser C.M.;
RT "Genome sequence of Chlamydomonas reinhardtii (Chlamydia sp.)
RT examining the role of niche-specific genes in the evolution of the
RT Chlamydiaceae."
RL Nucleic Acids Res. 31:2134-2147(2003).
CC -!- CATALYTIC ACTIVITY: Phosphatidyl-L-serine =
CC Phosphatidylethanolamine + CO(2).
CC -!- COFACTOR: Pyruvoyl group (By similarity).
CC -!- SIMILARITY: Belongs to the phosphatidylserine decarboxylase
CC family. Subfamily 2.
CC
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CC
CC EMBL; AE016997; AAP05666.1;
CC TIGR; CCA00927;
DR HAMAP; MF_00863;
DR InterPro; IPR003817; PS_Dcarboxylase.
DR InterPro; IPR005221; PS_Dcarboxylase.
DR Pfam; PF02666; PS_Dcarboxylase; 1.
DR TIGRFAMs; TIGR001163; PS_Dcarboxylase; 1.
DR TrEMBL; F02666; PS_Dcarboxylase; 1.
KW Complete proteome.
KW Complete proteome.
KW Complete proteome.
FT CHAIN 1 257 PHOSPHATIDYL SERINE DECARBOXYLASE BETA
FT CHAIN 258 299 CHAIN (BY SIMILARITY).
FT CHAIN 258 299 PHOSPHATIDYL SERINE DECARBOXYLASE ALPHA
FT CHAIN 258 299 CHAIN (BY SIMILARITY).
FT SITE 257 258 CLEAVAGE (NONHYDROLYTIC) (BY SIMILARITY).
FT MOD_RES 258 258 CONVERTED TO A PYRUVYL GROUP (BY
FT SIMILARITY).
FT SEQUENCE 299 AA; 34223 MW; 6F8E837D97E84E0 CRC64;
Query Match 50.7%; Score 38; DB 1; Length 299;
Best Local Similarity 43.8%; Pred. No. 11;
Matches 7; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
QY 1 MEKVQYLRTRSAIRRS 16
DB 1 MKKLQYIDRSTNQRT 16
RESULT 11
APAH ACTAC
ID APAH ACTAC STANDARD; PRT; 275 AA.
AC OS2655;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Bis(5'-nucleosyl)-tetraphosphatase, symmetrical (EC 3.6.1.41)
DE (Diadenosine tetraphosphatase) (APAH hydrolase) (Diadenosine 5',5'-
DE Pl, 5'-tetraphosphate pyrophosphohydrolase).
DE APAH.
OS Actinobacillus actinomycetemcomitans (Haemophilus
OS actinomycetemcomitans).

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RA Setubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities";
RL Nature 417:459-463 (2002).
CC
CC -!- FUNCTION: The sigma factor is an initiation factor that promotes
CC attachment of the RNA polymerase to specific initiation sites and
CC then is released. This is the primary sigma-factor of this
CC bacteria (By similarity).
CC
CC -!- SIMILARITY: Belongs to the sigma-70 factor family.
CC
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CC
CC EMBL: AE012027; AM38630.1; -
CC InterPro: IPR009043; RNA_pol_sigma.
CC InterPro: IPR007631; Sigma70_ner.
CC InterPro: IPR007127; Sigma70_r1.1.
CC InterPro: IPR009042; Sigma70_r1.2.
CC InterPro: IPR007627; Sigma70_r2.
CC InterPro: IPR007624; Sigma70_r3.
CC InterPro: IPR007630; Sigma70_r4.
CC InterPro: IPR000943; Sigma70.
CC Pfam: PF04546; sigma70_ner.1.
CC Pfam: PF03979; sigma70_r1.1; 1.
CC Pfam: PF00140; sigma70_r1.2; 1.
CC Pfam: PF04542; sigma70_r2; 1.
CC Pfam: PF04539; sigma70_r3; 1.
CC Pfam: PF04545; sigma70_r4; 1.
CC PRINTS: PR00046; SIGMA70FCT.
CC PROSITE: PS00715; SIGMA70_1; 1.
CC PROSITE: PS00716; SIGMA70_2; 1.
CC Transcription regulation; Sigma factor; DNA-directed RNA polymerase;
KW DNA-binding; complete proteome.
KW DOMAIN 414 427 POLYMERASE CORE BINDING (POTENTIAL).
FT DNA BIND 584 603 H-T-H MOTIF (BY SIMILARITY).
SQ SEQUENCE 625 AA; 70084 MW; 6B7032460884C850 CRC64;

Query Match 49.3%; Score 37; DB 1; Length 625;
Best Local Similarity 50.8%; Pred. No. 37;
Matches 8; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 1 MEKVQYLRSAIRAS 16
Db 358 MEKANYLTGLGEIKES 373

RESULT 13
H41_BLEJA
ID -H41_BLEJA STANDARD; PRT; 47 AA.
AC P80735;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Histone H4 (Fragment).
OS Blepharisma japonicum.
CC Eukaryota; Alveolata; Ciliophora; Heterotricha; Heterotrichida;
CC Blepharismidae; Blepharisma.
CC NCBI_TaxID=5961;
RN [1]
RP SEQUENCE OF 1-46, AND SEQUENCE OF 9-97 FROM N.A.
RC STRAIN=AS-3;
RX MEDLINE=97257506; PubMed=9103980;
RA Salvini M., Bini E., Santucci A., Batistoni R.;
RT Ciliophora, Heterotrichida;
RL FEMS Microbiol. Lett. 149:93-98 (1997).
CC -!- FUNCTION: Histone H4, along with histone H3, plays a central role
CC in nucleosome formation.
CC -!- SUBUNIT: The nucleosome is an octamer containing two molecules
CC each of H2A, H2B, H3 and H4. The octamer wraps approximately 146
CC bp of DNA.
CC -!- SIMILARITY: Belongs to the histone H4 family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: X97995; CA66634.1; -
CC InterPro: IPR007124; Hist_TAF.
CC InterPro: IPR007125; Histone_core_D.
CC InterPro: IPR001951; Histone_H4.
CC Pfam: PF00125; histone.1.
CC PRINTS: PR00623; HISTONEH4.
CC Prodom: PD001827; Histone_H4; 1.
CC SMART: SM00417; H4; 1.
CC DR PROSITE: PS00047; HISTONE_H4; PARTIAL.
CC Chromosomal protein; Nucleosome core; Nuclear protein; DNA-binding.
KW PROSITE; PS00047; HISTONE_H4; PARTIAL.
FT NON TER 97
SQ SEQUENCE 97 AA; 10722 MW; 64BBB2D65594607C CRC64;

Query Match 48.0%; Score 36; DB 1; Length 97;
Best Local Similarity 53.8%; Pred. No. 7;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

```

```

CC -!- SUBUNIT: The nucleosome is an octamer containing two molecules
CC each of H2A, H2B, H3 and H4. The octamer wraps approximately 146
CC bp of DNA.
CC -!- SIMILARITY: Belongs to the histone H4 family.
CC InterPro: IPR001951; Histone_H4.
CC PRINTS: PR00623; HISTONEH4.
CC Prodom: PD001827; Histone_H4; 1.
CC PROSITE: PS00047; HISTONE_H4; PARTIAL.
CC Chromosomal protein; Nucleosome core; Nuclear protein; DNA-binding.
KW PROSITE; PS00047; HISTONE_H4; PARTIAL.
FT NON TER 47
SQ SEQUENCE 47 AA; 4961 MW; D743BEA73B769ADA CRC64;

Query Match 48.0%; Score 36; DB 1; Length 47;
Best Local Similarity 53.8%; Pred. No. 3;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 EKVOYLRSAIR 14
Db 27 ENIQGITKPAIR 39

RESULT 14
H41_BLEJA
ID -H41_BLEJA STANDARD; PRT; 97 AA.
AC P80737; P90515;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Histone H4-1 (Fragment).
OS Blepharisma japonicum.
CC Eukaryota; Alveolata; Ciliophora; Heterotricha; Heterotrichida;
CC Blepharismidae; Blepharisma.
CC NCBI_TaxID=5961;
RN [1]
RP SEQUENCE OF 1-46, AND SEQUENCE OF 9-97 FROM N.A.
RC STRAIN=AS-3;
RX MEDLINE=97257506; PubMed=9103980;
RA Salvini M., Bini E., Santucci A., Batistoni R.;
RT Ciliophora, Heterotrichida;
RL FEMS Microbiol. Lett. 149:93-98 (1997).
CC -!- FUNCTION: Histone H4, along with histone H3, plays a central role
CC in nucleosome formation.
CC -!- SUBUNIT: The nucleosome is an octamer containing two molecules
CC each of H2A, H2B, H3 and H4. The octamer wraps approximately 146
CC bp of DNA.
CC -!- SIMILARITY: Belongs to the histone H4 family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: X97995; CA66634.1; -
CC InterPro: IPR007124; Hist_TAF.
CC InterPro: IPR007125; Histone_core_D.
CC InterPro: IPR001951; Histone_H4.
CC Pfam: PF00125; histone.1.
CC PRINTS: PR00623; HISTONEH4.
CC Prodom: PD001827; Histone_H4; 1.
CC SMART: SM00417; H4; 1.
CC DR PROSITE: PS00047; HISTONE_H4; PARTIAL.
CC Chromosomal protein; Nucleosome core; Nuclear protein; DNA-binding.
KW PROSITE; PS00047; HISTONE_H4; PARTIAL.
FT NON TER 97
SQ SEQUENCE 97 AA; 10722 MW; 64BBB2D65594607C CRC64;

Query Match 48.0%; Score 36; DB 1; Length 97;
Best Local Similarity 53.8%; Pred. No. 7;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

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Oy 2 EKQVYLTSAIRR 14
Db 26 ENIQITKPAIRR 38

RESULT 15
RL19 CORGL
ID RL19 CORGL STANDARD; PRT; 113 AA.
AC Q8PF56;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE 50S ribosomal protein L19.
GN RPLS OR C81932.
OS Corynebacterium efficiens.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=152794;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
RX MEDLINE=22723752; PubMed=12840036;
RA Nishio Y., Nakamura Y., Kawarabayashi Y., Usuda Y., Kimura E.,
RA Sugimoto S., Matsui K., Yamagishi A., Kikuchi H., Ikeo K.,
RA Gojobori T.;
RT "Comparative complete genome sequence analysis of the amino acid
RT replacements responsible for the thermostability of Corynebacterium
RT efficiens."
RL Genome Res. 13:1572-1575(2003).
CC -!- FUNCTION: This protein is located at the 30S-50S ribosomal subunit
CC interface and may play a role in the structure and function of the
CC aminoacyl-tRNA binding site (By similarity)
CC -!- SIMILARITY: Belongs to the L19p family of ribosomal proteins.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF005220; BAB99430.1; .
CC HAMAP; MF 00402; -; 1.
CC InterPro; IPR001857; Ribosomal L19.
CC Pfam; PF01245; Ribosomal L19; 1.
CC PRINTS; PR00061; RIBOSOMALL19.
CC PRODOM; PD002979; Ribosomal L19; 1.
CC TIGRFAMs; TIGR01024; rpls_bact; 1.
CC PROSITE; PS01015; RIBOSOMAL_L19; 1.
CC Ribosomal protein; Complete proteome.
CC KW Ribosomal L19; 1308 MW; 9BD1C9D25ADA453A CRC64;
CC SQ SEQUENCE 113 AA; 1308 MW; 9BD1C9D25ADA453A CRC64;

Query Match 48.0%; Score 36; DB 1; Length 113;
Best Local Similarity 40.0%; Pred. No. 9.1;
Matches 6; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Oy 1 MEKQVYLTSAIRRA 15
Db 80 LEKIEVVRGVDVRA 94

RESULT 16
RL19 CORGL
ID RL19 CORGL STANDARD; PRT; 113 AA.
AC Q8NNZ0;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 50S ribosomal protein L19.
GN RPLS OR C812037.
OS Corynebacterium glutamicum (Brevibacterium flavum).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

Oy 1 MEKQVYLTSAIRRA 15
Db 80 LEKIEVVRGVDVRA 94

Query Match 48.0%; Score 36; DB 1; Length 113;
Best Local Similarity 40.0%; Pred. No. 9.1;
Matches 6; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Oy 1 MEKQVYLTSAIRRA 15
Db 80 LEKIEVVRGVDVRA 94

RESULT 17
P2C1 ARATH
ID P2C1 ARATH STANDARD; PRT; 434 AA.
AC P49597; Q43717; Q94C87;
DT 01-FEB-1996 (Rel. 33, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Protein phosphatase 2C AB11 (EC 3.1.3.16) (P2C) (Abscissic acid-
DE insensitive 1).
GN AB11 OR AT4G26080 OR F20B18.190.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A., AND VARIANT ASP-180.
RC STRAIN=cv. Landsberg erecta;
RX MEDLINE=94255767; PubMed=8197457;
RA Meyer K., Leube M.P., Grill E.;
RT "A protein phosphatase 2C involved in ABA signal transduction in
RT Arabidopsis thaliana";
RL Science 264:1452-1455(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia; TISSUE=Leaf;
RX MEDLINE=95007758; PubMed=7923358;
RA Mindrinos M., Katagiri F., Yu G.L., Ausubel F.M.;
RT "The A. thaliana disease resistance gene RPS2 encodes a protein
RT containing a nucleotide-binding site and leucine-rich repeats.";
RL Cell 78:1085-1099(1994).
RN [3]

```

RC SEQUENCE FROM N.A.
 RC STRAIN=cv, Columbia; TISSUE=Leaf;
 RX MEDLINE=94255766; PubMed=7910981;
 RA Leung J., Bouvier-Durand M., Morris P.C., Guerrier D., Chefdor F.,
 RA Giraudat J.,
 RT "Arabidopsis ABA response gene AB1: features of a calcium-modulated
 RT protein phosphatase";
 RL Science 264:1448-1452(1994).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv, Columbia;
 RX MEDLINE=20083488; PubMed=10617198;
 RA Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G.,
 RA Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terryn N.,
 RA Harris B., Ansgore W., Brandt P., Grivell L.A., Rieger M.,
 RA Weichselgartner M., de Simone V., Obermaier B., Mache R., Mueller M.,
 RA Kreis M., Delseny M., Puigdomenech P., Watson M., Schmidheini T.,
 RA Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,
 RA Vos P., Kohlsel J., Zimmermann W., Wedler H., Ridley P.,
 RA Langham S.-A., McCullagh B., Bilham L., Robben J.,
 RA Van der Schueren J., Grymonprez B., Chuang Y.-J., Vandenbussche F.,
 RA Braeken M., Weijens I., Voet M., Bastiaens I., Aert R., Defoor E.,
 RA Weitzenegger T., Bothe G., Ransperger U., Hilbert H., Braun M.,
 RA Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W.,
 RA Moeljan P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,
 RA Bernauer S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,
 RA De Keyser A., Buyschaert C., Gielen J., Villarroel R., De Clercq R.,
 RA Van Montagu M., Rogers J., Cronin A., Quail M.A., Bray-Allen S.,
 RA Clark L., Doggett J., Hall S., Kay M., Lennard N., Mclay K., Mayes R.,
 RA Pettett A., Rajandream M.A., Lyne M., Benes V., Rechmann S.,
 RA Borkova D., Bloeker H., Scharte M., Grimm M., Loehnert T.-H.,
 RA Dose S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Partmann B., Granderath K., Dauner D., Herzl A.,
 RA Neumann S., Agirion F., Vitale D., Liguori R., Piravandi E.,
 RA Masseret O., Quigley F., Clabaud G., Muendlein A., Felber R.,
 RA Schnabl S., Hiller K., Schmidt W., Lecharny A., Casacuberta E.,
 RA Chefor F., Cooke R., Berger C., Montfort A., Casacuberta E.,
 RA Gibbons T., Weber N., Vandenbol M., Barques M., Terol J., Torres A.,
 RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,
 RA Heijnen L., Schwarz S., Scholler P., Heber S., Francis P., Bielke C.,
 RA Fishman D., Haase D., Lemcke K., Meves H.-W., Stocker S.,
 RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,
 RA Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L.,
 RA Sekhon M., Murray J., Sheet P., Cordes M., Abu-Irheidh J.,
 RA Sconeking T., Kallick J., Graves T., Harmon G., Edwards J.,
 RA Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
 RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
 RA Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.W.,
 RA Nelson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D.,
 RA Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Joshi C.,
 RA Antoniou B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
 RA Ma P., Zhong J., Preston R., Vil D., Shekner M., Matero A., Shah R.,
 RA Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S.,
 RA Granat S., Shohdy N., Hasegawa A., Hameed A., Lodhi M., Johnson A.,
 RA Chen E., Marra M.A., Martienssen R., McCombie W.R.;
 RT "Sequence and analysis of chromosome 4 of the plant Arabidopsis
 RT thaliana";
 RL Nature 402:769-777(1999).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv, Columbia;
 RX MEDLINE=22954850; PubMed=14593172;
 RA Yamada K., Lim J.M., Chen H., Shinn P., Palm C.J.,
 RA Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,
 RA Karlin-Newman G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,
 RA Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,
 RA Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Anesari Y.,
 RA Arakawa T., Bann J., Banno F., Bowser L.D., Brooks S.F., Carninci P.,
 RA Chao C., Choy N., Enju A., Goldsmith A.D., Gurtal M., Hansen N.F.,
 RA Hayashizaki Y., Johnson-Hopson C., Hsuan V.W., Iida K., Karnes M.,
 RA Khan S., Kossena E., Ishida J., Jiang P.X., Jones T., Kawai J.,
 RA Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,
 RA Satou M., Tamse R., Vaysberg M., Wallender E.K., Wong C., Yamamura Y.,

RA Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
 RT "Empirical analysis of transcriptional activity in the Arabidopsis
 RT genome";
 RL Science 302:842-846(2003).
 CC -!- FUNCTION: Involved in abscisic acid (ABA) signaling pathway.
 CC -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
 CC phosphate.
 CC -!- COFACTOR: Binds 2 magnesium or manganese ions (By similarity).
 CC -!- SIMILARITY: Belongs to the PP2C family.
 CC
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 CC
 CC EMBL: X78986; CAA55484.1; -
 CC EMBL: UL2856; AAS50237.1; -
 CC EMBL: X77116; CAA54383.1; -
 CC EMBL: AL049483; CAB39673.1; -
 CC EMBL: AL161564; CAB79463.1; -
 CC EMBL: AY035073; AAK59578.1; -
 CC FIR: T04263; T04263.
 CC HSSP: P35813; 1A6Q.
 CC InterPro: IPR002048; EF-hand.
 CC InterPro: IPR001332; PP2C-like.
 CC InterPro: IPR000222; PP2C.
 CC Pfam: PF00481; PP2C; 1.
 CC SMART: SM00331; PP2C SIG; 1.
 CC SMART: SM00332; PP2C; 1.
 CC PROSITE: PS00018; EF HAND; 1.
 CC PROSITE: PS01032; PP2C; 1.
 CC Hydrolase; Magnesium; Manganese; Multigene family; Calcium-binding.
 KW CALBIND 93 104
 FT DOMAIN 417 420
 FT VARIANT 190 180
 FT G -> D (WILTY PHENOTYPE AND ABA-
 FT INSENSITIVE SEED GERMINATION AND GROWTH).
 FT G -> R (IN REF. 5).
 FT CONFLICT 105 105 I -> V (IN REF. 1).
 FT SEQUENCE 434 AA; 47505 MW; 4A4C54F04195F572 CRC64;
 SQ
 Query Match. 48.0%; Score 36; DB 1; Length 434;
 Best Local Similarity 43.8%; Pred. No. 39;
 Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
 QY 1 MEKQVLTFRSAIRAS 16
 Db 396 MSAAEYLSKLAIQGS 411
 ID 2ASA HUMAN STANDARD; PRT; 486 AA.
 AC Q15172;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Serine/threonine protein phosphatase 2A, 56 kDa regulatory subunit,
 DE alpha isoform (PP2A, B subunit, B' alpha isoform) (PP2A, B
 DE subunit, RS alpha isoform).
 GN PPP2R5A.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Breast Cancer;
 RX MEDLINE=96064678; PubMed=7592815;
 RA McCright B., Virshup D.M.;

RT "Identification of a new family of protein phosphatase 2A regulatory subunits." J. Biol. Chem. 270:26123-26128(1995).

RN [2]

RP SEQUENCE OF 47-56; 129-132; 347-354; 448-462 AND 471-480.

RC TISSUE=Brain;

RX MEDLINE=96276417; PubMed=8694763;

RA Zolnierowicz S., van Hoof C., Andjelkovic N., Cron P., Stevens I., Marlevede W., Goris J., Hemmings B.A.;

RA "The variable subunit associated with protein phosphatase 2A defines a novel multimer family of regulatory subunits.";

RT Biochem. J. 317:187-194(1996).

RN [3]

RP PHOSPHORYLATION, AND SUBCELLULAR LOCATION.

RX MEDLINE=96355607; PubMed=8703017;

RA McCright B., Rivers A.M., Audlin S., Virshup D.M.;

RA "The B56 family of protein phosphatase 2A (PP2A) regulatory subunits encodes differentiation-induced phosphoproteins that target PP2A to both nucleus and cytoplasm.";

RT J. Biol. Chem. 271:22081-22089(1996).

CC -!- FUNCTION: The B regulatory subunit might modulate substrate selectivity and catalytic activity, and also might direct the localization of the catalytic enzyme to a particular subcellular compartment.

CC -!- SUBUNIT: PP2A consists of a common heterodimeric core enzyme, composed of a 36 kDa catalytic subunit (subunit C) and a 65 kDa constant regulatory subunit (PR65 or subunit A), that associates with a variety of regulatory subunits. Proteins that associate with the core dimer include three families of regulatory subunits B (the R2/B/PR55/B55, R3/B-/PR72/PR130/PR59 and R5/B-/B56 families), the 48 kDa variable regulatory subunit, viral proteins, and cell signaling molecules.

CC -!- SUBCELLULAR LOCATION: Cytoplasmic.

CC -!- TISSUE SPECIFICITY: Widely expressed with the highest expression in heart and skeletal muscle.

CC -!- PTM: Phosphorylated on serine residues.

CC -!- SIMILARITY: Belongs to the phosphatase 2A regulatory subunit B family.

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DR EMBL; L42373; AAC37601.1; -

DR PIR; I55449; I55449

DR Genbank; HGNC:9309; PFP2R5A.

DR MIM; 601643; -

DR GO; GO:0005737; C:cytoplasm; TAS.

DR GO; GO:0008601; F:protein phosphatase type 2A, intrinsic regu. . . ; TAS.

DR InterPro; IPR008938; ARM.

DR InterPro; IPR002554; B56.

DR Pfam; PF01603; B56; 1.

DR Phosphorylation; Multigene family.

KW DOMAIN 2 5 POLY-SER.

FT CONFLICT 52 52 E -> F (IN REF. 2; AA SEQUENCE).

FT CONFLICT 54 54 H -> S (IN REF. 2; AA SEQUENCE).

FT CONFLICT 451 451 R -> E (IN REF. 2; AA SEQUENCE).

SQ SEQUENCE 486 AA; 56193 MW; D314077032A6D44 CRC64;

Query Match 48.0%; Score 36; DB 1; Length 486;

Best Local Similarity 50.0%; Pred. No. 44;

Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 2 EKQVQLTSAIRRA 15

Db 19 EKVDGFTKSVRKA 32

RESULT 19

RPSD XANCP

ID RPSD XANCP STANDARD; PRT; 624 AA.

AC Q8P4E2;

DT 10-OCT-2003 (Rel. 42, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DE RNA polymerase sigma factor rpoD (Sigma-70).

DE RPOD OR XCC3736.

OS Xanthomonas campestris (pv. campestris).

OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;

OC Xanthomonadaceae; Xanthomonas.

OX NCBI_TaxID=340;

RN [1]

RP SEQUENCE FROM N.A.

RX STRAIN=ATCC 33913 / NCPPB 528;

RX MEDLINE=2202145; PubMed=12024217;

RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R., Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F., Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A., Cicarotte G., Cannavan F., Cardoso J., Chamberg F., Ciapina L.P., Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H., Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T., Formighieri E.F., Franco M.C., Greggio C.C., Gruber A., Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F., Locall E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M., Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H., Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R., Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F., Spindola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D., Trindade dos Santos M., Truffi D., Tsai S.M., White F.F., Serubal J.C., Kitajima J.P.;

RA "Comparison of the genomes of two Xanthomonas pathogens with differing host specificities.";

RT Nature 417:459-463(2002).

CC -!- FUNCTION: The sigma factor is an initiation factor that promotes attachment of the RNA polymerase to specific initiation sites and then is released. This is the primary sigma-factor of this bacteria (By similarity).

CC -!- SIMILARITY: Belongs to the sigma-70 factor family.

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DR EMBL; AE012494; AAM42993.1; -

DR InterPro; IPR009043; RNA_pol_sigma.

DR InterPro; IPR007631; Sigma70_ner.

DR InterPro; IPR007127; Sigma70_r1.

DR InterPro; IPR009042; Sigma70_r1_2.

DR InterPro; IPR007627; Sigma70_r2.

DR InterPro; IPR007624; Sigma70_r3.

DR InterPro; IPR007630; Sigma70_r4.

DR InterPro; IPR000943; Sigma70_r4.

DR Pfam; PF04546; sigma70_ner; 1.

DR Pfam; PF03979; sigma70_r1; 1.

DR Pfam; PF00140; sigma70_r1_2; 1.

DR Pfam; PF04542; sigma70_r2; 1.

DR Pfam; PF04539; sigma70_r3; 1.

DR Pfam; PF04545; sigma70_r4; 1.

DR PRINTS; PR00046; SIGMA70PCT.

DR PROSITE; PS00715; SIGMA70_1; 1.

DR PROSITE; PS00716; SIGMA70_2; 1.

KW Transcription regulation; Sigma factor; DNA-directed RNA polymerase;

KW DNA-binding; Complete proteome.

FT DOMAIN 413 426 POLYMERASE CORE BINDING (POTENTIAL).

FT DNA BIND 583 602 H-T-H MOTIF (BY SIMILARITY).

SQ SEQUENCE 624 AA; 69947 MW; 1F6C8CA093F7F1AF CRC64;

Query Match 48.0%; Score 36; DB 1; Length 624;

Best Local Similarity 50.0%; Pred. No. 57;
Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 MEKVOYLTRSAIRAS 16
DB 357 MEKANYLTAEIKDIS 372

RESULT 20
CHLD SYN7
ID CHLD SYN7 STANDARD; PRT; 677 AA.
AC 007345;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Magnesium-chelatase subunit CHLD (Mg-protoporphylin IX chelatase) (Mg-chelatase subunit D).
DB CHLD.
GN Synechococcus sp. (strain PCC 7942) (Anacystis nidulans R2).
OS Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
OX NCBI_TaxID=1140;
RN [1]
RP SEQUENCE FROM N.A.
RA Masuda T., Nakayama M., Ohta H., Takayama K.-I.;
RT "Cloning and sequencing of a chld gene encoding a subunit of
RT magnesium-chelatase from the cyanobacterium Synechococcus sp. PCC
RT 7942.";
RL (In) Plant Gene Register PGR97-091.
CC -!- FUNCTION: Involved in chlorophyll biosynthesis; introduces a
CC magnesium ion into protoporphylin IX to yield Mg-protoporphylin
CC IX.
CC -!- PATHWAY: Chlorophyll biosynthesis.
CC -!- SIMILARITY: BELONGS TO THE MG-CHELATASE SUBUNITS D/I FAMILY.
CC -!- SIMILARITY: Contains 1 VWFA domain.
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AB003135; BAA20346.1; -
CC InterPro; IPR003593; AAA_ATPase.
CC InterPro; IPR000523; MG_chelatase_chII.
CC InterPro; IPR002035; VWFA.
CC Pfam; PF01078; MG_chelatase; 1.
CC Pfam; PF00092; vwa; 1.
CC SMART; SM00382; AAA; 1.
CC SMART; SM00327; VWFA; 1.
CC PROSITE; PS0234; VWFA; 1.
KW Photosynthesis; Chlorophyll biosynthesis; ATP-binding.
FT DOMAIN 481 676
FT DOMAIN 329 333
FT SEQUENCE 677 AA; 73367 MW; 7E2988E096DF5506 CRC64;
Query Match 48.0%; Score 36; DB 1; Length 677;
Best Local Similarity 58.3%; Pred. No. 63;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 EKVOYLTRSAIR 13
DB 267 EQGYLVREAIR 278

RESULT 21
DVL2 XENLA
ID DVL2 XENLA STANDARD; PRT; 736 AA.
AC P51172;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE DE Segment polarity protein dishevelled homolog DVL-2 (Dishevelled-2)
DE (DSH homolog 2) (Xdeh).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RP TISSUE=Oocyte;
RX MEDLINE=95324391; PubMed=7600981;
RA Sokol S.Y., Klingensmith J., Perrimon N., Itoh K.;
RT "Dorsalizing and neuralizing properties of Xdeh, a maternally
RT expressed Xenopus homolog of dishevelled.";
RL Development 121:1637-1647(1995).
RN [2]
RP ERRATUM.
RX MEDLINE=96017659; PubMed=7588081;
RA Sokol S.Y., Klingensmith J., Perrimon N., Itoh K.;
RL Development 121:3487-3487(1995).
CC -!- FUNCTION: May play a role in the signal transduction pathway
CC mediated by multiple Wnt genes. Plays a role in dorsal axis
CC formation and in neural induction.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -!- TISSUE SPECIFICITY: Ubiquitous protein found equally distributed
CC in both animal-vegetal and dorsal-ventral directions.
CC -!- DEVELOPMENTAL STAGE: Maternal gene detected in different
CC developmental stages being most abundant in eggs.
CC -!- SIMILARITY: Belongs to the DSH family.
CC -!- SIMILARITY: Contains 1 DEP domain.
CC -!- SIMILARITY: Contains 1 PDZ/DHR domain.
CC -!- SIMILARITY: Contains 1 DIX domain.
CC
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CC
CC EMBL; U31552; AAB00688.1; -
CC PIR; I51691; I51691.
CC HSP; Q12923; 3PDZ.
CC InterPro; IPR000591; DEP.
CC InterPro; IPR008339; Dishevel.
CC InterPro; IPR003351; Dishevelled.
CC InterPro; IPR008341; Dishevelled_2.
CC InterPro; IPR001158; DIX.
CC InterPro; IPR001478; PDZ.
CC Pfam; PF00610; DEP; 1.
CC Pfam; PF02377; Dishevelled; 1.
CC Pfam; PF00778; DIX; 1.
CC Pfam; PF00595; PDZ; 1.
CC PRINTS; PR01760; DISHEVELLED.
CC PRINTS; PR01762; DISHEVELLED2.
CC ProDom; PD003639; DIX; 1.
CC SMART; SM00021; DAX; 1.
CC SMART; SM00049; DEP; 1.
CC SMART; SM00228; PDZ; 1.
CC PROSITE; PS50186; DEP; 1.
CC PROSITE; PS50641; DIX; 1.
CC PROSITE; PS50106; PDZ; 1.
KW Wnt signaling pathway; Developmental protein.
FT DOMAIN 1 82
FT DOMAIN 99 113
FT DOMAIN 222 227
FT DOMAIN 254 326
FT DOMAIN 428 502
FT DOMAIN 630 687
FT SEQUENCE 736 AA; 79787 MW; AF6C9A1662DD7CEB CRC64;
Query Match 48.0%; Score 36; DB 1; Length 736;

Best Local Similarity 70.0%; Pred. No. 69;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 5 QYLTRSAIRR 14
Db 624 EYSTRSSIRR 633

RESULT 22

HXK3 RAT
ID HXK3 RAT STANDARD; PRT; 924 AA.
AC P27926;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hexokinase type III (EC 2.7.1.1) (HK III).
GN HK3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=91378267; PubMed=1897938;
RA Schwab D.A.; Wilson J.E.;
RT "Complete amino acid sequence of the type III isozyme of rat hexokinase, deduced from the cloned cDNA";
RL Arch. Biochem. Biophys. 285:365-370(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA White J.A.;

RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.

CC -1- CATALYTIC ACTIVITY: ATP + D-hexose = ADP + D-hexose 6-phosphate.

CC -1- ENZYME REGULATION: Hexokinase is an allosteric enzyme inhibited by

CC its product Glc-6-P.

CC -1- PATHWAY: First step of several metabolic pathways.

CC -1- SUBUNIT: Monomer.

CC -1- DOMAIN: THE N- AND C-TERMINAL HALVES OF THIS HEXOKINASE SHOW

CC EXTENSIVE SEQUENCE SIMILARITY TO EACH OTHER. THE CATALYTIC

CC ACTIVITY IS ASSOCIATED WITH THE C-TERMINUS WHILE REGULATORY

CC FUNCTION IS ASSOCIATED WITH THE N-TERMINUS.

CC -1- MISCELLANEOUS: In vertebrates there are four major glucose-

CC phosphorylating isoenzymes, designated hexokinase I, II, III and

CC IV (glucokinase).

CC -1- SIMILARITY: Belongs to the hexokinase family.

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CC EMBL; U73859; AAB18253.1; --

DR PIR; S13913; S13913.

DR HSSP; P05708; 1B33.

DR InterPro; IPR001312; Hexokinase.

DR Pfam; PF03727; hexokinase2; 2.

DR PRINTS; PR00475; HEXOKINASE.

DR ProDom; PDC01109; Hexokinase; 2.

DR PROSITE; PS00378; HEXOKINASES; 2.

KW Transferase; Kinase; Glycolysis; Allosteric enzyme; Repeat;

KW ATP-binding; Membrane

FT DOMAIN 1 488 REGULATORY.

FT DOMAIN 489 924 CATALYTIC.

FT DOMAIN 162 188 GLUCOSE-BINDING (POTENTIAL).

FT DOMAIN 604 630 GLUCOSE-BINDING (POTENTIAL).

FT NP_BIND 95 100 ATP (POTENTIAL).

FT NP_BIND 542 547 ATP (POTENTIAL).

SQ SEQUENCE 924 AA; 100253 MW; 0162C1591AF040AC CRC64;

Query Match 48.0%; Score 36; DB 1; Length 924;

Best Local Similarity 61.5%; Pred. No. 88;

Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 EKVOYLTRSAIRR 14

Db 638 QDVVYLLREAIR 650

RESULT 23

RPOB_MESVI

ID RPOB_MESVI STANDARD; PRT; 1080 AA.

AC Q9MUS5;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE DNA-directed RNA polymerase beta chain (EC 2.7.7.6).

GN RPOB

OS Mesostigma viride.

OG Chloroplast.

OC Eukaryota; Viridiplantae; Streptophyta; Mesostigmatophyceae;

OC Mesostigmatales; Mesostigmataceae; Mesostigma.

OX NCBI_TaxID=41882;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=NIES-296;

RX MEDLINE=20150907; PubMed=10688199;

RA Lemieux C.; Otis C.; Turmel M.;

RT "Arcestral chloroplast genome in Mesostigma viride reveals an early

branch of green plant evolution.";

RL Nature 403:649-652(2000).

CC -1- FUNCTION: DNA-dependent RNA polymerase catalyzes the transcription

of DNA into RNA using the four ribonucleoside triphosphates as

substrates.

CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +

CC {RNA}(N).

CC -1- SUBUNIT: In chloroplasts, the RNA polymerase is composed of four

subunits: alpha, beta, beta', and beta''.

CC -1- SUBCELLULAR LOCATION: Chloroplast.

CC -1- SIMILARITY: Belongs to the RNA polymerase beta chain family.

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CC EMBL; AF166114; AAP43826.1; --

DR HSSP; Q9KWU7; JHQM.

DR InterPro; IPR007121; RNA_pol_B.

DR InterPro; IPR007644; RNA_pol_Rpb2_1.

DR InterPro; IPR007642; RNA_pol_Rpb2_2.

DR InterPro; IPR007645; RNA_pol_Rpb2_3.

DR InterPro; IPR007120; RNA_pol_Rpb2_6.

DR InterPro; IPR007641; RNA_pol_Rpb2_7.

DR Pfam; PF04563; RNA_pol_Rpb2_1; 1.

DR Pfam; PF04561; RNA_pol_Rpb2_2; 1.

DR Pfam; PF04565; RNA_pol_Rpb2_3; 1.

DR Pfam; PF00562; RNA_pol_Rpb2_6; 1.

DR Pfam; PF04560; RNA_pol_Rpb2_7; 1.

DR PROSITE; PS01166; RNA_POL_BETA; 1.

KW Transferase; DNA-directed RNA polymerase; Transcription; Chloroplast.

SQ SEQUENCE 1080 AA; 121910 MW; 6FECCLBDB547422A CRC64;

Query Match 48.0%; Score 36; DB 1; Length 1080;

Best Local Similarity 43.8%; Pred. No. 1e+02;

Matches 7; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MEKVQYLTRSAIRRAS 16

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Db      66 LKPKYNTERTSIRAS 81
RESULT 24
RL28 DRONE
ID      RL28 DRONE          STANDARD;          PRT;          144 AA.
AC      QVZS5;
DT      28-FEB-2003 (Rel. 41, Created)
DT      28-FEB-2003 (Rel. 41, Last sequence update)
DT      10-OCT-2003 (Rel. 42, Last annotation update)
DE      608 ribosomal protein L28.
CN      CG12740.
OS      Drosophila melanogaster (Fruit fly).
OC      Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC      Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC      Sphingroidea; Drosophilidae; Drosophila.
OX      NCBI_TaxID=7227;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=Berkeley;
RX      MEDLINE=20196006; PubMed=10731132;
RA      Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA      Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA      George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA      Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA      Brannon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA      Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA      Abril J.P., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA      Ballew R.M., Basu A., Baxendale J., Bayraktoglu L., Beasley E.M.,
RA      Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA      Borkova D., Botchan M.R., Bouck J., Brockstein P., Brotter P.,
RA      Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA      Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA      de Pablo S., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA      Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA      Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA      Fosler G., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA      Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA      Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA      Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA      Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA      Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA      Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA      Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA      Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA      Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA      Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclebb J.M.,
RA      Palazolo M., Fittman G.S., Pan S., Follard J., Puri V., Reese M.G.,
RA      Reinart K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA      Shue B.C., Siden-Klanos I., Simpson M., Skupski M.P., Smith T.,
RA      Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA      Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA      Wang Z.-Y., Wassman D.A., Weinstock G.M., Weissbach J.,
RA      Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA      Ye J., Yeh R.-F., Zavari J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA      Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA      Glöbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT      "The genome sequence of Drosophila melanogaster."
RL      Science 287:2185-2195(2000).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN=Berkeley;
RX      MEDLINE=22426066; PubMed=12537569;
RA      Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M.,
RA      George R.A., Guarin H., Krommiller B., Paclebb J.M., Park S., Wan K.H.,
RA      Rubin G.M., Celniker S.E.;
RT      "A Drosophila full-length cDNA resource."
RL      Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).
CC      -/- SIMILARITY: Belongs to the L28E family of ribosomal proteins.
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CC      -----
DR      EMBL; AE003477; AAF47742.1; -
DR      EMBL; AY071444; AAL49066.1; -
DR      FlyBase; FBgn0035422; CG12740.
DR      GO; GO:0005842; Cytoplasmic large ribosomal subunit (sensu Eu. . .; ISS.
DR      GO; GO:0003735; F:structural constituent of ribosome; ISS.
DR      GO; GO:0006412; P:protein biosynthesis; ISS.
DR      InterPro; IPR002672; Ribosomal_L28e.
DR      Pfam; PF01778; Ribosomal_L28e; 1.
DR      ProDom; PD010767; Ribosomal_L28e; 1.
KW      Ribosomal protein.
SQ      SEQUENCE 144 AA; 16029 MW; 14D5C7866F585113 CRC64;
Query Match 46.7%; Score 35; DB 1; Length 144;
Best Local Similarity 70.0%; Pred.No. 18;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY      7 LTRSAIRRAS 16
Db      110 LTRSAIRRAS 119
ID      AMIR_PSEAE          STANDARD;          PRT;          196 AA.
AC      P10332.
DT      01-JUL-1989 (Rel. 11, Created)
DT      16-OCT-2001 (Rel. 40, Last sequence update)
DT      10-OCT-2003 (Rel. 42, Last annotation update)
DE      Aliphatic amidase regulator.
GN      AMIR OR PA3363.
OS      Pseudomonas aeruginosa.
OC      Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC      Pseudomonadaceae; Pseudomonas.
OX      NCBI_TaxID=287;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=PAC433;
RX      MEDLINE=89211409; PubMed=2495988;
RA      Lowe N., Rice P.M., Drew R.E.;
RT      "Nucleotide sequence of the aliphatic amidase regulator gene (amir)
RL      of Pseudomonas aeruginosa."
RN      FEBS Lett. 246:39-43(1989).
RP      SEQUENCE FROM N.A.
RC      STRAIN=ATCC 15692 / PA01;
RX      MEDLINE=20437337; PubMed=10984043;
RA      Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,
RA      Hickey M.J., Brinkman F.S.L., Huftnagle W.O., Kowalik D.J., Lagrou M.,
RA      Garber R.L., Brinkman F.S.L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA      Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA      Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA      Reizer J., Salier M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT      "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RL      opportunistic pathogen."
RN      Nature 406:959-964(2000).
RN      [3]
RP      CHARACTERIZATION.
RX      MEDLINE=95286483; PubMed=7539417;
RA      Wilson S.A., Drew R.E.;
RT      "Transcriptional analysis of the amidase operon from Pseudomonas
RL      aeruginosa."
RN      J. Bacteriol. 177:3052-3057(1995).
RN      [4]
RP      X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF COMPLEX WITH AMIC.
RC      STRAIN=PAC1;
RX      MEDLINE=99437995; PubMed=10508151;
RA      O'Hara B.P., Norman R.A., Wan P.T., Roe S.M., Barrett T.E., Drew R.E.,

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RA Pearl L.H.;
RT "Crystal structure and induction mechanism of AmiC-AmiR: a
RL ligand-regulated transcription antitermination complex.";
CC EMBO J. 18:5175-5186(1999).
CC
CC -!- FUNCTION: Positive controlling element of amiE, the gene for
CC aliphatic amidase. Acts as a transcriptional antitermination
CC factor. It is thought to allow RNA polymerase read through a rho-
CC independent transcription terminator between the amiE promoter and
CC gene.
CC
CC -!- SUBUNIT: Forms a complex with amiC.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
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CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL; X13776; CAA32023.1; -.
CC EMBL; AE004758; AAG06751.1; -.
CC PIR; B83226; B83226.
CC PIR; S03884; S03884.
CC PDB; 1000; 23-DEC-99.
CC
CC InterPro; IPR005561; ANTA.
CC InterPro; IPR008327; Res_reg_antiterm.
CC Pfam; PF03861; ANTA; 1.
CC PIRSF; PIRSF036382; Res_reg_antiterm; 1.
CC Transcription regulation; Transcription antitermination; 3D-structure;
CC Complete proteome.
CC CONFLICT 48 48 S -> A (IN REF. 1).
CC CONFLICT 64 64 R -> G (IN REF. 1).
CC CONFLICT 141 141 E -> D (IN REF. 1).
CC CONFLICT 154 154 A -> V (IN REF. 1).
CC CONFLICT 170 170 Y -> H (IN REF. 1).
CC
CC HELIX 3 9
CC HELIX 10 12
CC STRAND 14 18
CC HELIX 23 35
CC TURN 36 36
CC STRAND 38 42
CC STRAND 55 59
CC TURN 64 64
CC TURN 65 75
CC TURN 78 79
CC STRAND 81 86
CC HELIX 91 100
CC TURN 101 101
CC STRAND 104 107
CC HELIX 112 114
CC HELIX 115 160
CC TURN 161 161
CC HELIX 164 176
CC TURN 177 179
CC HELIX 182 189
CC SEQUENCE 196 AA; 21903 MW; 306A4F30E8E4C6C0 CRC64;

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Query Match 46.7%; Score 35; DB 1; Length 196;
Best Local Similarity 53.8%; Pred No 26;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

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Oy 2 EKQYLTSAIRR 14
Db 166 EAHQYLSREAMKR 178

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Search completed: October 1, 2004, 12:18:16
Job time : 12.8 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 1, 2004, 11:56:56 ; Search time 50.8 Seconds
(without alignments)
99.376 Million cell updates/sec

Title: US-09-830-779-8

Perfect score: 75

Sequence: 1 MEKVQLTRSAIRAS 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

SPTREMBL_25:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_rhnc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriap:*

17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	54.7	116	16	Q82JW4
2	41	54.7	451	17	Q9U7T5
3	40	53.3	527	12	Q906Q3
4	40	53.3	998	11	Q8CFM4
5	40	53.3	1104	16	Q87GQ3
6	40	53.3	1108	17	Q58310
7	39	52.0	364	16	Q9A0Y9
8	39	52.0	406	16	Q88JL1
9	39	52.0	421	2	Q9AM36
10	39	52.0	481	17	Q9VLD2
11	39	52.0	644	5	Q868U8
12	38	50.7	119	17	Q285Z5
13	38	50.7	122	17	Q284N9
14	38	50.7	208	16	Q89J03
15	38	50.7	211	16	Q7UFR1
16	38	50.7	252	3	Q9HF62
					Q82JW4 streptomyc
					Q9U7T5 pyrococcus
					Q8CFM4 mus musculu
					Q87GQ3 vibrio para
					Q58310 pyrococcus
					Q9A0Y9 streptococ
					Q88JL1 pseudomonas
					Q9AM36 desulfovibr
					Q9VLD2 pyrococcus
					Q868U8 euplores ae
					Q285Z5 methanobact
					Q284N9 sulfolobus
					Q89J03 bradyrhizob
					Q7UFR1 rhodospirill
					Q9HF62 ashbya goss

Q99ZW6 streptococc
Q8P177 streptococc
Q87811 streptococc
Q8K7S streptococc
Q9F8B7 streptococc
Q84SQ7 oryza sativ
Q8MMG5 dictyosteli
Q8DJ60 synecococc
Q7UWM3 rhodospirill
Q8G413 bifidobacte
Q86701 methanobact
Q33293 mycobacteri
Q7TXV8 mycobacteri
Q32RES rhizobium m
Q8YZH6 anabaena sp
Q8E5S3 streptococc
Q8E046 streptococc
Q8DBN7 vibrio vuln
Q7VDP9 prochloroco
Q9HDW2 schizosacch
Q9V8I5 drosophila
Q9V8I6 drosophila
Q8MLH7 drosophila
Q9EB74 arabidopsis
Q61185 blepharisma
Q61184 blepharisma
Q61183 blepharisma
Q61182 blepharisma
Q62614 protozoaria
Q62586 blepharisma
Q8WM34 ursus marit
Q82VU6 nitrosomona
Q27875 trichomonas
Q07154 mycobacteri
Q8FP56 corynebacte
Q37BD7 thermoplasm
Q8CF99 rattus norv
Q27417 methanobact
Q87Q99 vibrio para
Q8IRB4 drosophila
Q89VD5 bradyrhizob
Q66251 actinobacil
Q96847 dictyosteli
Q23896 dictyosteli
Q92P22 rhizobium m
Q9VZC7 drosophila
Q82RM1 streptomyc
Q914C6 pseudomonas
Q64082 bacterioph
Q31939 bacillus su
Q9REV7 pseudomonas
Q8F7A1 leptospira
Q87XV4 oryza sativ
Q82158 salmonella
Q8TB19 homo sapien
Q97ZB3 sulfolobus
Q08348 xanthomonas
Q9E221 sodalis glo
Q8NFD2 homo sapien
Q9UVJ6 butyrilis ci
Q9XN93 oryza sativ
Q82HP5 streptomyc
Q861F1 dictyosteli
Q9TT68 myotis daub
Q9WSX6 marek's dis
Q8X8E7 escherichia
Q93859 nilaparvata
Q8XR14 ralstonia s
Q86W4 oryza sativ
Q81M84 oryza sativ
Q9E160 wheat strea
Q9VGW4 drosophila
Q9PB15 xanthomonas


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DR InterPro; IPR007095; RNA_pol_DS_PS.
DR InterPro; IPR007094; RNA_pol_PSVir.
DR Pfam; PF00978; RNA_dep_RNAPol2; 1.
KW RNA-directed RNA polymerase.
FT NON_TER 1
SQ SEQUENCE 527 AA; 59276 MW; C445CE1169846132 CRC64;

Query Match 53.3%; Score 40; DB 12; Length 527;
Best Local Similarity 80.0%; Pred. No. 59;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 QYLTRSAIR 14
Db 95 QYVRSAIR 104

RESULT 4
ID Q8CFM4 PRELIMINARY; PRT; 998 AA.
AC Q8CFM4;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Breast tumor;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013626; AA013626.1; -.
DR InterPro; IPR008160; Collagen.
DR Pfam; PF01391; Collagen; 12.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 998 AA; 95451 MW; 2AB4BA953B708AA6 CRC64;

Query Match 53.3%; Score 40; DB 11; Length 998;
Best Local Similarity 42.9%; Pred. No. 1.2e+02;
Matches 6; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MEKVQYLTRSAIR 14
Db 974 METIQWISRLTKR 987

RESULT 5
ID Q87GQ3 PRELIMINARY; PRT; 1104 AA.
AC Q87GQ3;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN VP01262.
OS Vibrio parahaemolyticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=670;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RIMD 2210633 / Serotype O3:K6;
RA MEDLINE=22508454; PubMed=12620739;
RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
RA Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
RT "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
RT distinct from that of V. cholerae."
RL Lancet 361:743-749(2003).
DR EMBL; AP005088; BAC62605.1; -.

KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 1104 AA; 125574 MW; 61C89EE3AB30C3DD CRC64;

Query Match 53.3%; Score 40; DB 16; Length 1104;
Best Local Similarity 42.9%; Pred. No. 1.3e+02;
Matches 6; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MEKVQYLTRSAIR 14
Db 853 LSKIEHTPSAVR 866

RESULT 6
ID O58310 PRELIMINARY; PRT; 1108 AA.
AC O58310;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-JAN-1999 (TrEMBLrel. 09, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 1108AA long hypothetical cell division control protein.
GN PH0606.
OS Pyrococcus horikoshii.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=53953;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OT3;
RX MEDLINE=98344137; PubMed=9679194;
RA Kawarabayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
RA Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb P.T., Horikoshi K.,
RA Mauchi Y., Shizuwa H., Kikuchi H.;
RT "Complete sequence and gene organization of the genome of a hyper-
RT thermophilic archaeobacterium, Pyrococcus horikoshii OT3."
RL DNA Res. 5:55-76(1998).
DR EMBL; AP000003; BAA29695.1; -.
DR PIR; E71104; E71104.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0008094; F:DNA dependent ATPase activity; IEA.
DR GO; GO:0000910; P:cytokinesis; IEA.
DR GO; GO:0006270; P:DNA replication initiation; IEA.
DR GO; GO:0016539; P:protein splicing; IEA.
DR InterPro; IPR003587; Hedgehog_hintC.
DR InterPro; IPR006142; INTEIN.
DR InterPro; IPR006141; Intein_S.
DR InterPro; IPR001208; MCM.
DR InterPro; IPR008045; MCM_2.
DR Pfam; PF00493; MCM; 1.
DR PRINTS; PR00379; INTEIN.
DR PRINTS; PR01657; MCMFAMILY.
DR PRINTS; PR01658; MCMPROTEIN2.
DR ProDom; PD001041; MCM; 2.
DR SMART; SM00305; HintC; 2.
DR SMART; SM00306; HintN; 2.
DR SMART; SM00350; MCM; 1.
DR TIGRFAMs; TIGR01443; intein_Cterm; 2.
DR TIGRFAMs; TIGR01445; intein_Nterm; 2.
DR PROSITE; PS00818; INTEIN_CTER; 2.
DR PROSITE; PS00817; INTEIN_NTER; 2.
DR PROSITE; PS00051; MCM_2_3.
KW Cell division; Complete proteome.
SQ SEQUENCE 1108 AA; 125567 MW; 92D2578B31351E75 CRC64;

Query Match 53.3%; Score 40; DB 17; Length 1108;
Best Local Similarity 53.3%; Pred. No. 1.3e+02;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
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QY 1 MEKVQYLTRSAIRRA 15
DB 668 MEVKDYLTREVERKA 682
|||:|:|
|||:|:|

Query Match 52.0%; Score 39; DB 16; Length 406;
Best Local Similarity 75.0%; Pred. No. 70;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 KVOYLTRSAIRR 14
DB 273 KQVLTREAIRR 284
|||:|:|
|||:|:|

RESULT 9
Q9AM36 PRELIMINARY; PRT; 421 AA.
ID Q9AM36;
AC Q9AM36;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Hypothetical protein SPY0549.
GN SPY0549.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
[1]
RN SEQUENCE FROM N.A.
RP STEIN=SF370 / ATCC 700294 / Serotype M1;
RC MEDLINE=21192684; PubMed=11296296;
RA Ferretti J.J., McShan W.M., Ajdic D.J., Savic G., Lyon K.,
RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,
RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
DR EMBL; AE006512; AAK33542.1; -.
DR Hypothetical protein; Complete proteome.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 364 AA; 41754 MW; 038B8D36F4234020 CRC64;

Query Match 52.0%; Score 39; DB 16; Length 364;
Best Local Similarity 53.8%; Pred. No. 62;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 EKVQYLTRSAIRR 14
DB 307 EKIQYQTRSMYKK 319
|||:|:|
|||:|:|

RESULT 8
Q88LL1 PRELIMINARY; PRT; 406 AA.
ID Q88LL1;
AC Q88LL1;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN Pseudomonas putida (strain KT2440).
OS Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=160488;
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=22423060; PubMed=12534463;
RA Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
RA Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
RA Brinkac L., Beanan M., DeBoy R.T., Daugherty S., Kolonay J.,
RA Madupu R., Nelson W., White O., Peterson J., Khouri H., Hance I.,
RA Chris Lee P., Holtzapple E., Scanlan D., Tran K., Moazzes A.,
RA Uterback T., Rizzo M., Lee K., Koeck D., Ncesti D., Wedler H.,
RA Lauber J., Stjepandic D., Hohnsels J., Straetz M., Helm S.,
RA Kiewitz C., Eisen J., Timmis K.N., Duisterhoef A., Tuemmli B.,
RA Fraser C.M.;
RT "Complete genome sequence and comparative analysis of the
RT metabolically versatile Pseudomonas putida KT2440.";
RL Environ. Microbiol. 4:799-808(2002).
DR EMBL; AE016781; AAN67537.1; -.
DR TIGR; PP1920; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 406 AA; 47318 MW; 7CD8C30DF0D3C6E2 CRC64;

Query Match 52.0%; Score 39; DB 2; Length 421;
Best Local Similarity 50.0%; Pred. No. 73;
Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRAS 16
DB 6 MEKIQVDQSPDPAN 21
|||:|:|
|||:|:|

RESULT 10
Q9VID2 PRELIMINARY; PRT; 481 AA.
ID Q9VID2;
AC Q9VID2;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Hypothetical protein PYRAB04950.
GN PYRAB04950 OR PAB0334.
OS Pyrococcus abyssi.
OC Archaea; Euryarchaeota; Thermococci; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=29292;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=GES / Orsay;
RA Heilig R.;
RT "Pyrococcus abyssi genome sequence: insights into archaeal chromosome
RT structure and evolution.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AT248284; CAB49417.1; -.
DR PIR; B75167; B75167.

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DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0005267; P:potassium channel activity; IEA.
DR GO: GO:0006813; P:potassium ion transport; IEA.
DR InterPro: IPR001622; K-channel pore.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 481 AA; 55655 MW; 685FE30056A45259 CRC64;

Query Match
Best Local Similarity 52.0%; Score 39; DB 17; Length 481;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 2 EKQVLTSAIRRA 15
Db 38 EKIKYIKRAFERA 51

RESULT 11
ID Q868U8 PRELIMINARY; PRT; 644 AA.
AC Q868U8;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Beta-gamma-plaetin precursor.
OS Euploceis aediculatus.
OC Eukaryota; Alveolata; Ciliophora; Spirotrichea; Hypotrichia;
OC Euplotida; Euplotidae; Euploetes.
OX NCBI_TaxID=5940;
[1]
RN R1
RP SEQUENCE FROM N.A.
RX PubMed=12615971;
RA Kioetzel J.A., Baroin-Tourancheau A., Miceli C., Barchetta S.,
FA Farmer J., Banerjee D., Fleury-Aubusson A.;
RT "Cytoskeletal proteins with N-terminal signal peptides: plateins in
the ciliate Euploetes define a new family of articulins.";
RL J. Cell Sci. 116:1291-1303(2003).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22559397; PubMed=12674476;
RA Kioetzel J.A., Baroin-Tourancheau A., Miceli C., Barchetta S.,
FA Farmer J., Banerjee D., Fleury-Aubusson A.;
RT "Plateins: a novel family of signal peptide-containing articulins in
euplotid ciliates.";
RL J. Eukaryot. Microbiol. 50:19-33(2003).
DR EMBL: AY124991; AAM94464.1; -.
KW Signal.
FT SIGNAL
SQ SEQUENCE 644 AA; 74972 MW; 7298E3148FE7417A CRC64;

Query Match
Best Local Similarity 52.0%; Score 39; DB 5; Length 644;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 3 KQVLTSAIR 13
Db 395 EIQVTEAVR 405

RESULT 12
ID O26525 PRELIMINARY; PRT; 119 AA.
AC O26525;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein MTH425.
GN MTH425.
OS Methanobacterium thermoautotrophicum.
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
OC Methanobacteriaceae; Methanothermobacter.
OX NCBI_TaxID=187420;
[1]
RN R1
RP SEQUENCE FROM N.A.

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RC STRAIN=Delta H;
RX MEDLINE=98037514; PubMed=9371463;
RA Smith D.R., Doucette-Stamm L.A., DeLoughery C., Lee H.-M., Dubois J.,
RA Aldridge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
RA Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
RA Jiwan N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
RA McDougall S., Shimer G., Goyal A., Pietrowski S., Church G.M.,
RA Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
RT "Complete genome sequence of Methanobacterium thermoautotrophicum
J. Bacteriol. 179:7135-7155(1997).
DR EMBL: AE000827; AAB84931.1; -.
DR PTR: D69155; D69155.
DR GO: GO:0005874; C:microtubule; IEA.
DR GO: GO:000525; P:GTP binding; IEA.
DR GO: GO:0005198; F:structural molecule activity; IEA.
DR GO: GO:0007018; P:microtubule-based movement; IEA.
DR InterPro: IPR002453; Beta tubulin.
DR PROSITE: PS00228; TUBULIN_B_AUTOREG; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 119 AA; 13045 MW; DBS119ED7630F098 CRC64;

Query Match
Best Local Similarity 50.7%; Score 38; DB 17; Length 119;
Matches 6; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MEKVQYLTSAIRRAS 16
Db 35 MDNMYLTQSTVQSS 50

RESULT 13
ID Q974N9 PRELIMINARY; PRT; 122 AA.
AC Q974N9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein ST0620.
GN ST0620.
OS Sulfolobus tokodaii.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OX NCBI_TaxID=111955;
[1]
RN R1
RP SEQUENCE FROM N.A.
RC STRAIN=JCM 10545 / 7;
RX MEDLINE=21456156; PubMed=11572479;
RA Kawarabayashi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
RA Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.,
RA Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
RA Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
RA Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
RA Oshima T., Kikuchi H.;
RT "Complete genome sequence of an aerobic thermoacidophilic
Crenarchaeon, Sulfolobus tokodaii strain 7.";
RL DNA Res. 8:123-140(2001).
DR EMBL: AP000983; BAB65618.1; -.
DR InterPro: IPR008301; UCP016498.
DR PIRSF: PIRSF016498; UCP016498; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 122 AA; 14467 MW; 98A31A274842EB3 CRC64;

Query Match
Best Local Similarity 50.7%; Score 38; DB 17; Length 122;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MEKVQYLTSAIRR 14
Db 26 MKKIKYLTTEALMK 39

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RESULT 14
Q89J03 ID Q89J03 PRELIMINARY; PRT; 208 AA.
AC Q89J03;
DT 01-JUN-2003 (TRENBLrel. 24, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE B115481 protein.
GN B115481.
OS Bradyrhizobium japonicum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Bradyrhizobium.
OX NCBI_TaxID=375;
RN [1]
RN SEQUENCE FROM N.A.
RP STRAIN=USDA 110;
RX MEDLINE=22484998; PubMed=12597275;
RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
RA Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
RA Kohara M., Matsumoto M., Shimo S., Tsurucka H., Wada T., Yamada M.,
RA Tabata S.;
RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
RT Bradyrhizobium japonicum USDA110."
RL DNA Res. 9:189-197(2002).
RW ENBL; APO05955; BAC50746.1; -.
KW Complete proteome.
SQ SEQUENCE 208 AA; 22494 MW; E461C88B14783C7A CRC64;

Query Match 50.7%; Score 38; DB 16; Length 208;
Best Local Similarity 72.7%; Pred. No. 53;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 QYLTRSAIRRA 15
Db 74 QELTRALRA 84

RESULT 15
Q7UFRI ID Q7UFRI PRELIMINARY; PRT; 211 AA.
AC Q7UFRI;
DT 01-OCT-2003 (TRENBLrel. 25, Created)
DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Thymidine kinase tdk (HC 2.7.1.21).
GN TDK OR RB8399.
OS Rhodospirillum rubrum.
OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
OC Planctomycetaceae; Pirellula.
OX NCBI_TaxID=117;
RN [1]
RN SEQUENCE FROM N.A.
RP STRAIN=1;
RX MEDLINE=22735913; PubMed=12835416;
RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
RA Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,
RA Schlesner H., Amann R., Reinhardt R.;
RT "Complete genome sequence of the marine planctomycete Pirellula sp.
RT strain 1."
RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
RW ENBL; BK294147; CAD78621.1; -.
KW Kinase; Transferrase; Complete proteome.
SQ SEQUENCE 211 AA; 23976 MW; 2FF54BF18F094376 CRC64;

Query Match 50.7%; Score 38; DB 16; Length 211;
Best Local Similarity 37.5%; Pred. No. 54;
Matches 6; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 1 MEKQVLTSAIRRAS 16
Db 86 VDBAQLTTRQVRLS 101

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RESULT 16
Q9HF62 ID Q9HF62 PRELIMINARY; PRT; 252 AA.
AC Q9HF62;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE YC1016C (Fragment).
GN YC1016C.
OS Ashbya gossypii (Yeast) (Bremothecium gossypii).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Ashbya.
OX NCBI_TaxID=33169;
RN [1]
RN SEQUENCE FROM N.A.
RP Wengland J., Philippsen P.;
RT "Isolation and characterization of the Ashbya gossypii BUD3 gene."
RT Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF210625; AAG41241.1; -.
FT NON TER 252 252
SQ SEQUENCE 252 AA; 27793 MW; 20B2C7F284042B76 CRC64;

Query Match 50.7%; Score 38; DB 3; Length 252;
Best Local Similarity 54.5%; Pred. No. 66;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 EKQVLTSAIRRAI 12
Db 228 ERIQLSRSTL 238

RESULT 17
Q99ZW6 ID Q99ZW6 PRELIMINARY; PRT; 376 AA.
AC Q99ZW6;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Putative coproporphyrinogen III oxidase (EC 1.3.3.3).
GN HEMN OR SPY1040.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RN SEQUENCE FROM N.A.
RP STRAIN-SF370 / ATCC 700294 / Serotype M1;
RX MEDLINE=21192684; PubMed=11296296;
RA Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,
RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes."
RT Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
RL EMBL; AE006549; AAK33932.1; -.
DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:0004109; F:coproporphyrinogen oxidase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006779; P:porphyrin biosynthesis; IEA.
DR InterPro; IPR006538; Elp3.
DR InterPro; IPR004559; HemeN_rel.
DR InterPro; IPR007197; Radical SAM.
DR Pfam; PF04055; Radical SAM.
DR SMART; SM00729; Elp3; 1.
DR TIGRfams; TIGR00539; hemN_rel; 1.
KW Oxidoreductase; Complete proteome.
SQ SEQUENCE 376 AA; 43111 MW; 737548C68DB358E3 CRC64;

Query Match 50.7%; Score 38; DB 16; Length 376;
Best Local Similarity 53.3%; Pred. No. 1e-02;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 EKQVLTSAIRRAS 16

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DR Pfam: PF04055; Radical SAM; 1.
SQ SEQUENCE 398 AA; 45841 MW; 669A0563D1206261 CRC64;

Query Match      50.7%; Score 38; DB 16; Length 398;
Best Local Similarity 53.3%; Pred.No. 1.1e+02;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 2 EKQVYLTSAIRRAS 16
Db 124 EXIAVLQSAVNRIS 138
      |||: |||: |||
      |||: |||: |||

RESULT 20
Q8K7R5 PRELIMINARY; PRT; 408 AA.
ID Q8K7R5
AC Q8K7R5;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Putative coproporphyrinogen III oxidase.
DE HEMN OR SPYM3_0673.
GN Streptococcus pyogenes (serotype M3).
OS Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=198466;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS315 / Serotype M3;
RX MEDLINE=22133808; PubMed=12132206;
RA Beres S.B., Sylva G.L., Barbican K.D., Lei B., Hoff J.S.,
RA Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D.,
RA Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
RA Schlievert P.M., Musser J.M.;
RT "Genome sequence of a serotype M3 strain of group A Streptococcus:
RT phage-encoded toxins, the high-virulence phenotype, and clone
RT emergence."
RL Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083 (2002).
RL EMBL; AF014150; AAM79280.1; -.
DR GO; GO:0005373; C:cytoplasm; IEA.
DR GO; GO:0004109; F:coproporphyrinogen oxidase activity; IEA.
DR GO; GO:0006779; P:porphyrin biosynthesis; IEA.
DR InterPro; IPR006638; E1p3
DR InterPro; IPR004559; HEMN_rel
DR InterPro; IPR007197; Radical_SAM.
DR Pfam; PF04055; Radical_SAM; 1.
DR SMART; SM00729; E1p3; 1.
DR TIGRFAMs; TIGR00539; hemN_rel; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 408 AA; 46987 MW; C31113FBA0B1A5AD CRC64;

Query Match      50.7%; Score 38; DB 16; Length 408;
Best Local Similarity 53.3%; Pred.No. 1.1e+02;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 2 EKQVYLTSAIRRAS 16
Db 134 EXIAVLQSAVNRIS 148
      |||: |||: |||
      |||: |||: |||

RESULT 21
Q9F8B7 PRELIMINARY; PRT; 578 AA.
ID Q9F8B7
AC Q9F8B7;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Deor regulator.
DE
OS Streptococcus agalactiae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1311;
RN [1]_
RP SEQUENCE FROM N.A.

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RX MEDLINE-20402586; PubMed-10944228;
RA Lachnauer C.S., Crell R., Michel J.L., Madoff L.C.;
RT "Mosaicism in the alpha-like protein genes of group B streptococci.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:9630-9635(2000).
CC -/- SIMILARITY: BELONGS TO THE DEOR FAMILY OF TRANSCRIPTIONAL
CC REGULATORS.
DR ENBL; AF248038; AAG09976.1; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR InterPro; IPR001034; HTH_Deor.
DR Pfam; PF0C455; deor; 1.
DR SMART; SW00420; HTH_Deor; 1.
DR PROSITE; PS00894; HTH_Deor; 1.
KW DNA-binding; Transcription; Transcription regulation.
SQ SEQUENCE 578 AA; 66770 MW; C1DE7AFB5943B8E3 CRC64;

Query Match 50.7%; Score 38; DB 2; Length 578;
Best Local Similarity 50.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 3 KVQLTRSAIRRAS 16
Db 306 KVQLTRQFIKQIS 319

RESULT 22
Q84S07 PRELIMINARY; PRT; 882 AA.
AC Q84S07;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein OSJNB0047D08.27.
GN OSJNB0047D08.27.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M.,
RA Overton II L.L., Tsitrin T., Kim M.M., Bera J.J., Jin S.S.,
RA Radosh D.W., Tallon L.J., Koo H., Zismann V., Hsiao J., Blunt S.,
RA Vanaken S.S., Riedmuller S.B., Utterback T.T., Feldhiyem T.V.,
RA Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J.,
RA White O., Salzberg S.L., Fraser C.M.;
RT "Oryza sativa chromosome 3 BAC OSJNB0047D08 genomic sequence.";
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Buell R.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR ENBL; AC137925; AAC7264.1; -.
KW Hypothetical protein.
SQ SEQUENCE 882 AA; 96573 MW; 5CDCB01A2569CE0 CRC64;

Query Match 50.7%; Score 38; DB 10; Length 882;
Best Local Similarity 56.2%; Pred. No. 2.5e+02;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 MEKVQLTRSAIRRAS 16
Db 300 VEYSQLLTRCAARRAN 315

RESULT 23
Q8WMG5 PRELIMINARY; PRT; 1223 AA.
ID Q8WMG5

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AC Q8WMG5;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to Homo sapiens (Human). Similar to SWI/SNF related, matrix
DE associated, actin dependent regulator of chromatin, subfamily C,
DE member 1.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AX4;
RA Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P.,
RA Lehmann R., Baumgart C., Parva G., April J.F., Guigo R., Kumpf K.,
RA Tunggal B., Cox B., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.;
RT "Sequence and analysis of chromosome 2 of Dictyostelium discoideum.";
RL Nature 418:79-85(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AX4;
RA Baumgart C.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR ENBL; AC116989; AAM43749.2; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001005; MYB_DNA_binding.
DR InterPro; IPR001673; S_mold_repeat.
DR Pfam; PF00526; S_mold_repeat; 13.
DR SMART; SM00717; SANT; 1.
DR PROSITE; PS0090; MYB_3; 1.
SQ SEQUENCE 1223 AA; 136240 MW; B7D92B2925F39C72 CRC64;

Query Match 50.7%; Score 38; DB 5; Length 1223;
Best Local Similarity 80.0%; Pred. No. 3.6e+02;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 QVLTSAIRR 14
Db 696 QVLTSAIRR 705

RESULT 24
Q8DJ60 PRELIMINARY; PRT; 1541 AA.
ID Q8DJ60;
AC Q8DJ60;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Ferredoxin-dependent glutamate synthase.
GN GLSF OR TLL1368.
OS Synechococcus elongatus (Thermosynechococcus elongatus).
OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
OX NCBI_TaxID=32046;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BP-1;
RX MEDLINE=2225144; PubMed=12240834;
RA Nakamura Y., Kareko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S.,
RA Watanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y.,
RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Nakazaki N.,
RA Shimo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the thermophilic cyanobacterium
RT Thermosynechococcus elongatus BP-1.";
RL DNA Res. 9:123-130(2002).
DR ENBL; AP005373; BAC0920.1; -.
DR GO; GO:0015930; P:glutamate synthase activity; IEA.
DR GO; GO:0006537; P:glutamate biosynthesis; IEA.
DR GO; GO:0006807; P:nitrogen metabolism; IEA.
DR InterPro; IPR002489; DUF14.
DR InterPro; IPR002932; Glu_synthase.
DR InterPro; IPR006982; Glu_synth_cent.

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DR InterPro; IPR006981; Glu synth_NTN.
DR Pfam; PF01645; Glu synthase; 1.
DR Pfam; PF04897; Glu synth_NTN; 1.
DR Pfam; PF04898; Glu synth_central; 1.
DR Pfam; PF01493; GXGXG; 1.
KW Complete proteome.
SQ SEQUENCE 1541 AA; 168017 MW; 9CB26077859306A6 CRC64;

Query Match 50.7%; Score 38; DB 16; Length 1541;
Best Local Similarity 53.3%; Pred. No. 4.6e+02;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MEKVQYLTRSAIRRA 15
Db 162 LERQLYLRKRIERA 176

RESULT 25

Q7UWM3 PRELIMINARY; PRT; 68 AA.
AC Q7UWM3;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN RB1931.
OS Rhodospirillum rubrum
OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
OC Planctomycetaceae; Firellula.
OX NCBI_TaxID=117;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1;
RX MEDLINE=22735913; PubMed=12835416;
RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
RA Ludwig W., Gade D., Beck A., Bozsym K., Heitmann K., Rabus R.,
RA Schliesner H., Amann R., Reinhardt R.;
RT "Complete genome sequence of the marine planctomycete Firellula sp.
strain 1."
RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
DR EMBL; BX294136; CAD72339.1; -
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 68 AA; 7494 MW; 7E1FDF98DB5F67C CRC64;

Query Match 50.0%; Score 37.5; DB 16; Length 68;
Best Local Similarity 66.7%; Pred. No. 20;
Matches 10; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

Qy 3 KVOYLTRSAI-RRAS 16
Db 44 KLFSLRSASIRRAS 58

Search completed: October 1, 2004, 12:17:31
Job time : 56.9 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 1, 2004, 11:56:15 ; Search time 63.2 Seconds

(without alignments)
71.531 Million cell updates/sec

Title: US-09-830-779-17_COPY_1_16

Perfect score: 75

Sequence: 1 MEKVQLTRSAIRAS 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : A_Geneseq_29Jan04:*

1: Geneseq1980s:*

2: Geneseq1990s:*

3: Geneseq2000s:*

4: Geneseq2001s:*

5: Geneseq2002s:*

6: Geneseq2003as:*

7: Geneseq2003bs:*

8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	75	100.0	16	3 AAY71009	Human Pho
2	75	100.0	35	3 AAY71012	Penetrati
3	75	100.0	36	3 AAY71011	Penetrati
4	75	100.0	36	8 ADE45175	Human SER
5	75	100.0	52	3 AAY71003	Human mut
6	75	100.0	52	3 AAY71002	Human Pho
7	75	100.0	52	5 ABP06592	Human ORF
8	75	100.0	52	8 ADE45172	Mouse SER
9	75	100.0	52	8 ADE45170	Rabbit SE
10	75	100.0	52	8 ADE45171	Rat SERCA
11	75	100.0	52	8 ADE45167	Human SER
12	75	100.0	79	3 AAY71019	Aay71019 H6 tagged
13	75	100.0	79	3 AAY71017	Hexahisti
14	72	96.0	52	3 AAY71006	Human mut
15	72	96.0	52	8 ADE45168	Pig SERCA
16	72	96.0	52	8 ADE45169	Dog SERCA
17	72	96.0	35	3 AAY71014	Penetrati
18	71	94.7	35	3 AAY71013	Penetrati
19	71	94.7	35	5 ABB79404	Human Pho
20	71	94.7	52	8 ADE45173	Chicken s
21	71	94.7	79	3 AAY71018	H6 tagged
22	70	93.3	52	3 AAY71005	Human mut
23	69	92.0	52	3 AAY71004	Human mut
24	66	88.0	52	3 AAY71007	Human mut
25	41	54.7	116	7 ADC87928	Ribosomal

26	41	54.7	451	4	AAB96582	Putative
27	40	53.3	121	6	ABU19318	Protein e
28	39	52.0	364	5	ABP29187	Streptoco
29	38	50.7	113	6	ABU26060	Protein e
30	38	50.7	389	2	AAR29657	TGF-beta
31	38	50.7	390	2	AAR27522	TGF-beta
32	38	50.7	408	5	ABP27526	Streptoco
33	37	49.3	339	4	ABP70120	Drosophil
34	37	49.3	376	5	ABP27525	Streptoco
35	37	49.3	569	4	ABG24741	Novel hum
36	36.5	48.7	331	2	AAW71592	Human mye
37	36	48.0	96	4	AAU47163	Propionib
38	36	48.0	96	6	ABM43682	Propionib
39	36	48.0	113	4	AGC91979	C glutami
40	36	48.0	114	6	ABU24569	Protein e
41	36	48.0	155	5	ABP04260	Human ORF
42	36	48.0	207	6	ABU43491	Protein e
43	36	48.0	275	4	ABU52746	Human met
44	36	48.0	387	4	ABE65660	Drosophil
45	36	48.0	401	4	ABB65661	Drosophil
46	36	48.0	409	6	ABU38335	Protein e
47	36	48.0	434	4	AAE01344	Arabidops
48	36	48.0	434	4	AAE01348	Arabidops
49	36	48.0	434	6	AAE36344	Arabidops
50	36	48.0	465	6	ABU20843	Protein e
51	36	48.0	486	7	ADE58782	Human Pro
52	36	48.0	511	4	AAU59773	Propionib
53	36	48.0	511	6	ABM56292	Propionib
54	36	48.0	596	6	ABM65049	Propionib
55	36	48.0	720	5	AAE25100	Human kin
56	36	48.0	765	4	ABE85514	Human pro
57	36	48.0	924	2	AAW37430	Rat hexok
58	36	48.0	924	2	AAW37443	Rat hexok
59	36	48.0	2400	6	ABM70712	Photornab
60	35.5	47.3	319	4	ABE69696	Drosophil
61	35	46.7	24	2	AAY36671	Fragment
62	35	46.7	24	6	ADA11925	Human nov
63	35	46.7	61	4	AAE21036	Peptide #
64	35	46.7	61	4	ABB43216	Peptide #
65	35	46.7	61	4	ABB41248	Peptide #
66	35	46.7	61	4	AAE35032	Peptide #
67	35	46.7	61	4	AAE37056	Peptide #
68	35	46.7	61	4	ABE25244	Protein #
69	35	46.7	61	4	ABE26300	Protein #
70	35	46.7	61	4	AAW74917	Human bon
71	35	46.7	61	4	AAW76948	Human bon
72	35	46.7	61	4	AAE64123	Human bra
73	35	46.7	61	4	ABG62113	Human liv
74	35	46.7	61	4	ABG58610	Human liv
75	35	46.7	61	5	ABG46055	Human pep
76	35	46.7	62	4	AAW94354	Human rep
77	35	46.7	69	4	AAU47311	Propionib
78	35	46.7	69	6	ABM43830	Propionib
79	35	46.7	76	5	ABP07326	Human ORF
80	35	46.7	96	5	ABP33456	Human ORF
81	35	46.7	113	6	ABU33987	Protein e
82	35	46.7	131	2	AAV36660	Fragment
83	35	46.7	131	6	ADA11914	Human nov
84	35	46.7	137	3	ABG08267	Arabidops
85	35	46.7	137	3	ABG48859	Arabidops
86	35	46.7	137	3	AAE14887	Arabidops
87	35	46.7	137	3	AAE48819	Arabidops
88	35	46.7	144	4	ABE58535	Drosophil
89	35	46.7	147	4	AAU46685	Propionib
90	35	46.7	147	6	ABM43204	Propionib
91	35	46.7	156	4	AAU23445	Novel hum
92	35	46.7	190	4	ABE24490	Human pro
93	35	46.7	207	6	ABU43247	Protein e
94	35	46.7	209	4	ABG02969	Novel hum
95	35	46.7	211	5	ABP40291	Staphyloc
96	35	46.7	220	3	AAE48818	Arabidops
97	35	46.7	220	3	AAE48858	Arabidops
98	35	46.7	220	3	AAE14886	Arabidops

99 35 46.7 220 3 AAG08266
100 35 46.7 234 6 ABU29277

Aag08266 Arabidops
Abu29277 Protein e

ALIGNMENTS

RESULT 1
AAV71009
ID AAV71009 standard; peptide; 16 AA.

AC AAV71009;
DT 29-AUG-2000 (first entry)
DE Human Phospholamban (PLB) cargo peptide.
KW Phospholamban; PLB; human; sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a;
KW cardiant; cardiomyocyte; transport peptide; penetratin; cargo peptide;
KW contractilin; cardiac contractility; inhibitor; cardiac disease;
KW treatment; heart failure; myocardial dysfunction.

OS Homo sapiens.
PN WO200025804-A2.
XX 11-MAY-2000.

XX 02-NOV-1999; 99WO-US025692.
XX 02-NOV-1998; 98US-0106718P.
XX 27-JUL-1999; 99US-0145883P.
XX (REGC) UNIV CALIFORNIA.

XX Chien K, Dillman W, Minamisawa S, He H, Hoshijima M, Meyer M;
XX Scott C, Wang Y, Silverman GJ;
XX WPI; 2000-365393/31.

XX Treating cardiac diseases, e.g. heart failure or myocardial dysfunction
XX comprises enhancing cardiac contractility by inhibiting interaction
XX between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine
XX triphosphatase.

XX Example 4; Page 50; 56pp; English.
XX The patent discloses a method for the treatment of heart failure, using
XX small peptide complexes and recombinant proteins, that induces
XX phospholamban (PLB) deficiency and inhibits the interaction between PLB
XX and sarcoplasmic reticulum Ca 2+ ATPase (SERCA2a) within cardiomyocytes.
XX The peptide complex comprises of transport peptide like penetratin and
XX cargo peptide selected from mutant PLB, native PLB or antibody against
XX PLB protein (contractilin). Penetratin-PLB peptide functions as a
XX dominant negative inhibitor of PLB-SERCA2a interaction, enhances cardiac
XX contractility and reduces blood pressure. This method is useful for the
XX treatment of cardiac disease e.g. heart failure and myocardial
XX dysfunction. The present amino acid sequence is the cargo peptide from
XX human PLB amino terminal residues 1-16; it could be derived from any
XX segment of wild type or mutant PLB protein. The cargo peptide is linked
XX to the transport peptide by a covalent linkage

XX Sequence 16 AA;

Query Match 100.0%; Score 75; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 1e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MEKVOYLTRGAIIRAS 16

DB 1 MEKVOYLTRGAIIRAS 16

RESULT 2
AAV71012
ID AAV71012 standard; peptide; 35 AA.

XX AAV71012;
DT 29-AUG-2000 (first entry)
DE Penetratin-based recombinant phospholamban peptide, TAT-PLB.

XX Phospholamban; PLB; human; sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a;
KW cardiant; cardiomyocyte; transport peptide; penetratin; cargo peptide;
KW contractilin; cardiac contractility; inhibitor; cardiac disease;
KW treatment; heart failure; myocardial dysfunction; recombinant peptide;
KW HIV, TAT protein.

OS Homo sapiens.
OS Human immunodeficiency virus.

XX Key Location/Qualifiers
XX 5. .15
FT Region /note= "Corresponds to denatured human immunodeficiency
FT virus (HIV) TAT protein"
FT 16. .35
FT /note= "Corresponds to human phospholamban (PLB) amino
FT terminal peptide"

PN WO200025804-A2.

XX 11-MAY-2000.

XX 02-NOV-1999; 99WO-US025692.

XX 02-NOV-1998; 98US-0106718P.
XX 27-JUL-1999; 99US-0145883P.

XX (REGC) UNIV CALIFORNIA.

XX Chien K, Dillman W, Minamisawa S, He H, Hoshijima M, Meyer M;
XX Scott C, Wang Y, Silverman GJ;
XX WPI; 2000-365393/31.

XX Treating cardiac diseases, e.g. heart failure or myocardial dysfunction
XX comprises enhancing cardiac contractility by inhibiting interaction
XX between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine
XX triphosphatase.

XX Example 5; Page 52; 56pp; English.

XX The patent discloses a method for the treatment of heart failure, using
XX small peptide complexes and recombinant proteins, that induces
XX phospholamban (PLB) deficiency and inhibits the interaction between PLB
XX and sarcoplasmic reticulum Ca 2+ ATPase (SERCA2a) within cardiomyocytes.
XX The peptide complex comprises of transport peptide like penetratin and
XX cargo peptide selected from mutant PLB, native PLB or antibody against
XX PLB protein (contractilin). Penetratin-PLB peptide functions as a
XX dominant negative inhibitor of PLB-SERCA2a interaction, enhances cardiac
XX contractility and reduces blood pressure. This method is useful for the
XX treatment of cardiac disease e.g. heart failure and myocardial
XX dysfunction. The present sequence is the penetratin-based recombinant
XX peptide TAT-PLB, comprising the amino terminal end of human PLB native
XX protein, attached to the 3' end of denatured human immunodeficiency virus
XX (HIV), TAT protein. Penetratin is a class of peptides, with translocating
XX properties having the ability to carry hydrophilic compounds across the
XX plasma membrane

XX Sequence 35 AA;

Query Match 100.0%; Score 75; DB 3; Length 35;
Best Local Similarity 100.0%; Pred. No. 2.4e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQLTRSAIRRAS 16
 DB 16 MEKVQLTRSAIRRAS 31

RESULT 3
 AAY71011
 ID AAY71011 standard; peptide; 36 AA.
 AC AAY71011;
 XX 29-AUG-2000 (first entry)
 DT Penetratin-based recombinant phospholamban peptide, PLB-ANT.
 DE Phospholamban; PLB; human; sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a;
 KW cardiactin; cardiomyocyte; transport peptide; penetratin; cargo peptide;
 KW contractilin; cardiac contractility; inhibitor; cardiac disease;
 KW treatment; heart failure; myocardial dysfunction; recombinant peptide;
 KW fruit fly; antennapedia; ANT.
 XX Homo sapiens.
 OS Drosophila sp.
 XX

Key Location/Qualifiers
 Region 1..20
 FT /note= "Corresponds to human phospholamban (PLB) amino
 FT terminal peptide"
 FT Region 21..36
 FT /note= "Corresponds to Drosophila antennapedia (ANT)
 FT transport peptide"
 XX WO200025804-A2.
 XX 11-MAY-2000.
 XX 02-NOV-1999; 99WO-US025692.
 XX 02-NOV-1998; 98US-0106718P.
 XX 27-JUL-1999; 99US-0145883P.
 XX (REGC) UNIV CALIFORNIA.
 XX Chien K, Dillman W, Minamisawa S, He H, Hoshijima M, Meyer M;
 PI Scott C, Wang Y, Silverman GJ;
 XX WPI; 2000-365393/31.
 XX Treating cardiac diseases; e.g. heart failure or myocardial dysfunction
 PT comprises enhancing cardiac contractility by inhibiting interaction
 PT between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine
 PT triphosphatase.
 XX

Example 5; Page 52; 56pp; English.

The patent discloses a method for the treatment of heart failure, using
 CC small peptide complexes and recombinant proteins, that induces
 CC phospholamban (PLB) deficiency and inhibits the interaction between PLB
 CC and sarcoplasmic reticulum Ca 2+ ATPase (SERCA2a) within cardiomyocytes.
 CC The peptide complex comprises of transport peptide like penetratin and
 CC cargo peptide selected from mutant PLB, native PLB or antibody against
 CC PLB protein (contractilin). Penetratin-PLB peptide functions as a
 CC dominant negative inhibitor of PLB-SERCA2a interaction, enhances cardiac
 CC contractility and reduces blood pressure. This method is useful for the
 CC treatment of cardiac disease e.g. heart failure and myocardial
 CC dysfunction. The present sequence is the penetratin-based recombinant
 CC peptide PLB-ANT, comprising the amino terminal end of human PLB native
 CC protein, attached to the 5' end of the Drosophila antennapedia (ANT)
 CC transport peptide. Penetratin is a class of peptides, with translocating
 CC properties having the ability to carry hydrophilic compounds across the
 CC plasma membrane
 XX

Sequence 36 AA;

Query Match 100.0%; Score 75; DB 3; Length 36;
 Best Local Similarity 100.0%; Pred. No. 2.5e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQLTRSAIRRAS 16
 DB 1 MEKVQLTRSAIRRAS 16

RESULT 4
 ADE45175
 ID ADE45175 standard; peptide; 36 AA.
 AC ADE45175;
 XX 29-JAN-2004 (first entry)
 DT Human SERCA_2 inhibitor phospholamban, cytosolic domain.
 DE Human; SERCA_2; phospholamban; PLB;
 KW Ca2+ ATPase of the sarco/endoplasmic reticulum; protein co-ordinate data;
 KW cardiactin.
 XX Homo sapiens.
 OS US6538022-B1.
 XX 25-MAR-2003.
 PD 18-FEB-1999; 99US-00252063.
 XX 24-SEP-1997; 97US-00937117.
 XX (ORIN) ORION CORP.
 XX Pollesello P, Ovasaka M, Tenhunen J, Vidgren J;
 PI Yliperttula-Ikonen M, Tilgmann C, Lotta T, Kaivola J;
 XX WPI; 2004-019625/02.
 XX New compound, useful for relieving inhibitory effects of phospholamban on
 PT cardiac SR Ca2+-ATPase by deactivating phospholamban and stimulating Ca2+
 PT -ATPase.
 XX Disclosure; SEQ ID NO 9; 65pp; English.

The invention relates to a compound which deactivates, and exhibits
 CC affinity for, a phospholamban (PLB) protein (an inhibitor of SERCA 2,
 CC Ca2+ ATPase of the sarco/endoplasmic reticulum) appearing as ADE45167-
 CC ADE45173. The compound has a structure containing three of the four
 CC moieties: an electronegative moiety associating with an S1 binding site
 CC of the phospholamban cytosolic domain when the compound is bound to it,
 CC the binding site comprises Tyr-6, Arg-9 and/or Arg-13; an electronegative
 CC moiety associating with an S2 binding site of the phospholamban cytosolic
 CC domain when the compound is bound to it, the S2 binding site comprises
 CC Arg-14; a hydrophobic moiety associating with an S3 binding site of the
 CC phospholamban cytosolic domain when the compound is bound, the binding
 CC site comprises Met-20, Lys-27 and/or Leu-28; and a hydrophobic moiety
 CC associating with an S4 binding site of the phospholamban cytosolic domain
 CC when the compound is bound, the binding site comprises Phe-32 and/or Phe-
 CC 35. The compound is not 3-benzyl-5,7-bis ((1H-tetrazol-5-yl)-methoxy)-4-
 CC -methyl-2H-methyl-2H-1-benzopyran-2-one. Also included are deactivating
 CC phospholamban, comprising administering the novel compound to stimulate
 CC the Ca 2+ -ATPase. The compound is useful for relieving the inhibitory
 CC effects of phospholamban on cardiac SERCA_2. The present sequence is the
 CC cytosolic domain of human phospholamban.

Sequence 36 AA;

Query Match 100.0%; Score 75; DB 8; Length 36;
 Best Local Similarity 100.0%; Pred. No. 2.5e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MEKVQYLTRSAIRRAS 16
 DB 1 MEKVQYLTRSAIRRAS 16

RESULT 5
 AAY71003
 ID AAY71003 standard; protein; 52 AA.

XX AC AAY71003;
 XX DT 29-AUG-2000 (first entry)
 XX DE Human mutant phospholamban (PLB) V49A protein.
 XX KW Phospholamban; PLB; human; sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a;
 KW cardiant; cardiomyocyte; transport peptide; penetratin; cargo peptide;
 KW contractilin; cardiac contractility; inhibitor; cardiac disease;
 KW treatment; heart failure; myocardial dysfunction; mutant.
 XX OS Homo sapiens.
 XX OS Synthetic.

XX FH Key Location/Qualifiers
 FT Misc-difference 49 /note= "Wild type Val replaced with Ala"
 FT WO200025804-A2.

XX PN 11-MAY-2000.
 XX PD 02-NOV-1999; 99WO-USO25692.
 XX PR 02-NOV-1998; 98US-0106718P.
 XX PR 27-JUL-1999; 99US-0145883P.
 XX PA (REGC) UNIV CALIFORNIA.

XX PI Chien K, Dillman W, Minamisawa S, He H, Hoshijima M, Meyer M;
 XX PI Scott C, Wang Y, Silverman GJ;
 XX DR WPI; 2000-365393/31.

XX PT Treating cardiac diseases, e.g. heart failure or myocardial dysfunction
 PT comprises enhancing cardiac contractility by inhibiting interaction
 PT between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine
 PT triphosphatase.

XX PS Disclosure; Page 48; 56pp; English.

XX CC The patent discloses a method for the treatment of heart failure, using
 CC small peptide complexes and recombinant proteins, that induces
 CC phospholamban (PLB) deficiency and inhibits the interaction between PLB
 CC and sarcoplasmic reticulum Ca 2+ ATPase (SERCA2a) within cardiomyocytes.
 CC The peptide complex comprises of transport peptide like penetratin and
 CC cargo peptide selected from mutant PLB, native PLB or antibody against
 CC PLB protein (contractilin). Penetratin-PLB peptide functions as a
 CC dominant negative inhibitor of PLB-SERCA2a interaction, enhances cardiac
 CC contractility and reduces blood pressure. This method is useful for the
 CC treatment of cardiac disease e.g. heart failure and myocardial
 CC dysfunction. The present amino acid sequence is the human mutant PLB
 CC protein, comprising a sense mutation Val49Ala. This mutant sequence when
 CC overexpressed in the transformed cardiomyocytes, shows increased
 CC contractility than the wild type PLB sequence

XX SQ Sequence 52 AA;

Query Match 100.0%; Score 75; DB 3; Length 52;
 Best Local Similarity 100.0%; Pred. No. 3.7e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MEKVQYLTRSAIRRAS 16

DB 1 MEKVQYLTRSAIRRAS 16

RESULT 6

AAY71002
 ID AAY71002 standard; protein; 52 AA.

XX AC AAY71002;
 XX DT 29-AUG-2000 (first entry)
 XX DE Human phospholamban (PLB) wild type protein.

XX KW Phospholamban; PLB; human; sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a;
 KW cardiant; cardiomyocyte; transport peptide; penetratin; cargo peptide;
 KW contractilin; cardiac contractility; inhibitor; cardiac disease;
 KW treatment; heart failure; myocardial dysfunction.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
 FT Domain 1..20
 FT /label= Domain Ia
 FT /note= "Rich in alpha-helical confirmation with a net
 FT positive charge"

FT FT Domain 21..30
 FT /label= Domain Ib
 FT /note= "Cytoplasmic sector of the monomer"

FT FT Domain 31..52
 FT /label= Domain II
 FT /note= "Transmembrane sector made of uncharged residues
 FT responsible for stabilising the pentamer formation"

XX PN WO200025804-A2.

XX PD 11-MAY-2000.

XX PR 02-NOV-1999; 99WO-USO25692.

XX PR 02-NOV-1998; 98US-0106718P.

XX PR 27-JUL-1999; 99US-0145883P.

XX PA (REGC) UNIV CALIFORNIA.

XX PI Chien K, Dillman W, Minamisawa S, He H, Hoshijima M, Meyer M;
 XX PI Scott C, Wang Y, Silverman GJ;

XX DR WPI; 2000-365393/31.

XX PT Treating cardiac diseases, e.g. heart failure or myocardial dysfunction
 PT comprises enhancing cardiac contractility by inhibiting interaction
 PT between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine
 PT triphosphatase.

XX PS Disclosure; Page 47; 56pp; English.

XX CC The patent discloses a method for the treatment of heart failure, using
 CC small peptide complexes and recombinant proteins, that induces
 CC phospholamban (PLB) deficiency and inhibits the interaction between PLB
 CC and sarcoplasmic reticulum Ca 2+ ATPase (SERCA2a) within cardiomyocytes.
 CC The peptide complex comprises of transport peptide like penetratin and
 CC cargo peptide selected from mutant PLB, native PLB or antibody against
 CC PLB protein (contractilin). Penetratin-PLB peptide functions as a
 CC dominant negative inhibitor of PLB-SERCA2a interaction, enhances cardiac
 CC contractility and reduces blood pressure. This method is useful for the
 CC treatment of cardiac disease e.g. heart failure and myocardial
 CC dysfunction. The present amino acid sequence is the human PLB wild type
 CC protein, a potent inhibitor of SERCA2a activity. It primarily exists in a
 CC pentameric form. It is a mediator in the regulation of myocardial
 CC function by catecholamines through the cAMP cascade

XX SQ Sequence 52 AA;

[illegible]

Db ADE45167
ID ADE45167 standard; protein; 52 AA.
XX ADE45167;
XX
XX 29-JAN-2004 (first entry)
XX Human SERCA_2 inhibitor phospholamban.
XX Human; SERCA_2; phospholamban; PLB;
KW Ca2+ ATPase of the sarco/endoplasmic reticulum; protein co-ordinate data;
KW cardiant.
XX Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT Binding-site 6 /note= "S1 binding site residue claimed in claim 1"
FT Binding-site 9 /note= "S1 binding site residue claimed in claim 1"
FT Binding-site 13 /note= "S1 binding site residue claimed in claim 1"
FT Binding-site 14 /note= "S2 binding site residue claimed in claim 1"
FT Binding-site 20 /note= "S3 binding site residue claimed in claim 1"
FT Binding-site 27 /note= "S3 binding site residue claimed in claim 1"
FT Binding-site 28 /note= "S3 binding site residue claimed in claim 1"
FT Binding-site 32 /note= "S4 binding site residue claimed in claim 1"
FT Binding-site 35 /note= "S4 binding site residue claimed in claim 1"
XX
XX US6538022-B1.
XX 25-MAR-2003.
XX 18-FEB-1999; 99US-00252063.
XX 24-SEP-1997; 97US-00937117.
XX (ORIN) ORION CORP.
XX Pollesello P, Ovasa M, Tenhunen J, Vidgren J;
XX Yliperttula-Ikonen M, Tiiigmann C, Lotta T, Kaivola J;
XX WPI; 2004-019625/02.
XX
XX New compound, useful for relieving inhibitory effects of phospholamban on
XX cardiac SR Ca2+-ATPase by deactivating phospholamban and stimulating Ca2+
XX -ATPase.
XX
XX Claim 1; SEQ ID NO 1; 65pp; English.
XX
XX The invention relates to a compound which deactivates, and exhibits
XX affinity for, a phospholamban (PLB) protein (an inhibitor of SERCA_2,
XX Ca2+ ATPase of the sarco/endoplasmic reticulum) appearing as ADE45167-
XX ADE45173. The compound has a structure containing three of the four
XX moieties: an electronegative moiety associating with an S1 binding site
XX of the phospholamban cytosolic domain when the compound is bound to it.
XX the binding site comprises Tyr-6, Arg-9 and/or Arg-13; an electronegative
XX moiety associating with an S2 binding site of the phospholamban cytosolic
XX domain when the compound is bound to it, the S2 binding site comprises
XX Arg-14; a hydrophobic moiety associating with an S3 binding site of the
XX phospholamban cytosolic domain when the compound is bound, the binding
XX site comprises Met-20, Lys-27 and/or Leu-28; and a hydrophobic moiety

CC associating with an S4 binding site of the phospholamban cytosolic domain
CC when the compound is bound, the binding site comprises Phe-32 and/or Phe-
CC 35. The compound is act 3-benzyl-5,7-bis ((1H-tetrazol-5-yl)-methoxy)-4-
CC -methyl-2H-methyl-2H-1-benzopyran-2-one. Also included are deactivating
CC phospholamban, comprising administering the novel compound to stimulate
CC the Ca 2+ -ATPase. The compound is useful for relieving the inhibitory
CC effects of phospholamban on cardiac SERCA_2. The present sequence is
CC human phospholamban.
XX
SQ Sequence 52 AA;
Query Match 100.0%; Score 75; DB 8; Length 52;
Best Local Similarity 100.0%; Pred. No. 3.7e-06; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 0;
Qy 1 MEKQYLTRSAIRRAS 16
Db 1 MEKQYLTRSAIRRAS 16
RESULT 12
AAY71019
ID AAY71019 standard; protein; 79 AA.
XX
XX AAY71019;
XX
DT 29-AUG-2000 (first entry)
XX
DE H6 tagged penetratin-based recombinant protein, H6-(V49A)mutantPLB-ANT.
XX
KW Phospholamban; PLB; human; sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a;
KW cardiant; cardiomyocyte; transport peptide; penetratin; cargo peptide;
KW contractilin; cardiac contractility; inhibitor; cardiac disease; mutant;
KW treatment; heart failure; myocardial dysfunction; recombinant protein;
KW fruit fly; ANT; antennapedia; H6 tag; hexahistidine.
XX
XX Homo sapiens.
OS Drosophila sp.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Region 1..52 /note= "Corresponds to mutant human phospholamban (PLB)
FT protein"
FT Misc-difference 49 /note= "Wild type Val replaced with Ala"
FT Region 53..58 /note= "Corresponds to hexahistidine tag (H6)"
FT Region 63..78 /note= "Corresponds to Drosophila antennapedia (ANT)
FT transport peptide"
XX
XX WO200025804-A2.
XX
PD 11-MAY-2000.
XX
XX 02-NOV-1999; 99WO-US025692.
XX
XX 02-NOV-1998; 98US-0106718P.
XX 27-JUL-1999; 99US-0145883P.
XX
XX (REGC) UNIV CALIFORNIA.
XX
XX Chien K, Dillman W, Minamisawa S, He H, Hoshijima M, Meyer M;
XX Scott C, Wang Y, Silverman GJ;
XX WPI; 2000-365393/31.
XX
XX Treating cardiac diseases, e.g. heart failure or myocardial dysfunction
XX comprises enhancing cardiac contractility by inhibiting interaction
XX between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine
XX triphosphatase.
XX

PS Example 6; Page 56; 56pp; English.

XX The patent discloses a method for the treatment of heart failure, using
CC small peptide complexes and recombinant proteins, that induces
CC phospholamban (PLB) deficiency and inhibits the interaction between PLB
CC and sarcoplasmic reticulum Ca²⁺ ATPase (SERCA2a) within cardiomyocytes.
CC The peptide complex comprises of transport peptide like penetratin and
CC cargo peptide selected from mutant PLB, native PLB or antibody against
CC PLB protein (contractilin). Penetratin-PLB peptide functions as a
CC dominant negative inhibitor of PLB-SERCA2a interaction, enhances cardiac
CC contractility and reduces blood pressure. This method is useful for the
CC treatment of cardiac disease e.g. heart failure and myocardial
CC dysfunction. The present sequence is the hexahistidine (H6) tagged
CC penetratin-based recombinant protein H6-mutantPLB-ANT, comprising the
CC human mutant (Val19Ala) PLB protein and Drosophila antennapedia (ANT)
CC transport peptide attached by a hexahistidine tag. This sequence is
CC expressed in Escherichia coli cells

XX Sequence 79 AA;

Query Match 100.0%; Score 75; DB 3; Length 79;
Best Local Similarity 100.0%; Pred. No. 5.8e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRAS 16
DB 1 MEKVQYLTRSAIRRAS 16

RESULT 13

AAAY71017
ID AAY71017 standard; protein; 79 AA.

XX AC AAY71017;

XX 29-AUG-2000 (first entry)

XX Hexahistidine tagged penetratin-based recombinant protein, H6-wtPLB-ANT.
XX Phospholamban; PLB; human; sarcoplasmic reticulum Ca²⁺ ATPase; SERCA2a;
XX cardiant; cardiomyocyte; transport peptide; penetratin; cargo peptide;
XX contractilin; cardiac contractility; inhibitor; cardiac disease;
XX treatment; heart failure; myocardial dysfunction; recombinant protein;
XX fruit fly; ANT; antennapedia; H6 tag; hexahistidine.

XX Homo sapiens.

XX Drosophila sp.

XX Synthetic.

XX Key Location/Qualifiers

FT Region 1..52 /note= "Corresponds to Human phospholamban (PLB) protein"

FT Region 53..58 /note= "Corresponds to hexahistidine tag (H6)"

FT Region 63..78 /note= "Corresponds to Drosophila antennapedia (ANT)

FT /note= "transport peptide"

XX WO2000025804-A2.

XX 11-MAY-2000.

XX 02-NOV-1999; 99WO-US025692.

XX 02-NOV-1998; 98US-0106718P.

XX 27-JUL-1999; 99US-0145883P.

XX (REGC) UNIV CALIFORNIA.

XX Chien K, Dillman W, Minamisawa S, He H, Hoshijima M, Meyer M;

XX Scott C, Wang Y, Silverman GJ;

XX WPI; 2000-365393/31.

XX

PT Treating cardiac diseases, e.g. heart failure or myocardial dysfunction
PT comprises enhancing cardiac contractility by inhibiting interaction
PT between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine
PT triphosphatase.

XX Example 6; Page 54-55; 56pp; English.

XX The patent discloses a method for the treatment of heart failure, using
CC small peptide complexes and recombinant proteins, that induces
CC phospholamban (PLB) deficiency and inhibits the interaction between PLB
CC and sarcoplasmic reticulum Ca²⁺ ATPase (SERCA2a) within cardiomyocytes.
CC The peptide complex comprises of transport peptide like penetratin and
CC cargo peptide selected from mutant PLB, native PLB or antibody against
CC PLB protein (contractilin). Penetratin-PLB peptide functions as a
CC dominant negative inhibitor of PLB-SERCA2a interaction, enhances cardiac
CC contractility and reduces blood pressure. This method is useful for the
CC treatment of cardiac disease e.g. heart failure and myocardial
CC dysfunction. The present sequence is the hexahistidine (H6) tagged
CC type human PLB protein and Drosophila antennapedia (ANT) transport
CC peptide attached by a hexahistidine tag. This sequence is expressed in
CC Escherichia coli cells

XX Sequence 79 AA;

Query Match 100.0%; Score 75; DB 3; Length 79;
Best Local Similarity 100.0%; Pred. No. 5.8e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRAS 16

DB 1 MEKVQYLTRSAIRRAS 16

RESULT 14

AAAY71006

ID AAY71006 standard; protein; 52 AA.

XX AC AAY71006;

XX 29-AUG-2000 (first entry)

XX Human mutant phospholamban (PLB) S16N protein.

XX Phospholamban; PLB; human; sarcoplasmic reticulum Ca²⁺ ATPase; SERCA2a;

XX cardiant; cardiomyocyte; transport peptide; penetratin; cargo peptide;

XX contractilin; cardiac contractility; inhibitor; cardiac disease;

XX treatment; heart failure; myocardial dysfunction; mutant.

XX Homo sapiens.

XX Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 16 /note= "Wild type Ser replaced with Asn"

XX WO2000025804-A2.

XX 11-MAY-2000.

XX 02-NOV-1999; 99WO-US025692.

XX 02-NOV-1998; 98US-0106718P.

XX 27-JUL-1999; 99US-0145883P.

XX (REGC) UNIV CALIFORNIA.

XX Chien K, Dillman W, Minamisawa S, He H, Hoshijima M, Meyer M;

XX Scott C, Wang Y, Silverman GJ;

XX WPI; 2000-365393/31.

PT Treating cardiac diseases, e.g. heart failure or myocardial dysfunction
 PT comprises enhancing cardiac contractility by inhibiting interaction
 PT between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine
 PT triphosphatase.

PS Disclosure; Page 49; 56pp; English.

CC The patent discloses a method for the treatment of heart failure, using
 CC small peptide complexes and recombinant proteins, that induces
 CC phospholamban (PLB) deficiency and inhibits the interaction between PLB
 CC and sarcoplasmic reticulum Ca 2+ ATPase (SERCA2a) within cardiomyocytes.
 CC The peptide complex comprises of transport peptide like penetratin and
 CC cargo peptide selected from mutant PLB, native PLB or antibody against
 CC PLB protein (contractilin). Penetratin-PLB peptide functions as a
 CC dominant negative inhibitor of PLB-SERCA2a interaction, enhances cardiac
 CC contractility and reduces blood pressure. This method is useful for the
 CC treatment of cardiac disease e.g. heart failure and myocardial
 CC dysfunction. The present amino acid sequence is the human mutant PLB
 CC protein, comprising the mutation Ser16Asn. This mutant sequence when
 CC overexpressed in the transformed cardiomyocytes, shows increased
 CC contractility than the wild type PLB sequence

XX Sequence 52 AA;

Query Match 96.0%; Score 72; DB 3; Length 52;

Best Local Similarity 93.8%; Pred. No. 1.3e-05; Indels 0; Gaps 0;

Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEKVQYLTRSAIRRAS 16

Db 1 MEKVQYLTRSAIRRAAN 16

RESULT 15

ADE45168
 ID ADE45168 standard; protein; 52 AA.

XX

AC ADE45168;

XX

DT 29-JAN-2004 (first entry)

XX

DE Pig SERCA_2 inhibitor phospholamban.

XX

KW Pig; SERCA_2; phospholamban; PLB;

KW Ca2+ ATPase of the sarco/endoplasmic reticulum; protein co-ordinate data;

KW cardiant.

XX

OS Sus sp.

XX

PN US6538022-B1.

XX

PD 25-MAR-2003.

XX

PF 18-FEB-1999; 99US-00252063.

XX

PR 24-SEP-1997; 97US-00937117.

XX

PA (ORIN) ORION CORP.

XX

PI Pollesello P, Ovaska M, Tenhunen J, Vidgren J;

XX

PI Yliperttula-Ikonen M, Tilgmann C, Lotta T, Kaivola J;

XX

DR WPI; 2004-019625/02.

XX

PT New compound, useful for relieving inhibitory effects of phospholamban on

PT cardiac SR Ca2+-ATPase by deactivating phospholamban and stimulating Ca2+

PT -ATPase.

XX

PS Claim 1; SEQ ID NO 2; 65pp; English.

XX

XX The invention relates to a compound which deactivates, and exhibits

XX affinity for, a phospholamban (PLB) protein (an inhibitor of SERCA_2,

CC Ca2+ ATPase of the sarco/endoplasmic reticulum) appearing as ADE45167-

CC ADE45173. The compound has a structure containing three of the four
 CC moieties: an electronegative moiety associating with an S1 binding site
 CC of the phospholamban cytosolic domain when the compound is bound to it,
 CC the binding site comprises Tyr-6, Arg-9 and/or Arg-13; an electronegative
 CC moiety associating with an S2 binding site of the phospholamban cytosolic
 CC domain when the compound is bound to it, the S2 binding site comprises
 CC Arg-14; a hydrophobic moiety associating with an S3 binding site of the
 CC phospholamban cytosolic domain when the compound is bound, the binding
 CC site comprises Met-20, Lys-27 and/or Leu-28; and a hydrophobic moiety
 CC associating with an S4 binding site of the phospholamban cytosolic domain
 CC when the compound is bound, the binding site comprises Phe-32 and/or Phe-
 CC 35. The compound is not 3-benzyl-5,7-bis ((1H-tetrazol-5-yl)-methoxy)-4-
 CC methyl-2H-methyl-2H-1-benzopyran-2-one. Also included are deactivating
 CC phospholamban, comprising administering the novel compound to stimulate
 CC the Ca 2+ -ATPase. The compound is useful for relieving the inhibitory
 CC effects of phospholamban on cardiac SERCA_2. The present sequence is a
 CC phospholamban.

XX Sequence 52 AA;

Query Match 96.0%; Score 72; DB 8; Length 52;

Best Local Similarity 93.8%; Pred. No. 1.3e-05; Indels 0; Gaps 0;

Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEKVQYLTRSAIRRAS 16

Db 1 MDKVQYLTRSAIRRAS 16

RESULT 16

ADE45169

ID ADE45169 standard; protein; 52 AA.

XX

AC ADE45169;

XX

DT 29-JAN-2004 (first entry)

XX

DE Dog SERCA_2 inhibitor phospholamban.

XX

KW Dog; SERCA_2; phospholamban; PLB;

KW Ca2+ ATPase of the sarco/endoplasmic reticulum; protein co-ordinate data;

KW cardiant.

XX

OS Canis sp.

XX

PN US6538022-B1.

XX

PD 25-MAR-2003.

XX

PF 18-FEB-1999; 99US-00252063.

XX

PR 24-SEP-1997; 97US-00937117.

XX

PA (ORIN) ORION CORP.

XX

PI Pollesello P, Ovaska M, Tenhunen J, Vidgren J;

XX

PI Yliperttula-Ikonen M, Tilgmann C, Lotta T, Kaivola J;

XX

DR WPI; 2004-019625/02.

XX

PT New compound, useful for relieving inhibitory effects of phospholamban on

PT cardiac SR Ca2+-ATPase by deactivating phospholamban and stimulating Ca2+

PT -ATPase.

XX

PS Claim 1; SEQ ID NO 3; 65pp; English.

XX

XX The invention relates to a compound which deactivates, and exhibits

XX affinity for, a phospholamban (PLB) protein (an inhibitor of SERCA_2,

CC Ca2+ ATPase of the sarco/endoplasmic reticulum) appearing as ADE45167-

CC moiety associating with an S2 binding site of the phospholamban cytosolic
 CC domain when the compound is bound to it, the S2 binding site comprises
 CC Arg-14; a hydrophobic moiety associating with an S3 binding site of the
 CC phospholamban cytosolic domain when the compound is bound, the binding
 CC site comprises Met-20, Lys-27 and/or Leu-28; and a hydrophobic moiety
 CC associating with an S4 binding site of the phospholamban cytosolic domain
 CC when the compound is bound, the binding site comprises Phe-32 and/or Phe-
 CC 35. The compound is not 3-benzyl-5,7-bis ((1H-tetrazol-5-yl)-methyloxy)-4
 CC -methyl-2H-methyl-2H-1-benzopyran-2-one. Also included are deactivating
 CC phospholamban, comprising administering the novel compound to stimulate
 CC the Ca²⁺ + ATPase. The compound is useful for relieving the inhibitory
 CC effects of phospholamban on cardiac SERCA₂. The present sequence is a
 CC phospholamban.
 XX
 SQ Sequence 52 AA;

Query Match 96.0%; Score 72; DB 8; Length 52;
 Best Local Similarity 93.8%; Pred. No. 1.3e-05;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQLTRSAIRRAS 16
 | : |||||
 DB 1 MDKVQLTRSAIRRAS 16

RESULT 17
 AAY71014
 ID AAY71014 standard; peptide; 35 AA.

AC AAY71014;
 XX 29-AUG-2000 (first entry)
 XX Penetratin-based recombinant phospholamban peptide, TAT-mutant PLB.
 XX Phospholamban; PLB; human; sarcoplasmic reticulum Ca²⁺ ATPase; SERCA2a;
 KW cardiant; cardiomyocyte; transport peptide; penetratin; cargo peptide;
 KW contractilin; cardiac contractility; inhibitor; cardiac disease; mutant;
 KW treatment; heart failure; myocardial dysfunction; recombinant protein;
 KW HIV; TAT protein.
 XX
 XX Homo sapiens.
 OS Human immunodeficiency virus.

XX Key Location/Qualifiers
 XX Region 5. .15
 FT /note= "Corresponds to denatured human immunodeficiency
 FT virus (HIV) TAT protein"
 FT Region 16. .35
 FT /note= "Corresponds to mutant human phospholamban (PLB)
 FT amino terminal peptide"
 FT Misc-difference 31
 FT /note= "Wild type Ser replaced with Glu"

XX WO200025804-A2.
 XX 11-MAY-2000.
 XX 02-NOV-1999; 99WO-US025692.
 XX 02-NOV-1998; 98US-0106718P.
 XX 27-JUN-1999; 99US-0145883P.

XX (REGC) UNIV CALIFORNIA.
 XX Chien K, Dillman W, Minamisawa S, He H, Hoshijima M, Meyer M;
 PI Scott C, Wang Y, Silverman GJ;
 XX WPI; 2000-365393/31.

XX Treating cardiac diseases, e.g. heart failure or myocardial dysfunction
 PT comprises enhancing cardiac contractility by inhibiting interaction
 PT between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine

PT triphosphatase.
 XX Example 5; Page 53; 56pp; English.
 XX The patent discloses a method for the treatment of heart failure, using
 CC small peptide complexes and recombinant proteins, that induces
 CC phospholamban (PLB) deficiency and inhibits the interaction between PLB
 CC and sarcoplasmic reticulum Ca²⁺ ATPase (SERCA2a) within cardiomyocytes.
 CC The peptide complex comprises of transport peptide like penetratin and
 CC cargo peptide selected from mutant PLB, native PLB or antibody against
 CC PLB protein (contractilin). Penetratin-PLB peptide functions as a
 CC dominant negative inhibitor of PLB-SERCA2a interaction, enhances cardiac
 CC contractility and reduces blood pressure. This method is useful for the
 CC treatment of cardiac disease e.g. heart failure and myocardial
 CC dysfunction. The present sequence is the penetratin-based recombinant
 CC peptide TAT-mutant PLB, comprising the amino terminal end of human PLB
 CC mutant (Ser31Glu) protein, attached to the 3' end of denatured human
 CC immunodeficiency virus (HIV), TAT protein. Penetratin is a class of
 CC peptides, with translocating properties having the ability to carry
 CC hydrophilic compounds across the plasma membrane
 XX
 SQ Sequence 35 AA;

Query Match 94.7%; Score 71; DB 3; Length 35;
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQLTRSAIRRA 15
 | : |||||
 DB 16 MEKVQLTRSAIRRA 30

RESULT 18
 AAY71013
 ID AAY71013 standard; peptide; 36 AA.

AC AAY71013;
 XX 29-AUG-2000 (first entry)
 XX Penetratin-based recombinant phospholamban peptide, mutant PLB-ANT.
 XX Phospholamban; PLB; human; sarcoplasmic reticulum Ca²⁺ ATPase; SERCA2a;
 KW cardiant; cardiomyocyte; transport peptide; penetratin; cargo peptide;
 KW contractilin; cardiac contractility; inhibitor; cardiac disease; mutant;
 KW treatment; heart failure; myocardial dysfunction; recombinant protein;
 KW fruit fly; ANT; antennapedia.
 XX
 XX Homo sapiens.
 OS Drosophila sp.

XX Key Location/Qualifiers
 XX Region 1. .20
 FT /note= "Corresponds to mutant human phospholamban (PLB)
 FT amino terminal peptide"
 FT Misc-difference 16
 FT /note= "Wild type Ser replaced with Glu"
 FT Region 21. .36
 FT /note= "Corresponds to Drosophila antennapedia (ANT)
 FT transport peptide"

XX WO200025804-A2.
 XX 11-MAY-2000.

XX 02-NOV-1999; 99WO-US025692.
 XX 02-NOV-1998; 98US-0106718P.
 XX 27-JUL-1999; 99US-0145883P.

XX (REGC) UNIV CALIFORNIA.

XX Chien K, Dillman W, Minamisawa S, He H, Hoshijima M, Meyer M;

PI Scott C, Wang Y, Silverman GJ;
 DR WPI; 2000-365393/31.
 XX
 PT Treating cardiac diseases, e.g. heart failure or myocardial dysfunction
 PT comprises enhancing cardiac contractility by inhibiting interaction
 PT between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine
 PT triphosphatase.
 XX
 PS Example 5; Page 53; 56pp; English.
 XX
 CC The patent discloses a method for the treatment of heart failure, using
 CC small peptide complexes and recombinant proteins, that induces
 CC phospholamban (PLB) deficiency and inhibits the interaction between PLB
 CC and sarcoplasmic reticulum Ca 2+ ATPase (SERCA2a) within cardiomyocytes.
 CC The peptide complex comprises of transport peptide like penetratin and
 CC cargo peptide selected from mutant PLB, native PLB or antibody against
 CC PLB protein (contractilin). Penetratin-PLB peptide functions as a
 CC dominant negative inhibitor of PLB-SERCA2a interaction, enhances cardiac
 CC contractility and reduces blood pressure. This method is useful for the
 CC treatment of cardiac disease e.g. heart failure and myocardial
 CC dysfunction. The present sequence is the penetratin-based recombinant
 CC peptide, mutant PLB-ANT, comprising the amino terminal end of human PLB
 CC mutant (Ser16Glu) protein, attached to the 5' end of the Drosophila
 CC antennapedia (ANT) transport peptide. Penetratin is a class of peptides,
 CC with translocating properties having the ability to carry hydrophilic
 CC compounds across the plasma membrane
 XX
 SQ Sequence 36 AA;
 Query Match 94.7%; Score 71; DB 3; Length 36;
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MEKVQYLTRSAIRRA 15
 |||||
 DB 1 MEKVQYLTRSAIRRA 15
 |||||
 RESULT 19
 ABB79404
 ID ABB79404 standard; peptide; 52 AA.
 AC ABB79404;
 XX
 DT 24-JUN-2002 (first entry)
 XX
 DE Human phospholamban pseudophosphorylation mutant S16E PLB.
 XX
 KW Human; phospholamban; PLB; cardiant; heart disease; gene therapy;
 KW cardiac function; mutant; mutain.
 XX
 OS Homo sapiens.
 XX
 PH Key Location/Qualifiers
 FT Misc-difference 16
 FT /note= "Wildtype Ser substituted by Glu"
 XX
 PN US2002032167-A1.
 XX
 PD 14-MAR-2002.
 XX
 PF 11-SEP-2001; 2001US-00954571.
 XX
 PR 11-SEP-2000; 2000US-0231821P.
 XX
 PA (CHIE/) CHEN K. R.
 PA (HOSH/) HOSHIMURA M.
 PA (ROSS/) ROSS J.
 PA (IKED/) IKEDA Y.
 XX
 PI Chien KR, Hoshijma M, Ross J, Ikeda Y;
 XX

DR WPI; 2002-361185/39.
 XX
 PT Delivering a dose of a gene expression cassette in a fluid selectively to
 PT heart for sustained expression, useful for improving or enhancing cardiac
 PT function, by employing a viral vector together with a vascular
 PT permeabilizing agent.
 XX
 PS Example 6; Fig 1; 12pp; English.
 XX
 CC The invention relates to delivering a therapeutic dose of a gene
 CC expression cassette in a fluid selectively to heart for sustained
 CC expression, comprising employing a viral vector together with a vascular
 CC permeabilizing agent. The method is useful for gene therapy delivering
 CC genes for improving or enhancing cardiac function, particularly in
 CC hamster models of heart disease. The present sequence is that of a
 CC pseudophosphorylation mutant of phospholamban (S16EPLB). This point
 CC mutant is among a number of dominant negative mutants identified and
 CC characterised in WO00/25804 and used in the method of the present
 CC invention
 XX
 SQ Sequence 52 AA;
 Query Match 94.7%; Score 71; DB 5; Length 52;
 Best Local Similarity 100.0%; Pred. No. 2e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MEKVQYLTRSAIRRA 15
 |||||
 DB 1 MEKVQYLTRSAIRRA 15
 |||||
 RESULT 20
 ADE45173
 ID ADE45173 standard; protein; 52 AA.
 AC ADE45173;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Chicken SERCA_2 inhibitor phospholamban.
 XX
 KW Chicken; SERCA 2; phospholamban; PLB;
 KW Ca2+ ATPase of the sarco/endoplasmic reticulum; protein co-ordinate data;
 KW cardiant.
 XX
 OS Gallus sp.
 XX
 PN US6538022-B1.
 XX
 PD 25-MAR-2003.
 XX
 PF 18-FEB-1999; 99US-00252063.
 XX
 PR 24-SEP-1997; 97US-00937117.
 XX
 PA (ORIN) ORION CORP.
 XX
 PI Pollesello P, Ovaska M, Tenhunen J, Vidgren J;
 PI Yliperttula-Ikonen M, Tilgmann C, Lotta T, Kaivola J;
 XX
 DR WPI; 2004-019625/02.
 XX
 PT New compound, useful for relieving inhibitory effects of phospholamban on
 PT cardiac SR Ca2+-ATPase by deactivating phospholamban and stimulating Ca2+
 PT -ATPase.
 XX
 PS Claim 1; SEQ ID NO 7; 65pp; English.
 XX
 CC The invention relates to a compound which deactivates, and exhibits
 CC affinity for, a phospholamban (PLB) protein (an inhibitor of SERCA 2,
 CC Ca2+ ATPase of the sarco/endoplasmic reticulum) appearing as ADE45167-
 CC ADE45173. The compound has a structure containing three of the four
 CC moieties: an electronegative moiety associating with an S1 binding site

CC of the phospholamban cytosolic domain when the compound is bound to it.
 CC the binding site comprises Tyr-6, Arg-9 and/or Arg-13; an electronegative
 CC moiety associating with an S2 binding site of the phospholamban cytosolic
 CC domain when the compound is bound to it, the S2 binding site comprises
 CC Arg-14; a hydrophobic moiety associating with an S3 binding site of the
 CC phospholamban cytosolic domain when the compound is bound, the binding
 CC site comprises Met-20, Lys-27 and/or Leu-28; and a hydrophobic moiety
 CC associating with an S4 binding site of the phospholamban cytosolic domain
 CC when the compound is bound, the binding site comprises Phe-32 and/or Phe-
 CC 35. The compound is not 3-benzyl-5,7-bis ((1H-tetrazol-5-yl)-methoxy)-4
 CC -methyl-2H-1-benzopyran-2-one. Also included are deactivating
 CC phospholamban, comprising administering the novel compound to stimulate
 CC the Ca 2+ -ATPase. The compound is useful for relieving the inhibitory
 CC effects of phospholamban on cardiac SERCA_2. The present sequence is a
 CC phospholamban.
 XX
 SQ Sequence 52 AA;

Query Match 94.7%; Score 71; DB 8; Length 52;
 Best Local Similarity 87.5%; Pred. No. 2e-05;
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MEKVQYLTRSAIRRAS 16
 DQ 1 MEKVQYLTRSAIRRAS 16
 |||||:|||||

RESULT 21
 ID AAY71018 standard; protein; 79 AA.
 XX
 AC AAY71018;
 XX
 DT 29-AUG-2000 (first entry)
 XX
 DE H6 tagged penetratin-based recombinant protein, H6- (S16E) mutant PLB-ANT.
 XX
 KW Phospholamban; PLB; human; sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a;
 KW cardiant; cardiomyocyte; transport peptide; penetratin; cargo peptide;
 KW contractilin; cardiac contractility; inhibitor; cardiac disease; mutant;
 KW treatment; heart failure; myocardial dysfunction; recombinant protein;
 KW fruit fly; ANT; antennapedia; H6 tag; hexahistidine.
 XX
 OS Homo sapiens.
 OS Drosophila sp.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT Region 1..52
 FT /note= "Corresponds to mutant human phospholamban (PLB)
 FT protein"
 FT Misc-difference 16
 FT /note= "Wild type Ser replaced with Glu"
 FT Region 53..58
 FT /note= "Corresponds to hexahistidine tag (H6)"
 FT Region 63..78
 FT /note= "Corresponds to Drosophila antennapedia (ANT)
 FT transport peptide"
 XX
 FN WO2000025804-A2.
 XX
 PD 11-MAY-2000.
 XX
 PF 02-NOV-1999; 99WO-US025692.
 XX
 PR 02-NOV-1998; 98US-0106718P.
 PR 27-JUL-1999; 99US-0145883P.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Chien K, Dillman W, Minamisawa S, He H, Hoshijima M, Meyer M;
 PI Scott C, Wang Y, Silverman GJ;
 XX

DR WPI; 2000-365393/31.
 XX Treating cardiac diseases, e.g. heart failure or myocardial dysfunction
 PT comprises enhancing cardiac contractility by inhibiting interaction
 PT between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine
 PT triphosphatase.
 XX
 PS Example 6; Page 55; 56pp; English.
 XX
 CC The patent discloses a method for the treatment of heart failure, using
 CC small peptide complexes and recombinant proteins, that induces
 CC phospholamban (PLB) deficiency and inhibits the interaction between PLB
 CC and sarcoplasmic reticulum Ca 2+ ATPase (SERCA2a) within cardiomyocytes.
 CC The peptide complex comprises of transport peptide like penetratin and
 CC cargo peptide selected from mutant PLB, native PLB or antibody against
 CC PLB protein (contractilin). Penetratin-PLB peptide functions as a
 CC dominant negative inhibitor of PLB-SERCA2a interaction, enhances cardiac
 CC contractility and reduces blood pressure. This method is useful for the
 CC treatment of cardiac disease e.g. heart failure and myocardial
 CC dysfunction. The present sequence is the hexahistidine (H6) tagged
 CC penetratin-based recombinant protein H6-mutant PLB-ANT, comprising the
 CC human mutant (Ser16Glu) PLB protein and Drosophila antennapedia (ANT)
 CC transport peptide attached by a hexahistidine tag. This sequence is
 CC expressed in Escherichia coli cells
 XX
 SQ Sequence 79 AA;

Query Match 94.7%; Score 71; DB 3; Length 79;
 Best Local Similarity 100.0%; Pred. No. 3.1e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MEKVQYLTRSAIRRA 15
 DQ 1 MEKVQYLTRSAIRRA 15
 |||||:|||||

RESULT 22
 ID AAY71005 standard; protein; 52 AA.
 XX
 AC AAY71005;
 XX
 DT 29-AUG-2000 (first entry)
 XX
 DE Human mutant phospholamban (PLB) R14E protein.
 XX
 KW Phospholamban; PLB; human; sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a;
 KW cardiant; cardiomyocyte; transport peptide; penetratin; cargo peptide;
 KW contractilin; cardiac contractility; inhibitor; cardiac disease;
 KW treatment; heart failure; myocardial dysfunction; mutant.
 XX
 OS Homo sapiens.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT Misc-difference 14
 FT /note= "Wild type Arg replaced with Glu"
 XX
 FN WO2000025804-A2.
 XX
 PD 11-MAY-2000.
 XX
 PF 02-NOV-1999; 99WO-US025692.
 XX
 PR 02-NOV-1998; 98US-0106718P.
 PR 27-JUL-1999; 99US-0145883P.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Chien K, Dillman W, Minamisawa S, He H, Hoshijima M, Meyer M;
 PI Scott C, Wang Y, Silverman GJ;
 XX
 DR WPI; 2000-365393/31.

XX Treating cardiac diseases, e.g. heart failure or myocardial dysfunction
 PT comprises enhancing cardiac contractility by inhibiting interaction
 PT between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine
 PT triphosphatase.
 XX
 XX Disclosure; Page 48-49; 56pp; English.
 XX
 XX The patent discloses a method for the treatment of heart failure, using
 CC small peptide complexes and recombinant proteins, that induces
 CC phospholamban (PLB) deficiency and inhibits the interaction between PLB
 CC and sarcoplasmic reticulum Ca 2+ ATPase (SERCA2a) within cardiomyocytes.
 CC The peptide complex comprises of transport peptide like penetratin and
 CC cargo peptide selected from mutant PLB, native PLB or antibody against
 CC PLB protein (contractilin). Penetratin-PLB peptide functions as a
 CC dominant negative inhibitor of PLB-SERCA2a interaction, enhances cardiac
 CC contractility and reduces blood pressure. This method is useful for the
 CC treatment of cardiac disease e.g. heart failure and myocardial
 CC dysfunction. The present amino acid sequence is the human mutant PLB
 CC protein, comprising a sense mutation Arg14Glu. This mutant sequence when
 CC overexpressed in the transformed cardiomyocytes, shows increased
 CC contractility than the wild type PLB sequence
 XX
 XX Sequence 52 AA;
 SQ

Query Match 93.3%; Score 70; DB 3; Length 52;
 Best Local Similarity 93.8%; Pred. No. 3e-05;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MEKQVYLTRSAIRRAS 16
 |||||
 Db 1 MEKQVYLTRSAIRRAS 16
 |||||

RESULT 23
 AAY71004
 ID AAY71004 standard; protein; 52 AA.
 XX
 XX AAY71004;
 XX
 XX 29-AUG-2000 (first entry)
 XX
 XX Human mutant phospholamban (PLB) E2A protein.
 XX Phospholamban; PLB; human; sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a;
 KW cadiant; cardiomyocyte; transport peptide; penetratin; cargo peptide;
 KW contractilin; cardiac contractility; inhibitor; cardiac disease;
 KW treatment; heart failure; myocardial dysfunction; mutant.
 XX
 XX Homo sapiens.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 2 /note= "Wild type Glu replaced with Ala"
 FT Misc-difference 2 /note= "Wild type Glu replaced with Ala"
 FT
 XX
 XX WO200025804-A2.
 XX
 XX 11-MAY-2000.
 XX
 XX 02-NOV-1999; 99WO-US025692.
 XX
 XX 02-NOV-1998; 98US-0106718P.
 PR 27-JUL-1999; 99US-0145883P.
 XX
 XX (REGC) UNIV CALIFORNIA.
 PA
 XX Chien K, Dillman W, Minamisawa S, He H, Hoshijima M, Meyer M;
 PI Scott C, Wang Y, Silverman GJ;
 XX
 XX WPI; 2000-365393/31.
 XX
 XX Treating cardiac diseases, e.g. heart failure or myocardial dysfunction
 PT

PT comprises enhancing cardiac contractility by inhibiting interaction
 PT between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine
 PT triphosphatase.
 XX
 XX Disclosure; Page 48; 56pp; English.
 XX
 XX The patent discloses a method for the treatment of heart failure, using
 CC small peptide complexes and recombinant proteins, that induces
 CC phospholamban (PLB) deficiency and inhibits the interaction between PLB
 CC and sarcoplasmic reticulum Ca 2+ ATPase (SERCA2a) within cardiomyocytes.
 CC The peptide complex comprises of transport peptide like penetratin and
 CC cargo peptide selected from mutant PLB, native PLB or antibody against
 CC PLB protein (contractilin). Penetratin-PLB peptide functions as a
 CC dominant negative inhibitor of PLB-SERCA2a interaction, enhances cardiac
 CC contractility and reduces blood pressure. This method is useful for the
 CC treatment of cardiac disease e.g. heart failure and myocardial
 CC dysfunction. The present amino acid sequence is the human mutant PLB
 CC protein, comprising the mutation Glu24Ala. This mutant sequence when
 CC overexpressed in the transformed cardiomyocytes, shows increased
 CC contractility than the wild type PLB sequence
 XX
 XX Sequence 52 AA;
 SQ

Query Match 92.0%; Score 69; DB 3; Length 52;
 Best Local Similarity 93.8%; Pred. No. 4.6e-05;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MEKQVYLTRSAIRRAS 16
 |||||
 Db 1 MAKQVYLTRSAIRRAS 16
 |||||

RESULT 24
 AAY71007
 ID AAY71007 standard; protein; 52 AA.
 XX
 XX AAY71007;
 XX
 XX 29-AUG-2000 (first entry)
 XX
 XX Human mutant phospholamban (PLB) K3E/R14E protein.
 XX Phospholamban; PLB; human; sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a;
 KW cadiant; cardiomyocyte; transport peptide; penetratin; cargo peptide;
 KW contractilin; cardiac contractility; inhibitor; cardiac disease;
 KW treatment; heart failure; myocardial dysfunction; mutant.
 XX
 XX Homo sapiens.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 3 /note= "Wild type Lys replaced with Glu"
 FT Misc-difference 14 /note= "Wild type Arg replaced with Glu"
 FT
 XX
 XX WO200025804-A2.
 XX
 XX 11-MAY-2000.
 XX
 XX 02-NOV-1999; 99WO-US025692.
 XX
 XX 02-NOV-1998; 98US-0106718P.
 PR 27-JUL-1999; 99US-0145883P.
 XX
 XX (REGC) UNIV CALIFORNIA.
 PA
 XX Chien K, Dillman W, Minamisawa S, He H, Hoshijima M, Meyer M;
 PI Scott C, Wang Y, Silverman GJ;
 XX
 XX WPI; 2000-365393/31.
 XX
 XX Treating cardiac diseases, e.g. heart failure or myocardial dysfunction
 PT

PT comprises enhancing cardiac contractility by inhibiting interaction
 PT between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine
 PT triphosphate.
 XX
 XX Disclosure; Page 49; 56pp; English.
 XX
 XX The patent discloses a method for the treatment of heart failure, using
 CC small peptide complexes and recombinant proteins, that induces
 CC phospholamban (PLB) deficiency and inhibits the interaction between PLB
 CC and sarcoplasmic reticulum Ca²⁺ ATPase (SERCA2a) within cardiomyocytes.
 CC The peptide complex comprises of transport peptide like penetratin and
 CC cargo peptide selected from mutant PLB, native PLB or antibody against
 CC PLB protein (concratinin). Penetratin-PLB peptide functions as a
 CC dominant negative inhibitor of PLB-SERCA2a interaction, enhances cardiac
 CC contractility and reduces blood pressure. This method is useful for the
 CC treatment of cardiac disease e.g. heart failure and myocardial
 CC dysfunction. The present amino acid sequence is the human mutant PLB
 CC protein, comprising the double mutation Lys3Glu and Arg15Glu. This mutant
 CC sequence, when overexpressed in the transformed cardiomyocytes, shows
 CC increased contractility than the wild type PLB sequence
 XX
 XX Sequence 52 AA;

Query Match 88.0%; Score 66; DB 3; Length 52;
 Best Local Similarity 87.5%; Pred. No. 0.00016;
 Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MEKVQYLTSAIRRAS 16
 ||:|||||
 DB 1 MEEVQYLTSAIRAS 16

RESULT 25

ID ADC87928 standard; protein; 116 AA.

AC ADC87928;

DT 01-JAN-2004 (first entry)

DE Ribosomal protein similar to FCWP1 #144.

XX Antifungal protein; ribosomal protein; FCWP1; AlyAPP;
 XX plant fungal infection; Alternaria; Ascochyta; Botrytis; Cercospora;
 XX Colletotrichum; Diplodia; Fusarium; Gaemanomyces; Helminthosporium;
 XX Macrophomina; Mycosphaerella; Nectria; Peronospora; Phoma;
 XX Phymatotrichum; Phytophthora; Plasmopara; Podospaera; Puccinia; Puthium;
 XX Pyrenophora; Pyricularia; Pythium; Rhizoctonia; Sclerotium; Sclerotinia;
 XX Septoria; Thielaviopsis; Venturia; Verticillium.

XX Unidentified.

XX US6573361-B1.

XX 03-JUN-2003.

XX 07-DEC-2000; 2000US-00732210.

XX 07-DEC-1999; 99US-0169340P.

XX 07-DEC-1999; 99US-0169513P.

XX (MONS) MONSANTO TECHNOLOGY LLC.

XX Bunkers GJ, Liang J, Mittanck CA, Seale JW, Wu YS;

XX WPI; 2003-754558/71.

XX Novel antifungal protein FCWP1, isolated from Fusarium culmorum, useful
 XX for controlling fungal infections in plants.

XX Example 21; SEQ ID NO 181; 27pp; English.

XX The invention relates to an isolated antifungal ribosomal protein from

CC fusarium culmorum, FCWP1. Also included is a fusion protein between the
 CC signal peptide of the antifungal protein AlyAPP from Alyssum and FCWP1.
 CC encoded by the nucleic acid appearing as ADC87758. The FCWP1 proteins are
 CC useful for controlling fungal infections in plants, such as those caused
 CC by Alternaria (e.g. Ascochyta blight), Botrytis (e.g. Botrytis cinerea),
 CC Cercospora (e.g. Cercospora kikuchii, Cercospora zea-maydis),
 CC Colletotrichum (e.g. Colletotrichum lindemuthianum), Diplodia (e.g.
 CC Diplodia maydis), Fusarium (e.g. Fusarium nivale, Fusarium oxysporum,
 CC Fusarium graminearum, Fusarium culmorum, Fusarium solani, Fusarium
 CC moniliforme, Fusarium roseum), Gaemanomyces (e.g. Gaemanomyces
 CC graminis f.sp. tritici), Helminthosporium (e.g. Helminthosporium turcicum
 CC Helminthosporium carbonum, Helminthosporium maydis), Macrosporiina
 CC (e.g. Macrosporiina phaseolina, Magnaporthe grisea), Mycosphaerella
 CC (e.g. Mycosphaerella figiensis), Nectria (Nectria haematococca), Phoma
 CC peronospora (e.g. Peronospora manshurica, Peronospora tabacina), Phoma
 CC (e.g. Phoma betae), Phymatotrichum (e.g. Phymatotrichum omnivorum),
 CC Phytophthora (e.g. Phytophthora cinnamomi, Phytophthora cactorum,
 CC Phytophthora phaseoli, Phytophthora parasitica, Phytophthora
 CC citrophthora, Phytophthora megasperma f.sp. sojae, Phytophthora
 CC Podospaera leucotricha), Puccinia (e.g. Puccinia sorghi, Puccinia
 CC striiformis, Puccinia graminis f.sp. tritici, Puccinia asparagi,
 CC Puccinia recondita, Puccinia arachidis), Puthium (e.g. Puthium
 CC aphanidermatum), Pyrenophora (e.g. Pyrenophora tritici-repentens),
 CC Pyricularia (e.g. Pyricularia oryzae), Pythium (e.g. Pythium ultimum),
 CC Rhizoctonia (e.g. Rhizoctonia solani, Rhizoctonia cerealis), Sclerotium
 CC (e.g. Sclerotium rolfsii), Sclerotinia (e.g. Sclerotinia sclerotiorum),
 CC Septoria (e.g. Septoria lycopersici, Septoria glycines, Stagonospora
 CC nodorum / Phaeosphaeria nodorum, Septoria tritici), Thielaviopsis (e.g.
 CC Thielaviopsis basicola), Uncinula (e.g. Uncinula necator), Venturia
 CC (e.g. Venturia inaequalis) or Verticillium (e.g. Verticillium dahliae,
 CC Verticillium albo-atrum). Mutations in the proteolytic consensus
 CC sequences contained within FCWP1 provides improved stability of its
 CC antifungal activity. Also disclosed are ribosomal proteins with similar
 CC PI (>71) and molecular weight (<20kDa) to FCWP1, which may act as
 CC antifungal proteins. The present sequence represents one of the ribosomal
 CC proteins similar to FCWP1. Note: The sequence data for this patent did
 CC not form part of the printed specification, but was obtained in
 CC electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?DocID=6573361B1.

XX Sequence 116 AA;

Query Match. 54.7%; Score 41; DB 7; Length 116;

Best Local Similarity 46.7%; Pred. No. 14;

Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 MEKVQYLTSAIRRA 15

DB 81 VEKIELVTRGVDREA 95

Search completed: October 1, 2004, 12:13:15

Job time : 63.2 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 1, 2004, 12:07:51 ; Search time 17 Seconds
(without alignments)
48.589 Million cell updates/sec

Title: US-09-830-779-17_COPY_1_16

Perfect score: 75

Sequence: 1 MEKQVLTGSAIRAS 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Issued Patents AA:

1: /cgn2_6/ptodata/2/iaa/5A COMB.pep.*

2: /cgn2_6/ptodata/2/iaa/5B COMB.pep.*

3: /cgn2_6/ptodata/2/iaa/6A COMB.pep.*

4: /cgn2_6/ptodata/2/iaa/6B COMB.pep.*

5: /cgn2_6/ptodata/2/iaa/PTUS COMB.pep.*

6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	75	100.0	36	4	US-09-252-063-9
2	75	100.0	52	4	US-09-252-063-1
3	75	100.0	52	4	US-09-252-063-4
4	75	100.0	52	4	US-09-252-063-5
5	75	100.0	52	4	US-09-252-063-6
6	75	100.0	52	4	US-09-252-063-7
7	72	96.0	52	4	US-09-252-063-2
8	72	96.0	52	4	US-09-252-063-3
9	72	96.0	52	4	US-09-252-063-7
10	71	94.7	52	4	US-09-252-063-7
11	41	54.7	116	4	US-09-732-210-181
12	37	49.3	631	4	US-09-252-991A-18000
13	36	48.0	98	4	US-09-489-039A-7319
14	36	48.0	134	4	US-09-489-039A-11071
15	36	48.0	686	4	US-09-252-991A-19332
16	36	48.0	765	4	US-09-252-991A-24791
17	36	48.0	924	2	US-08-588-983-18
18	36	48.0	924	2	US-08-588-976-18
19	35	46.7	210	4	US-09-252-991A-28362
20	35	46.7	211	4	US-09-134-001C-5136
21	35	46.7	216	4	US-09-134-001C-6395
22	35	46.7	357	4	US-09-910-174B-14
23	35	46.7	357	4	US-09-620-461-14
24	35	46.7	497	4	US-09-277-262-4
25	35	46.7	516	4	US-09-277-262-2
26	34.5	46.0	835	2	US-08-568-751-4
27	34.5	46.0	864	4	US-09-323-872A-28

864	4	US-09-072-433-16	Sequence 16, Appl
230	4	US-09-540-236-2466	Sequence 2466, Ap
238	4	US-09-107-532A-5165	Sequence 5165, Ap
310	4	US-09-107-532A-5580	Sequence 5580, Ap
331	4	US-09-328-352-5369	Sequence 5369, Ap
53	4	US-09-673-395A-511	Sequence 511, App
24	4	US-09-561-490E-3	Patent No. 5169933
50	6	5169933-31	Sequence 3, Appl
71	4	US-09-489-039A-9691	Sequence 9691, Ap
204	4	US-09-134-001C-4945	Sequence 4945, Ap
172	4	US-09-252-991A-24148	Sequence 24148, A
180	4	US-09-252-991A-18799	Sequence 18799, A
235	4	US-09-198-452A-752	Sequence 752, App
276	2	US-08-712-072C-4	Sequence 4, Appl
297	4	US-09-252-991A-16808	Sequence 16808, A
313	4	US-09-413-814-9	Sequence 9, Appl
320	4	US-09-543-681A-6146	Sequence 6146, Ap
327	6	5171684-6	Patent No. 5171684
350	4	US-08-637-670-39	Sequence 39, Appl
373	4	US-09-328-352-5753	Sequence 5753, Ap
374	4	US-09-679-279-6	Sequence 6, Appl
409	4	US-09-533-029-104	Sequence 104, App
495	4	US-09-107-532A-3679	Sequence 3679, Ap
573	4	US-09-328-352-6420	Sequence 6420, Ap
612	4	US-09-489-039A-10702	Sequence 10702, A
787	4	US-09-489-039A-7628	Sequence 7628, Ap
804	4	US-09-107-532A-6348	Sequence 6348, Ap
807	4	US-09-252-991A-18831	Sequence 18831, A
972	3	US-08-335-844A-24	Sequence 24, Appl
972	4	US-09-129-365-24	Sequence 24, Appl
1124	4	US-09-191-786-1	Sequence 1, Appl
1100	4	US-09-732-210-1175	Sequence 1175, Ap
113	4	US-09-732-210-681	Sequence 681, App
139	4	US-08-065-844A-8	Sequence 8, Appl
169	4	US-09-252-991A-32083	Sequence 32083, A
213	4	US-09-328-352-6122	Sequence 6122, Ap
390	1	US-07-669-171-2	Sequence 2, Appl
390	1	US-08-132-405-1	Sequence 1, Appl
390	1	US-08-395-939A-1	Sequence 1, Appl
390	5	PCI-US91-01861-1	Sequence 1, Appl
390	6	5168051-2	Patent No. 5168051
394	5	PCI-US94-03705-5	Sequence 5, Appl
412	4	US-09-252-991A-28034	Sequence 28034, A
420	4	US-09-134-001C-3805	Sequence 3805, Ap
443	4	US-09-328-352-7207	Sequence 7207, Ap
457	3	US-09-416-213-2	Sequence 2, Appl
457	4	US-09-416-214-2	Sequence 2, Appl
457	4	US-09-038-676-2	Sequence 2, Appl
483	4	US-09-252-991A-11365	Sequence 11365, A
571	4	US-09-489-039A-14334	Sequence 14334, A
589	4	US-09-328-352-7592	Sequence 7592, Ap
604	4	US-09-391-104-30	Sequence 30, Appl
607	3	US-09-000-041A-2	Sequence 2, Appl
607	3	US-09-211-704A-10	Sequence 10, Appl
622	4	US-09-252-991A-19802	Sequence 19802, A
664	2	US-08-428-125-7	Sequence 7, Appl
664	2	US-08-455-355-7	Sequence 7, Appl
664	2	US-09-367-512-6	Sequence 6, Appl
667	2	US-08-428-125-6	Sequence 6, Appl
667	2	US-08-455-355-6	Sequence 6, Appl
667	2	US-09-367-512-5	Sequence 5, Appl
682	4	US-09-252-991A-31275	Sequence 31275, A
784	4	US-09-252-991A-20416	Sequence 20416, A
812	4	US-09-198-452A-978	Sequence 978, App
978	2	US-08-415-593-43	Sequence 43, Appl
1044	4	US-09-252-991A-22493	Sequence 22493, A
1154	4	US-09-489-039A-7724	Sequence 7724, Ap
1799	4	US-09-134-000C-5178	Sequence 5178, Ap
2568	4	US-09-866-108A-3	Sequence 3, Appl
343	4	US-09-489-039A-10330	Sequence 10330, A
1729	4	US-09-553-680-2	Sequence 2, Appl
36	1	US-08-487-890A-29	Sequence 29, Appl
31	41.3		Sequence 29, Appl
31	41.3		

ALIGNMENTS

RESULT 1
 US-09-252-063-9
 ; Sequence 9, Application US/09252063
 ; Patent No. 6538022
 ; GENERAL INFORMATION:
 ; APPLICANT: Pollesello, Piero
 ; APPLICANT: Ovaska, Martti
 ; APPLICANT: Tenhunen, Jukka
 ; APPLICANT: Vidgren, Jukka
 ; APPLICANT: Yliperttula-Ikonen, Marjo
 ; APPLICANT: Tilgmann, Carola
 ; APPLICANT: Lotta, Timo
 ; APPLICANT: Kaivola, Juha
 ; TITLE OF INVENTION: Compounds for Deactivating Phospholamban Function on
 ; FILE REFERENCE: 1102.0250001
 ; CURRENT APPLICATION NUMBER: US/09/252,063
 ; EARLIER FILING DATE: 1999-02-18
 ; EARLIER APPLICATION NUMBER: 08/937,117
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 9
 ; LENGTH: 36
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; OTHER INFORMATION: Description of Artificial Sequence: cystolic part
 ; OTHER INFORMATION: of phospholamban peptide
 US-09-252-063-9

Query Match 100.0%; Score 75; DB 4; Length 36;
 Best Local Similarity 100.0%; Pred. No. 2e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MEKVQLTRSAIRRAS 16
 DB 1 MEKVQLTRSAIRRAS 16

RESULT 2
 US-09-252-063-1
 ; Sequence 1, Application US/09252063
 ; Patent No. 6538022
 ; GENERAL INFORMATION:
 ; APPLICANT: Pollesello, Piero
 ; APPLICANT: Ovaska, Martti
 ; APPLICANT: Tenhunen, Jukka
 ; APPLICANT: Vidgren, Jukka
 ; APPLICANT: Yliperttula-Ikonen, Marjo
 ; APPLICANT: Tilgmann, Carola
 ; APPLICANT: Lotta, Timo
 ; APPLICANT: Kaivola, Juha
 ; TITLE OF INVENTION: Compounds for Deactivating Phospholamban Function on
 ; FILE REFERENCE: 1102.0250001
 ; CURRENT APPLICATION NUMBER: US/09/252,063
 ; EARLIER FILING DATE: 1999-02-18
 ; EARLIER APPLICATION NUMBER: 08/937,117
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 1
 ; LENGTH: 52
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-252-063-1

Query Match 100.0%; Score 75; DB 4; Length 52;
 Best Local Similarity 100.0%; Pred. No. 3e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MEKVQLTRSAIRRAS 16
 DB 1 MEKVQLTRSAIRRAS 16

RESULT 3
 US-09-252-063-4
 ; Sequence 4, Application US/09252063
 ; Patent No. 6538022
 ; GENERAL INFORMATION:
 ; APPLICANT: Pollesello, Piero
 ; APPLICANT: Ovaska, Martti
 ; APPLICANT: Tenhunen, Jukka
 ; APPLICANT: Vidgren, Jukka
 ; APPLICANT: Yliperttula-Ikonen, Marjo
 ; APPLICANT: Tilgmann, Carola
 ; APPLICANT: Lotta, Timo
 ; APPLICANT: Kaivola, Juha
 ; TITLE OF INVENTION: Compounds for Deactivating Phospholamban Function on
 ; FILE REFERENCE: 1102.0250001
 ; CURRENT APPLICATION NUMBER: US/09/252,063
 ; EARLIER FILING DATE: 1999-02-18
 ; EARLIER APPLICATION NUMBER: 08/937,117
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 4
 ; LENGTH: 52
 ; TYPE: PRT
 ; ORGANISM: Oryctolagus cuniculus
 US-09-252-063-4

Query Match 100.0%; Score 75; DB 4; Length 52;
 Best Local Similarity 100.0%; Pred. No. 3e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MEKVQLTRSAIRRAS 16
 DB 1 MEKVQLTRSAIRRAS 16

RESULT 4
 US-09-252-063-5
 ; Sequence 5, Application US/09252063
 ; Patent No. 6538022
 ; GENERAL INFORMATION:
 ; APPLICANT: Pollesello, Piero
 ; APPLICANT: Ovaska, Martti
 ; APPLICANT: Tenhunen, Jukka
 ; APPLICANT: Vidgren, Jukka
 ; APPLICANT: Yliperttula-Ikonen, Marjo
 ; APPLICANT: Tilgmann, Carola
 ; APPLICANT: Lotta, Timo
 ; APPLICANT: Kaivola, Juha
 ; TITLE OF INVENTION: Compounds for Deactivating Phospholamban Function on
 ; FILE REFERENCE: 1102.0250001
 ; CURRENT APPLICATION NUMBER: US/09/252,063
 ; EARLIER FILING DATE: 1999-02-18
 ; EARLIER APPLICATION NUMBER: 08/937,117
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 5
 ; LENGTH: 52
 ; TYPE: PRT
 ; ORGANISM: Rattus sp.
 US-09-252-063-5

Query Match 100.0%; Score 75; DB 4; Length 52;
Best Local Similarity 100.0%; Pred. No. 3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEKVQYLTRSAIRRAS 16
Db 1 MEKVQYLTRSAIRRAS 16

RESULT 5

US-09-252-063-6
; Sequence 6, Application US/09252063
; Patent No. 6538022
; GENERAL INFORMATION:
; APPLICANT: Pollesello, Piero
; APPLICANT: Ovaska, Martti
; APPLICANT: Tenhunen, Jukka
; APPLICANT: Vidgren, Jukka
; APPLICANT: Yliperttula-Ikonen, Marjo
; APPLICANT: Tilgmann, Carola
; APPLICANT: Lotta, Timo
; APPLICANT: Kaivola, Juha
; TITLE OF INVENTION: Compounds for Deactivating Phospholamban Function on
; FILE REFERENCE: 1102.0250001
; CURRENT APPLICATION NUMBER: US/09/252,063
; CURRENT FILING DATE: 1999-02-18
; EARLIER APPLICATION NUMBER: 08/937,117
; EARLIER FILING DATE: 1997-09-24
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 6
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-252-063-6

Query Match 100.0%; Score 75; DB 4; Length 52;
Best Local Similarity 100.0%; Pred. No. 3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEKVQYLTRSAIRRAS 16
Db 1 MEKVQYLTRSAIRRAS 16

RESULT 6

US-09-549-872B-15
; Sequence 15, Application US/09549872B
; Patent No. 6540996
; GENERAL INFORMATION:
; APPLICANT: Zwaal, Richard
; APPLICANT: Groenen, Jose
; APPLICANT: Bogaert, Thierry
; TITLE OF INVENTION: COMPOUND SCREENING METHODS
; FILE REFERENCE: D00590/70008 (JRV/RE)
; CURRENT APPLICATION NUMBER: US/09/549,872B
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: GB 9508670.4
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: US 60/129,596
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: GB 9512736.7
; PRIOR FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 15
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-549-872B-15

Query Match 100.0%; Score 75; DB 4; Length 52;
Best Local Similarity 100.0%; Pred. No. 3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEKVQYLTRSAIRRAS 16
Db 1 MEKVQYLTRSAIRRAS 16

RESULT 7

US-09-252-063-2
; Sequence 2, Application US/09252063
; Patent No. 6538022
; GENERAL INFORMATION:
; APPLICANT: Pollesello, Piero
; APPLICANT: Ovaska, Martti
; APPLICANT: Tenhunen, Jukka
; APPLICANT: Vidgren, Jukka
; APPLICANT: Yliperttula-Ikonen, Marjo
; APPLICANT: Tilgmann, Carola
; APPLICANT: Lotta, Timo
; APPLICANT: Kaivola, Juha
; TITLE OF INVENTION: Compounds for Deactivating Phospholamban Function on
; FILE REFERENCE: 1102.0250001
; CURRENT APPLICATION NUMBER: US/09/252,063
; CURRENT FILING DATE: 1999-02-18
; EARLIER APPLICATION NUMBER: 08/937,117
; EARLIER FILING DATE: 1997-09-24
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Sus sp.
US-09-252-063-2

Query Match 96.0%; Score 72; DB 4; Length 52;
Best Local Similarity 93.8%; Pred. No. 1.1e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEKVQYLTRSAIRRAS 16
Db 1 MDKVQYLTRSAIRRAS 16

RESULT 8

US-09-252-063-3
; Sequence 3, Application US/09252063
; Patent No. 6538022
; GENERAL INFORMATION:
; APPLICANT: Pollesello, Piero
; APPLICANT: Ovaska, Martti
; APPLICANT: Tenhunen, Jukka
; APPLICANT: Vidgren, Jukka
; APPLICANT: Yliperttula-Ikonen, Marjo
; APPLICANT: Tilgmann, Carola
; APPLICANT: Lotta, Timo
; APPLICANT: Kaivola, Juha
; TITLE OF INVENTION: Compounds for Deactivating Phospholamban Function on
; FILE REFERENCE: 1102.0250001
; CURRENT APPLICATION NUMBER: US/09/252,063
; CURRENT FILING DATE: 1999-02-18
; EARLIER APPLICATION NUMBER: 08/937,117
; EARLIER FILING DATE: 1997-09-24
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 3
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Canis sp.
US-09-252-063-3

Query Match 96.0%; Score 72; DB 4; Length 52;
Best Local Similarity 93.8%; Pred. No. 1.1e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRAS 16
|:|||||:|||||:
DB 1 MDKVQYLTRSAIRRAS 16

RESULT 9
US-09-549-872B-14
; Sequence 14, Application US/09549872B
; Patent No. 6540996
; GENERAL INFORMATION:
; APPLICANT: Zwaal, Richard
; APPLICANT: Groenen, Jose
; APPLICANT: Bogaert, Thierry
; TITLE OF INVENTION: COMPOUND SCREENING METHODS
; FILE REFERENCE: D00590/70008 (JRV/RE)
; CURRENT APPLICATION NUMBER: US/09/549,872B
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: GB 9908670.4
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: US 60/129,596
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: GB 9912736.7
; PRIOR FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 14
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Sus sp.
US-09-549-872B-14

Query Match 96.0%; Score 72; DB 4; Length 52;
Best Local Similarity 93.8%; Pred. No. 1.1e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRAS 16
|:|||||:|||||:
DB 1 MDKVQYLTRSAIRRAS 16

RESULT 10
US-09-252-063-7
; Sequence 7, Application US/09252063
; Patent No. 6538022
; GENERAL INFORMATION:
; APPLICANT: Pollesello, Piero
; APPLICANT: Ovaska, Martti
; APPLICANT: Teshunen, Jukka
; APPLICANT: Viikgren, Jukka
; APPLICANT: Yli-Perttula-Ikonen, Marjo
; APPLICANT: Tilgmann, Carola
; APPLICANT: Lotta, Timo
; APPLICANT: Kaivola, Juha
; TITLE OF INVENTION: Compounds for Deactivating Phospholamban Function on
; FILE REFERENCE: 1102.0250001
; CURRENT APPLICATION NUMBER: US/09/252,063
; CURRENT FILING DATE: 1999-02-18
; EARLIER APPLICATION NUMBER: 08/937,117
; EARLIER FILING DATE: 1997-09-24
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 7
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Gallus sp.
US-09-252-063-7

Query Match 94.7%; Score 71; DB 4; Length 52;
Best Local Similarity 87.5%; Pred. No. 1.7e-06;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRAS 16
|:|||||:|||||:
DB 1 MEKVQYLTRSAIRRAS 16

RESULT 11
US-09-732-210-181
; Sequence 181, Application US/09732210
; Patent No. 6573361
; GENERAL INFORMATION:
; APPLICANT: Bunkers, Greg J.
; APPLICANT: Liang, Jihong
; APPLICANT: Mittanck, Cindy A.
; APPLICANT: Seale, Jeffrey W.
; APPLICANT: Wu, Yennie S.
; TITLE OF INVENTION: Anti-fungal Proteins and Methods for Their Use
; FILE REFERENCE: 38-21(15036)H
; CURRENT APPLICATION NUMBER: US/09/732,210
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/169,513
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: US 60/169,340
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 1753
; SEQ ID NO 181
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Streptomyces coelicolor
US-09-732-210-181

Query Match 54.7%; Score 41; DB 4; Length 116;
Best Local Similarity 46.7%; Pred. No. 2;
Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRA 15
|:|:|:|:|:|:|:
DB 81 VEKIELVTRGVDVRA 95

RESULT 12
US-09-252-991A-18000
; Sequence 18000, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 18000
; LENGTH: 631
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18000

Query Match 49.3%; Score 37; DB 4; Length 631;
Best Local Similarity 50.0%; Pred. No. 76;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRR 14
|:|:|:|:|:|:|:
DB 430 VELLOFLPRSEVR 443

RESULT 13

US-09-489-039A-7319
; Sequence 7319, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:

; APPLICANT: Gary Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 7319
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae

US-09-489-039A-7319

Query Match 48.0%; Score 36; DB 4; Length 98;
Best Local Similarity 58.3%; Pred. No. 15;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 KVOYLTRSAIR 14

Db 51 KPOHLTRSGMRK 62

RESULT 14

US-09-489-039A-11071
; Sequence 11071, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:

; APPLICANT: Gary Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 11071
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae

US-09-489-039A-11071

Query Match 48.0%; Score 36; DB 4; Length 194;
Best Local Similarity 58.3%; Pred. No. 32;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAI 12

Db 111 MERVYLQSQI 122

RESULT 15

US-09-252-991A-19332
; Sequence 19332, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 19332
; LENGTH: 686
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19332

Query Match 48.0%; Score 36; DB 4; Length 686;
Best Local Similarity 77.8%; Pred. No. 1.3e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 VOYLTRSAI 12

Db 522 VOYLTRSGL 530

RESULT 16

US-09-252-991A-24791
; Sequence 24791, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 24791
; LENGTH: 765
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-24791

Query Match 48.0%; Score 36; DB 4; Length 765;
Best Local Similarity 50.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 EKVQYLTRSAIRRA 15

Db 502 EQVRMLDRELRA 515

RESULT 17

US-08-388-983-18
; Sequence 18, Application US/08588983
; Patent No. 5854067
; GENERAL INFORMATION:

; APPLICANT: Christopher B. Newgard, et al.
; TITLE OF INVENTION: Methods and Compositions
; TITLE OF INVENTION: for Inhibiting Hexokinase
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: US
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/588,983
; FILING DATE: Concurrently herewith
; CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
NAME: Fussey, Shelley P.M.
REGISTRATION NUMBER: 39,458
REFERENCE/DOCKET NUMBER: UTSD:424/FUS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
TELEX: n/a
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 924 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-588-983-18

Query Match 48.0%; Score 36; DB 2; Length 924;
Best Local Similarity 61.5%; Pred. No. 1.8e+02;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 EKVOYLTRSAIRR 14
Db 638 QDVVLLRAIRR 650

RESULT 18
US-08-588-976-18
Sequence 18, Application US/08588976
Patent No. 5891717
GENERAL INFORMATION:
APPLICANT: Christopher B. Newgard, et al.
TITLE OF INVENTION: Methods and Compositions for
Inhibiting Hexokinase
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: US
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/588,976
FILING DATE: Concurrently herewith
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fussey, Shelley P.M.
REGISTRATION NUMBER: 39,458
REFERENCE/DOCKET NUMBER: UTSD:481/FUS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
TELEX: n/a
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 924 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-588-976-18

Query Match 48.0%; Score 36; DB 2; Length 924;
Best Local Similarity 61.5%; Pred. No. 1.8e+02;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 EKVOYLTRSAIRR 14
Db 638 QDVVLLRAIRR 650

RESULT 19
US-09-252-991A-28362
Sequence 28362, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 28362
LENGTH: 210
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28362

Query Match 46.7%; Score 35; DB 4; Length 210;
Best Local Similarity 53.8%; Pred. No. 54;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 EKVOYLTRSAIRR 14
Db 180 EAOYLSREAKR 192

RESULT 20
US-09-134-001C-5136
Sequence 5136, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: CTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 5136
LENGTH: 211
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5136

Query Match 46.7%; Score 35; DB 4; Length 211;
Best Local Similarity 46.7%; Pred. No. 54;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 EKVOYLTRSAIRRAS 16
Db 182 EKVDPLTKETERTT 196

RESULT 21
US-09-134-000C-6395
Sequence 6395, Application US/09134000C
Patent No. 6617156
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032

; CURRENT APPLICATION NUMBER: US/09/134,000C
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6395
; LENGTH: 216
; TYPE: PR1
; ORGANISM: Enterococcus faecalis
US-09-134-000C-6395

Query Match 46.7%; Score 35; DB 4; Length 216;
Best Local Similarity 50.0%; Pred. No. 56;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 5 QYLTRSAIRRAS 16
Db 161 QYINRETLRVS 172

RESULT 22

US-09-910-174B-14
; Sequence 14, Application US/09910174B
; Patent No. 6630575
; GENERAL INFORMATION:
; APPLICANT: Coyle, Anthony J.
; APPLICANT: Fraser, Christopher C.
; APPLICANT: Manning, Stephen
; TITLE OF INVENTION: B7-H2 Molecules, No. 6630575el Members of the B7
; FILE REFERENCE: 35800/236924
; CURRENT APPLICATION NUMBER: US/09/910,174B
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 09/620,461
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 357
; TYPE: PR1
; ORGANISM: Homo sapiens
US-09-910-174B-14

Query Match 46.7%; Score 35; DB 4; Length 357;
Best Local Similarity 75.0%; Pred. No. 97;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EKQVYLTR 9
Db 313 KKIQLTR 320

RESULT 23

US-09-620-461-14
; Sequence 14, Application US/09620461
; Patent No. 6635750
; GENERAL INFORMATION:
; APPLICANT: Coyle, Anthony J.
; APPLICANT: Fraser, Christopher C.
; APPLICANT: Manning, Stephen
; TITLE OF INVENTION: B7-H2 Molecules, No. 6635750el Members of the B7
; FILE REFERENCE: 5800-149
; CURRENT APPLICATION NUMBER: US/09/620,461
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 357
; TYPE: PR1
; ORGANISM: Homo sapiens
US-09-620-461-14

Query Match 46.7%; Score 35; DB 4; Length 357;
Best Local Similarity 75.0%; Pred. No. 97;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EKQVYLTR 9
Db 313 KKIQLTR 320

RESULT 24

US-09-277-262-4
; Sequence 4, Application US/09277262
; Patent No. 6395482
; GENERAL INFORMATION:
; APPLICANT: Karavliorgou, Maria
; APPLICANT: Gogos, Joseph A.
; TITLE OF INVENTION: METHODS OF DETERMINING A SUSCEPTIBILITY TO OR PRESENCE
; TITLE OF INVENTION: OF SCHIZOPHRENIA, OR A DISEASE OR DISORDER RELATED
; FILE REFERENCE: 600-1-223 CIP
; CURRENT APPLICATION NUMBER: US/09/277,262
; CURRENT FILING DATE: 1999-03-26
; EARLIER APPLICATION NUMBER: 09/229,530
; EARLIER FILING DATE: 1999-01-13
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 497
; TYPE: PR1
; ORGANISM: Mus musculus
US-09-277-262-4

Query Match 46.7%; Score 35; DB 4; Length 497;
Best Local Similarity 43.8%; Pred. No. 1.4e+02;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MEKVQYLTRSAIRRAS 16
Db 452 MEVLPYLSRALENS 467

RESULT 25

US-09-277-262-2
; Sequence 2, Application US/09277262
; Patent No. 6395482
; GENERAL INFORMATION:
; APPLICANT: Karavliorgou, Maria
; APPLICANT: Gogos, Joseph A.
; TITLE OF INVENTION: METHODS OF DETERMINING A SUSCEPTIBILITY TO OR PRESENCE
; TITLE OF INVENTION: OF SCHIZOPHRENIA, OR A DISEASE OR DISORDER RELATED
; FILE REFERENCE: 600-1-223 CIP
; CURRENT APPLICATION NUMBER: US/09/277,262
; CURRENT FILING DATE: 1999-03-26
; EARLIER APPLICATION NUMBER: 09/229,530
; EARLIER FILING DATE: 1999-01-13
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 516
; TYPE: PR1
; ORGANISM: Homo sapiens
US-09-277-262-2

Query Match 46.7%; Score 35; DB 4; Length 516;
Best Local Similarity 43.8%; Pred. No. 1.5e+02;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MEKVQYLTRSAIRRAS 16
Db 471 MEVLPYLSRALENS 486

Fri Oct 1 16:13:03 2004

us-09-830-779-17_copy_1_16.ra1

Page 8

Search completed: October 1, 2004, 12:21:10
Job time : 17 secs

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OM protein - protein search, using sw model

Run on: October 1, 2004, 12:18:23 ; Search time 63.4 Seconds
(without alignments)
81.211 Million cell updates/sec

Title: US-09-830-779-17_COPY_1_16

Perfect score: 75

Sequence: 1 MEKVQLTRSAIRAS 16

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Total number of hits satisfying chosen parameters: 1351062

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications AA:
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2: /cgn2_5/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_5/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_5/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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7: /cgn2_5/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_5/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_5/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
10: /cgn2_5/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_5/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
12: /cgn2_5/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_5/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
14: /cgn2_5/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
15: /cgn2_5/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
16: /cgn2_5/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_5/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_5/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	75	100.0	16	US-10-705-791-8	Sequence 8, Appl
2	75	100.0	35	US-10-705-791-11	Sequence 11, Appl
3	75	100.0	36	US-10-705-791-10	Sequence 10, Appl
4	75	100.0	52	US-09-954-571-2	Sequence 2, Appl
5	75	100.0	52	US-09-954-571-1	Sequence 4, Appl
6	75	100.0	52	US-09-954-571-5	Sequence 5, Appl
7	75	100.0	52	US-10-371-101-15	Sequence 15, Appl
8	75	100.0	52	US-10-408-765A-478	Sequence 478, Appl
9	75	100.0	52	US-10-705-791-2	Sequence 1, Appl
10	75	100.0	52	US-10-705-791-1	Sequence 2, Appl
11	75	100.0	79	US-10-705-791-17	Sequence 17, Appl
12	75	100.0	79	US-10-705-791-19	Sequence 18, Appl
13	72	96.0	52	US-09-954-571-3	Sequence 3, Appl
14	72	96.0	52	US-10-371-101-14	Sequence 14, Appl
15	72	96.0	52	US-10-705-791-5	Sequence 5, Appl

16	71	94.7	35	16	US-10-705-791-13	Sequence 13, Appl
17	71	94.7	36	16	US-10-705-791-12	Sequence 12, Appl
18	71	94.7	52	12	US-09-954-571-1	Sequence 1, Appl
19	71	94.7	79	16	US-10-705-791-18	Sequence 18, Appl
20	70	93.3	52	16	US-10-705-791-4	Sequence 4, Appl
21	69	92.0	52	16	US-10-705-791-3	Sequence 3, Appl
22	66	88.0	52	16	US-10-705-791-6	Sequence 6, Appl
23	41	54.7	44	12	US-10-424-599-238702	Sequence 238702, A
24	41	54.7	68	12	US-10-425-114-46161	Sequence 46161, A
25	41	54.7	116	14	US-10-156-761-10177	Sequence 10177, A
26	41	54.7	451	15	US-10-369-493-21630	Sequence 21630, A
27	40	53.3	121	12	US-10-282-122A-47242	Sequence 47242, A
28	40	53.3	1108	15	US-10-369-493-1247	Sequence 1247, Ap
29	40	53.3	452	16	US-10-369-493-20314	Sequence 20314, A
30	39	52.0	113	12	US-10-437-963-201301	Sequence 201301, A
31	38	50.7	113	12	US-10-282-122A-53984	Sequence 53984, A
32	38	50.7	931	16	US-10-437-963-139951	Sequence 139951, A
33	38	50.7	931	16	US-10-437-963-188757	Sequence 188757, A
34	37	49.3	112	12	US-10-424-599-175485	Sequence 175485, A
35	36.5	48.7	331	14	US-10-197-844-2	Sequence 2, Appl
36	36	48.0	75	16	US-10-437-963-202409	Sequence 202409, A
37	36	48.0	111	12	US-10-424-599-170920	Sequence 170920, A
38	36	48.0	111	12	US-10-424-599-195661	Sequence 195661, A
39	36	48.0	113	9	US-09-738-626-5733	Sequence 5733, Ap
40	36	48.0	114	12	US-10-282-122A-52593	Sequence 52593, A
41	36	48.0	119	16	US-10-767-701-55916	Sequence 55916, A
42	36	48.0	207	12	US-10-282-122A-71415	Sequence 71415, A
43	36	48.0	297	16	US-10-437-963-195227	Sequence 195227, A
44	36	48.0	344	15	US-10-131-410-177	Sequence 177, App
45	36	48.0	401	14	US-10-156-761-7673	Sequence 7673, Ap
46	36	48.0	409	12	US-10-282-122A-66259	Sequence 66259, A
47	36	48.0	417	12	US-10-389-647-494	Sequence 494, App
48	36	48.0	434	14	US-10-171-404A-46	Sequence 46, Appl
49	36	48.0	465	12	US-10-282-122A-48867	Sequence 48867, A
50	36	48.0	556	15	US-10-369-493-4879	Sequence 4879, Ap
51	36	48.0	629	16	US-10-437-963-153082	Sequence 153082, A
52	36	48.0	690	16	US-10-437-963-195233	Sequence 195233, A
53	36	48.0	720	16	US-10-433-794-20	Sequence 20, Appl
54	36	48.0	765	12	US-10-182-243-56	Sequence 56, Appl
55	36	48.0	765	14	US-10-128-174-3	Sequence 3, Appl
56	36	48.0	765	14	US-10-128-174-34	Sequence 34, Appl
57	36	48.0	765	14	US-10-128-174-35	Sequence 35, Appl
58	36	48.0	765	14	US-10-128-174-36	Sequence 36, Appl
59	36	48.0	765	14	US-10-128-174-37	Sequence 37, Appl
60	36	48.0	765	14	US-10-128-174-38	Sequence 38, Appl
61	36	48.0	765	14	US-10-128-174-39	Sequence 39, Appl
62	36	48.0	765	14	US-10-128-174-40	Sequence 40, Appl
63	36	48.0	765	14	US-10-128-174-41	Sequence 41, Appl
64	36	48.0	765	14	US-10-128-174-44	Sequence 44, Appl
65	36	48.0	808	16	US-10-437-963-198225	Sequence 198225, A
66	36	48.0	861	14	US-10-156-761-11000	Sequence 11000, A
67	36	48.0	867	15	US-10-369-493-10043	Sequence 10043, A
68	36	48.0	1138	16	US-10-437-963-128344	Sequence 128344, A
69	36	48.0	1465	16	US-10-437-963-128382	Sequence 128382, A
70	36	48.0	1489	16	US-10-437-963-128335	Sequence 128335, A
71	36	48.0	1572	16	US-10-437-963-128334	Sequence 128334, A
72	36	48.0	1639	16	US-10-437-963-128536	Sequence 128536, A
73	36	48.0	1806	16	US-10-437-963-128590	Sequence 128590, A
74	36	48.0	1841	16	US-10-437-963-128482	Sequence 128482, A
75	36	48.0	1859	16	US-10-437-963-128415	Sequence 128415, A
76	36	48.0	1875	16	US-10-437-963-128379	Sequence 128379, A
77	36	48.0	1908	16	US-10-437-963-128442	Sequence 128442, A
78	36	48.0	1936	16	US-10-437-963-128450	Sequence 128450, A
79	36	48.0	1966	16	US-10-437-963-128339	Sequence 128339, A
80	36	48.0	1987	16	US-10-437-963-128617	Sequence 128617, A
81	36	48.0	2093	16	US-10-437-963-128540	Sequence 128540, A
82	35	46.7	24	14	US-10-372-876-453	Sequence 453, App
83	35	46.7	24	14	US-10-097-065-453	Sequence 453, App
84	35	46.7	61	9	US-09-864-761-40542	Sequence 40542, A
85	35	46.7	61	9	US-09-864-761-41598	Sequence 41598, A
86	35	46.7	62	10	US-09-764-891-3012	Sequence 3012, Ap
87	35	46.7	90	16	US-10-437-963-144511	Sequence 144511, A
88	35	46.7	96	11	US-09-864-408A-4858	Sequence 4858, Ap

Sequence 152503,
Sequence 147002,
Sequence 61911, A
Sequence 103091,
Sequence 442, App
Sequence 442, App
Sequence 464, App
Sequence 71171, A
Sequence 57201, A
Sequence 164, App
Sequence 2255, App
Sequence 52269, A

ALIGNMENTS

US-10-705-791-8 99 12 US-10-424-599-152503
US-10-437-963-147002
US-10-282-122A-61911
US-10-437-963-103091
US-10-372-876-442
US-10-097-065-442
US-10-112-944-464
US-10-282-122A-71171
US-10-282-122A-57201
US-10-093-463-164
US-10-104-047-2255
US-10-425-114-52269

35 46.7 99 12
35 46.7 106 16
35 46.7 113 12
35 46.7 114 16
35 46.7 131 12
35 46.7 131 14
35 46.7 132 12
35 46.7 132 12
35 46.7 207 12
35 46.7 224 12
35 46.7 240 15
35 46.7 248 15
100 35 46.7 296 12

US-10-705-791-8
; Sequence 8, Application US/10705791
; Publication No. US20040121942A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; APPLICANT: Chien, Kenneth
; APPLICANT: Dillmann, Wolfgang
; APPLICANT: Minamisawa, Susanne
; APPLICANT: He, Huaping
; APPLICANT: Hoshijima, Masahiko
; APPLICANT: Meyer, Markus
; APPLICANT: Scott, Christopher
; APPLICANT: Wang, Yibin
; APPLICANT: Silverman, Gregg J.
; TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
; FILE REFERENCE: 6627-PA9025
; CURRENT APPLICATION NUMBER: US/10/705,791
; PRIOR FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: 60/106,718
; PRIOR FILING DATE: 1998-11-02
; PRIOR APPLICATION NUMBER: PCT/US99/25692
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens

Query Match 100.0%; Score 75; DB 16; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEKVQYLTRSAIRRAS 16
Db 1 MEKVQYLTRSAIRRAS 16

US-10-705-791-11
; Sequence 11, Application US/10705791
; Publication No. US20040121942A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; APPLICANT: Chien, Kenneth
; APPLICANT: Dillmann, Wolfgang
; APPLICANT: Minamisawa, Susanne
; APPLICANT: He, Huaping
; APPLICANT: Hoshijima, Masahiko
; APPLICANT: Meyer, Markus
; APPLICANT: Scott, Christopher
; APPLICANT: Wang, Yibin
; APPLICANT: Silverman, Gregg J.

US-10-705-791-11
; TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
; FILE REFERENCE: 6627-PA9025
; CURRENT APPLICATION NUMBER: US/10/705,791
; PRIOR FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: 60/106,718
; PRIOR FILING DATE: 1998-11-02
; PRIOR APPLICATION NUMBER: PCT/US99/25692
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Homo sapiens

Query Match 100.0%; Score 75; DB 16; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEKVQYLTRSAIRRAS 16
Db 16 MEKVQYLTRSAIRRAS 31

US-10-705-791-10
; Sequence 10, Application US/10705791
; Publication No. US20040121942A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; APPLICANT: Chien, Kenneth
; APPLICANT: Dillmann, Wolfgang
; APPLICANT: Minamisawa, Susanne
; APPLICANT: He, Huaping
; APPLICANT: Hoshijima, Masahiko
; APPLICANT: Meyer, Markus
; APPLICANT: Scott, Christopher
; APPLICANT: Wang, Yibin
; APPLICANT: Silverman, Gregg J.
; TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
; FILE REFERENCE: 6627-PA9025
; CURRENT APPLICATION NUMBER: US/10/705,791
; PRIOR FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: 60/106,718
; PRIOR FILING DATE: 1998-11-02
; PRIOR APPLICATION NUMBER: PCT/US99/25692
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Homo sapiens

Query Match 100.0%; Score 75; DB 16; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEKVQYLTRSAIRRAS 16
Db 1 MEKVQYLTRSAIRRAS 16

US-09-954-571-2
; Sequence 2, Application US/09954571
; Publication No. US20020032167A1
; GENERAL INFORMATION:
; APPLICANT: Chien, Kenneth R

; APPLICANT: Hoshijima, Masahiko
; APPLICANT: Ross, John
; APPLICANT: Ikeda, Yasuhiro
; TITLE OF INVENTION: HIGH EFFICIENCY CARDIAC GENE TRANSFER
; FILE REFERENCE: 6627-PA0123
; CURRENT APPLICATION NUMBER: US/09/954,571
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: 60/231,821
; PRIOR FILING DATE: 2000-11-09
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 2
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-954-571-2

Query Match 100.0%; Score 75; DB 12; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEKVQYLTRSAIRRAS 16
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Db 1 MEKVQYLTRSAIRRAS 16

RESULT 5
US-09-954-571-4
; Sequence 4, Application US/09954571
; Publication No. US20020032167A1
; GENERAL INFORMATION:
; APPLICANT: Chien, Kenneth R
; APPLICANT: Hoshijima, Masahiko
; APPLICANT: Ross, John
; APPLICANT: Ikeda, Yasuhiro
; TITLE OF INVENTION: HIGH EFFICIENCY CARDIAC GENE TRANSFER
; FILE REFERENCE: 6627-PA0123
; CURRENT APPLICATION NUMBER: US/09/954,571
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: 60/231,821
; PRIOR FILING DATE: 2000-11-09
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 4
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-954-571-4

Query Match 100.0%; Score 75; DB 12; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEKVQYLTRSAIRRAS 16
| | | | | | | | | | | | | | | | | |
Db 1 MEKVQYLTRSAIRRAS 16

RESULT 6
US-09-954-571-5
; Sequence 5, Application US/09954571
; Publication No. US20020032167A1
; GENERAL INFORMATION:
; APPLICANT: Chien, Kenneth R
; APPLICANT: Hoshijima, Masahiko
; APPLICANT: Ross, John
; APPLICANT: Ikeda, Yasuhiro
; TITLE OF INVENTION: HIGH EFFICIENCY CARDIAC GENE TRANSFER
; FILE REFERENCE: 6627-PA0123
; CURRENT APPLICATION NUMBER: US/09/954,571
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: 60/231,821
; PRIOR FILING DATE: 2000-11-09

; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 5
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Oryctolagus cuniculus
US-09-954-571-5

Query Match 100.0%; Score 75; DB 12; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEKVQYLTRSAIRRAS 16
| | | | | | | | | | | | | | | | | |
Db 1 MEKVQYLTRSAIRRAS 16

RESULT 7
US-10-371-101-15
; Sequence 15, Application US/10371101
; Publication No. US2003014995A1
; GENERAL INFORMATION:
; APPLICANT: Zwaal, Richard
; APPLICANT: Groenen, Jose
; APPLICANT: Bogaert, Thierry
; TITLE OF INVENTION: COMPOUND SCREENING METHODS
; FILE REFERENCE: D00590.70035.US
; CURRENT APPLICATION NUMBER: US/10/371,101
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: GB 9908670.4
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: US 60/129,596
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: GB 9912736.7
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: 09/549,872
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 15
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-371-101-15

Query Match 100.0%; Score 75; DB 14; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEKVQYLTRSAIRRAS 16
| | | | | | | | | | | | | | | | | |
Db 1 MEKVQYLTRSAIRRAS 16

RESULT 8
US-10-408-765A-478
; Sequence 478, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Robin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Waincock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 478
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-478

Query Match          100.0%; Score 75; DB 16; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRAS 16
   |||||
Db 1 MEKVQYLTRSAIRRAS 16

RESULT 9
US-10-705-791-1
; Sequence 1, Application US/10705791
; Publication No. US20040121942A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; APPLICANT: Chien, Kenneth
; APPLICANT: Dillmann, Wolfgang
; APPLICANT: Minamisawa, Susanne
; APPLICANT: He, Huaping
; APPLICANT: Hoshijima, Masahiko
; APPLICANT: Meyer, Markus
; APPLICANT: Scott, Christopher
; APPLICANT: Wang, Yibin
; APPLICANT: Silverman, Gregg J.
; TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
; FILE REFERENCE: 6627-PA9025
; CURRENT APPLICATION NUMBER: US/10/705,791
; CURRENT FILING DATE: 2003-11-10
; PRIOR FILING DATE: 1998-11-02
; PRIOR APPLICATION NUMBER: PCT/US99/25692
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-705-791-1

Query Match          100.0%; Score 75; DB 16; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRAS 16
   |||||
Db 1 MEKVQYLTRSAIRRAS 16

RESULT 10
US-10-705-791-2
; Sequence 2, Application US/10705791
; Publication No. US20040121942A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; APPLICANT: Chien, Kenneth
; APPLICANT: Dillmann, Wolfgang
; APPLICANT: Minamisawa, Susanne
; APPLICANT: He, Huaping
; APPLICANT: Hoshijima, Masahiko
; APPLICANT: Meyer, Markus
; APPLICANT: Scott, Christopher
; APPLICANT: Wang, Yibin
; APPLICANT: Silverman, Gregg J.
; TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
; FILE REFERENCE: 6627-PA9025
; CURRENT APPLICATION NUMBER: US/10/705,791
; CURRENT FILING DATE: 2003-11-10
; PRIOR FILING DATE: 1998-11-02
; PRIOR APPLICATION NUMBER: PCT/US99/25692
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-705-791-1
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; FILE REFERENCE: 6627-PA9025
; CURRENT APPLICATION NUMBER: US/10/705,791
; CURRENT FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: 60/106,718
; PRIOR FILING DATE: 1998-11-02
; PRIOR APPLICATION NUMBER: PCT/US99/25692
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-705-791-2

Query Match          100.0%; Score 75; DB 16; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRAS 16
   |||||
Db 1 MEKVQYLTRSAIRRAS 16

RESULT 11
US-10-705-791-17
; Sequence 17, Application US/10705791
; Publication No. US20040121942A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; APPLICANT: Chien, Kenneth
; APPLICANT: Dillmann, Wolfgang
; APPLICANT: Minamisawa, Susanne
; APPLICANT: He, Huaping
; APPLICANT: Hoshijima, Masahiko
; APPLICANT: Meyer, Markus
; APPLICANT: Scott, Christopher
; APPLICANT: Wang, Yibin
; APPLICANT: Silverman, Gregg J.
; TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
; FILE REFERENCE: 6627-PA9025
; CURRENT APPLICATION NUMBER: US/10/705,791
; CURRENT FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: 60/106,718
; PRIOR FILING DATE: 1998-11-02
; PRIOR APPLICATION NUMBER: PCT/US99/25692
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 79
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-705-791-17

Query Match          100.0%; Score 75; DB 16; Length 79;
Best Local Similarity 100.0%; Pred. No. 3e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRAS 16
   |||||
Db 1 MEKVQYLTRSAIRRAS 16

RESULT 12
US-10-705-791-19
; Sequence 19, Application US/10705791
; Publication No. US20040121942A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; APPLICANT: Chien, Kenneth
; APPLICANT: Dillmann, Wolfgang
```

APPLICANT: Minamisawa, Susanne
APPLICANT: He, Huaping
APPLICANT: Hoshijima, Masahiko
APPLICANT: Meyer, Markus
APPLICANT: Scott, Christopher
APPLICANT: Wang, Yibin
APPLICANT: Silverman, Gregg J.
TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
FILE REFERENCE: 6627-PA9025
CURRENT APPLICATION NUMBER: US/10/705,791
PRIOR FILING DATE: 2003-11-10
PRIOR APPLICATION NUMBER: 60/106,718
PRIOR FILING DATE: 1998-11-02
PRIOR APPLICATION NUMBER: PCT/US99/25692
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn version 3.2
SEQ ID NO 19
LENGTH: 79
TYPE: PRT
ORGANISM: Escherichia coli
US-10-705-791-19

Query Match 100.0%; Score 75; DB 16; Length 79;
Best Local Similarity 100.0%; Pred. No. 3e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEKVQYLTRSAIRRAS 16
Db 1 MEKVQYLTRSAIRRAS 16

RESULT 13
US-09-954-571-3
Sequence 3, Application US/09954571
Publication No. US20020022167A1
GENERAL INFORMATION:
APPLICANT: Chien, Kenneth R
APPLICANT: Hoshijima, Masahiko
APPLICANT: Ross, John
APPLICANT: Ikeda, Yasuhiro
TITLE OF INVENTION: HIGH EFFICIENCY CARDIAC GENE TRANSFER
FILE REFERENCE: 6627-PA0123
CURRENT APPLICATION NUMBER: US/09/954,571
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: 60/231,821
PRIOR FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.2
SEQ ID NO 3
LENGTH: 52
TYPE: PRT
ORGANISM: Canis familiaris
US-09-954-571-3

Query Match 96.0%; Score 72; DB 12; Length 52;
Best Local Similarity 93.8%; Pred. No. 6.9e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEKVQYLTRSAIRRAS 16
Db 1 MEKVQYLTRSAIRRAS 16

RESULT 14
US-10-371-101-14
Sequence 14, Application US/10371101
Publication No. US20030149995A1
GENERAL INFORMATION:
APPLICANT: Zwaal, Richard
APPLICANT: Groenen, Jose
APPLICANT: Bogaert, Thierry

TITLE OF INVENTION: COMPOUND SCREENING METHODS
FILE REFERENCE: D00590.70035 US
CURRENT APPLICATION NUMBER: US/10/371,101
CURRENT FILING DATE: 2003-02-21
PRIOR APPLICATION NUMBER: GB 9908670.4
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: US 60/129,596
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: GB 9912736.7
PRIOR FILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: 09/549,872
PRIOR FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn ver. 2.0
SEQ ID NO 14
LENGTH: 52
TYPE: PRT
ORGANISM: Sus sp.
US-10-371-101-14

Query Match 96.0%; Score 72; DB 14; Length 52;
Best Local Similarity 93.8%; Pred. No. 6.9e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEKVQYLTRSAIRRAS 16
Db 1 MEKVQYLTRSAIRRAS 16

RESULT 15
US-10-705-791-5
Sequence 5, Application US/10705791
Publication No. US20040121942A1
GENERAL INFORMATION:
APPLICANT: The Regents of the University of California
APPLICANT: Chien, Kenneth
APPLICANT: Dillmann, Wolfgang
APPLICANT: Minamisawa, Susanne
APPLICANT: He, Huaping
APPLICANT: Hoshijima, Masahiko
APPLICANT: Meyer, Markus
APPLICANT: Scott, Christopher
APPLICANT: Wang, Yibin
APPLICANT: Silverman, Gregg J.
TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT

FILE REFERENCE: 6627-PA9025
CURRENT APPLICATION NUMBER: US/10/705,791
CURRENT FILING DATE: 2003-11-10
PRIOR APPLICATION NUMBER: 60/106,718
PRIOR FILING DATE: 1998-11-02
PRIOR APPLICATION NUMBER: PCT/US99/25692
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn version 3.2
SEQ ID NO 5
LENGTH: 52
TYPE: PRT
ORGANISM: Homo sapiens
US-10-705-791-5

Query Match 96.0%; Score 72; DB 16; Length 52;
Best Local Similarity 93.8%; Pred. No. 6.9e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEKVQYLTRSAIRRAS 16
Db 1 MEKVQYLTRSAIRRAS 16

RESULT 16
US-10-705-791-13
Sequence 13, Application US/10705791

Publication No. US20040121942A1
GENERAL INFORMATION:
APPLICANT: The Regents of the University of California
APPLICANT: Chien, Kenneth
APPLICANT: Dillmann, Wolfgang
APPLICANT: Minamisawa, Susanne
APPLICANT: He, Huaping
APPLICANT: Hoshijima, Masahiko
APPLICANT: Meyer, Markus
APPLICANT: Scott, Christopher
APPLICANT: Wang, Yibin
APPLICANT: Silverman, Gregg J.
TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBEAN ACTIVITY FOR THE TREATMENT
FILE REFERENCE: 6627-PA9025
CURRENT APPLICATION NUMBER: US/10/705,791
CURRENT FILING DATE: 2003-11-10
PRIOR APPLICATION NUMBER: 60/106,718
PRIOR FILING DATE: 1998-11-02
PRIOR APPLICATION NUMBER: PCT/US99/25692
PRIOR FILING DATE: 1999-11-02
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patent in version 3.2
SEQ ID NO 13
LENGTH: 35
TYPE: PRT
ORGANISM: Homo sapiens
US-10-705-791-13

Query Match 94.7%; Score 71; DB 16; Length 35;
Best Local Similarity 100.0%; Pred. No. 6.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRA 15
DB 16 MEKVQYLTRSAIRRA 30

RESULT 17
US-10-705-791-12
Sequence 12, Application US/10705791
Publication No. US20040121942A1
GENERAL INFORMATION:
APPLICANT: The Regents of the University of California
APPLICANT: Chien, Kenneth
APPLICANT: Dillmann, Wolfgang
APPLICANT: Minamisawa, Susanne
APPLICANT: He, Huaping
APPLICANT: Hoshijima, Masahiko
APPLICANT: Meyer, Markus
APPLICANT: Scott, Christopher
APPLICANT: Wang, Yibin
APPLICANT: Silverman, Gregg J.
TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBEAN ACTIVITY FOR THE TREATMENT
FILE REFERENCE: 6627-PA9025
CURRENT APPLICATION NUMBER: US/10/705,791
CURRENT FILING DATE: 2003-11-10
PRIOR APPLICATION NUMBER: 60/106,718
PRIOR FILING DATE: 1998-11-02
PRIOR APPLICATION NUMBER: PCT/US99/25692
PRIOR FILING DATE: 1999-11-02
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patent in version 3.2
SEQ ID NO 12
LENGTH: 36
TYPE: PRT
ORGANISM: Homo sapiens
US-10-705-791-12

Query Match 94.7%; Score 71; DB 16; Length 36;
Best Local Similarity 100.0%; Pred. No. 7.2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRA 15
DB 1 MEKVQYLTRSAIRRA 15

RESULT 18
US-09-954-571-1
Sequence 1, Application US/09954571
Publication No. US20020032167A1
GENERAL INFORMATION:
APPLICANT: Chien, Kenneth R
APPLICANT: Hoshijima, Masahiko
APPLICANT: Ross, John
APPLICANT: Ikeda, Yasuhiro
TITLE OF INVENTION: HIGH EFFICIENCY CARDIAC GENE TRANSFER
FILE REFERENCE: 6627-PA0123
CURRENT APPLICATION NUMBER: US/09/954,571
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: 60/231,821
PRIOR FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patent in version 3.2
SEQ ID NO 1
LENGTH: 52
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Mutant form of human protein sequence
US-09-954-571-1

Query Match 94.7%; Score 71; DB 12; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRA 15
DB 1 MEKVQYLTRSAIRRA 15

RESULT 19
US-10-705-791-18
Sequence 18, Application US/10705791
Publication No. US20040121942A1
GENERAL INFORMATION:
APPLICANT: The Regents of the University of California
APPLICANT: Chien, Kenneth
APPLICANT: Dillmann, Wolfgang
APPLICANT: Minamisawa, Susanne
APPLICANT: He, Huaping
APPLICANT: Hoshijima, Masahiko
APPLICANT: Meyer, Markus
APPLICANT: Scott, Christopher
APPLICANT: Wang, Yibin
APPLICANT: Silverman, Gregg J.
TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBEAN ACTIVITY FOR THE TREATMENT
FILE REFERENCE: 6627-PA9025
CURRENT APPLICATION NUMBER: US/10/705,791
CURRENT FILING DATE: 2003-11-10
PRIOR APPLICATION NUMBER: 60/106,718
PRIOR FILING DATE: 1998-11-02
PRIOR APPLICATION NUMBER: PCT/US99/25692
PRIOR FILING DATE: 1999-11-02
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patent in version 3.2
SEQ ID NO 18
LENGTH: 79
TYPE: PRT
ORGANISM: Escherichia coli
US-10-705-791-18

Query Match 94.7%; Score 71; DB 16; Length 79;

Best Local Similarity 100.0%; Pred. No. 1.7e-05; Indels 0; Gaps 0; Mismatches 0;
Matches 15; Conservative 0;
Qy 1 MEKQVYLTRSAIRRA 15
| | | | | | | | | | | | | | | | |
Db 1 MEKQVYLTRSAIRRA 15
| | | | | | | | | | | | | | | | |
RESULT 20
US-10-705-791-4
; Sequence 4, Application US/10705791
; Publication No. US20040121942A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; APPLICANT: Chien, Kenneth
; APPLICANT: Dillmann, Wolfgang
; APPLICANT: Minamisawa, Susanne
; APPLICANT: He, Huaping
; APPLICANT: Hoshijima, Masahiko
; APPLICANT: Meyer, Markus
; APPLICANT: Scott, Christopher
; APPLICANT: Wang, Yibin
; APPLICANT: Silverman, Gregg J.
; TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
; FILE REFERENCE: 6627-PA9025
; CURRENT APPLICATION NUMBER: US/10/705,791
; PRIOR FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: 60/106,718
; PRIOR FILING DATE: 1998-11-02
; PRIOR APPLICATION NUMBER: PCT/US99/25692
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 4
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-705-791-4
Query Match 93.3%; Score 70; DB 16; Length 52;
Best Local Similarity 93.8%; Pred. No. 1.6e-05;
Matches 15; Conservative 0; Mismatches 1; Indels 0;
Qy 1 MEKQVYLTRSAIRRAS 16
| | | | | | | | | | | | | | | | |
Db 1 MEKQVYLTRSAIRRAS 16
| | | | | | | | | | | | | | | | |
RESULT 21
US-10-705-791-3
; Sequence 3, Application US/10705791
; Publication No. US20040121942A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; APPLICANT: Chien, Kenneth
; APPLICANT: Dillmann, Wolfgang
; APPLICANT: Minamisawa, Susanne
; APPLICANT: He, Huaping
; APPLICANT: Hoshijima, Masahiko
; APPLICANT: Meyer, Markus
; APPLICANT: Scott, Christopher
; APPLICANT: Wang, Yibin
; APPLICANT: Silverman, Gregg J.
; TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
; FILE REFERENCE: 6627-PA9025
; CURRENT APPLICATION NUMBER: US/10/705,791
; PRIOR FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: 60/106,718
; PRIOR FILING DATE: 1998-11-02
; PRIOR APPLICATION NUMBER: PCT/US99/25692
; PRIOR FILING DATE: 1999-11-02

NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 3
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-705-791-3
Query Match 92.0%; Score 69; DB 16; Length 52;
Best Local Similarity 93.8%; Pred. No. 2.5e-05;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MEKQVYLTRSAIRRAS 16
| | | | | | | | | | | | | | | | |
Db 1 MEKQVYLTRSAIRRAS 16
| | | | | | | | | | | | | | | | |
RESULT 22
US-10-705-791-6
; Sequence 6, Application US/10705791
; Publication No. US20040121942A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; APPLICANT: Chien, Kenneth
; APPLICANT: Dillmann, Wolfgang
; APPLICANT: Minamisawa, Susanne
; APPLICANT: He, Huaping
; APPLICANT: Hoshijima, Masahiko
; APPLICANT: Meyer, Markus
; APPLICANT: Scott, Christopher
; APPLICANT: Wang, Yibin
; APPLICANT: Silverman, Gregg J.
; TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
; FILE REFERENCE: 6627-PA9025
; CURRENT APPLICATION NUMBER: US/10/705,791
; PRIOR FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: 60/106,718
; PRIOR FILING DATE: 1998-11-02
; PRIOR APPLICATION NUMBER: PCT/US99/25692
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 6
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-705-791-6
Query Match 88.0%; Score 66; DB 16; Length 52;
Best Local Similarity 87.5%; Pred. No. 9.1e-05;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MEKQVYLTRSAIRRAS 16
| | | | | | | | | | | | | | | | |
Db 1 MEKQVYLTRSAIRRAS 16
| | | | | | | | | | | | | | | | |
RESULT 23
US-10-424-599-238702
; Sequence 238702, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684

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; SEQ ID NO 238702
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_57573C.1.bep
US-10-424-599-238702

Query Match          54.7%; Score 41; DB 12; Length 44;
Best Local Similarity 46.2%; Pred. No. 3.5;
Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy      1 MEKVQVILTRSAIR 13
      :||:|||||
Db      25 LEKIEVITTRERIK 37

; LENGTH: 116
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-10177

Query Match          54.7%; Score 41; DB 14; Length 116;
Best Local Similarity 46.7%; Pred. No. 10;
Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy      1 MEKVQVILTRSAIRRA 15
      :||:|||||
Db      81 VEKIELVTRGDVRRRA 95

Search completed: October 1, 2004, 12:48:43
Job time : 64.4 secs

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RESULT 24
US-10-425-114-46161
; Sequence 46161, Application US/10425114
; Publication NO. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 46161
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 701164165_FLI.pep
US-10-425-114-46161

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 1, 2004, 12:05:26 ; Search time 15.6 Seconds

(without alignments)
98.658 Million cell updates/sec

Title: US-09-830-779-17_COPY_1_16

Perfect score: 75

Sequence: 1 MEKVQYLRSATRRAS 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : PIR 78.*

1: p1r1.*

2: p1r2.*

3: p1r3.*

4: p1r4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	75	100.0	52	1 A40424	phospholamban - hu
2	75	100.0	52	1 S37638	phospholamban - ra
3	75	100.0	52	1 A49057	phospholamban - ra
4	75	100.0	52	1 B40424	phospholamban - ra
5	72	96.0	52	1 A28002	phospholamban - do
6	72	96.0	52	1 S05540	phospholamban - pi
7	71	94.7	52	1 A39535	phospholamban - ch
8	41	54.7	116	2 T34780	ribosomal protein
9	41	54.7	451	2 F75083	phospho-sugar muta
10	40	53.3	121	2 E70187	ribosomal protein
11	40	53.3	1108	2 E71104	probable cell divi
12	39	52.0	481	2 B75167	hypothetical prote
13	38	50.7	119	2 D69155	hypothetical prote
14	37	49.3	283	2 H69179	conserved hypotet
15	37	49.3	296	2 F70879	hypothetical prote
16	37	49.3	308	2 AC1867	hypothetical prote
17	37	49.3	2712	2 T05113	hypothetical prote
18	36	48.0	236	2 D69048	conserved hypotet
19	36	48.0	294	2 T00104	probable ddbp-4-de
20	36	48.0	335	2 A24785	hypothetical prote
21	36	48.0	409	2 F83493	probable MFS trans
22	36	48.0	410	2 T12833	hypothetical prote
23	36	48.0	417	2 H83370	hydrogen cyanide s
24	36	48.0	434	2 T04263	phosphoprotein pho
25	36	48.0	462	2 AH1053	probable exported
26	36	48.0	486	2 I55449	gene P2A protein
27	36	48.0	549	2 A90253	hypothetical prote
28	36	48.0	622	2 JC5425	transcription init
29	36	48.0	736	2 I51691	dishevelled homolo

30	36	48.0	924	1 S13913	hexokinase (EC 2.7
31	36	48.0	1148	2 D90815	transcription-tepa
32	36	48.0	1148	2 H85674	hypothetical prote
33	35	46.7	185	2 AG2026	hypothetical prote
34	35	46.7	196	2 B93226	aliphatic amidase
35	35	46.7	283	2 G83754	transcription regu
36	35	46.7	307	2 T1879	hypothetical prote
37	35	46.7	390	2 T09000	cysteine synthase
38	35	46.7	390	2 S53487	porphobilinogen sy
39	35	46.7	403	2 B69338	conserved hypotet
40	35	46.7	444	2 S68122	tubulin beta-4 cha
41	35	46.7	455	2 H71028	hypothetical prote
42	35	46.7	515	2 S02194	DNA-directed RNA p
43	35	46.7	535	2 T37183	hypothetical prote
44	35	46.7	561	2 G50303	hypothetical prote
45	35	46.7	626	1 S34120	DNA-directed DNA p
46	35	46.7	781	2 T50055	CDH2 zinc finger p
47	35	46.7	1013	2 T31211	trwC protein homol
48	35	46.7	1102	2 S65235	probable membrane
49	35	46.7	1710	2 T14005	phospholipase D (E
50	34.5	46.0	452	2 T34542	hypothetical prote
51	34.5	46.0	813	2 C97292	ATPases with chape
52	34.5	46.0	1027	2 T46296	hypothetical prote
53	34.5	46.0	1120	2 JC7765	mitotic spindle as
54	34	45.3	101	2 T39075	hypothetical prote
55	34	45.3	108	2 D85482	hypothetical prote
56	34	45.3	108	2 E90631	hypothetical prote
57	34	45.3	134	1 LNCM16	16k galactose-bind
58	34	45.3	170	2 T36571	hypothetical prote
59	34	45.3	172	2 S62166	NADH2 dehydrogenas
60	34	45.3	172	2 S62167	NADH2 dehydrogenas
61	34	45.3	173	2 S44396	NADH2 dehydrogenas
62	34	45.3	173	2 S44397	NADH2 dehydrogenas
63	34	45.3	185	1 R52M6M	ribosomal protein
64	34	45.3	185	2 T03233	probable ribosomal
65	34	45.3	191	2 A65137	hypothetical 21.0
66	34	45.3	191	2 H91160	hypothetical prote
67	34	45.3	191	2 G86006	hypothetical prote
68	34	45.3	200	2 A6C788	cytochrome c-type
69	34	45.3	214	2 E81270	probable outer mem
70	34	45.3	239	2 T20603	hypothetical prote
71	34	45.3	292	2 G95926	probable saccharid
72	34	45.3	321	2 T44336	hypothetical prote
73	34	45.3	328	2 S70885	UDP-galactose 4-ep
74	34	45.3	367	2 A62494	hypothetical prote
75	34	45.3	395	2 T00574	probable protein x
76	34	45.3	409	2 H81831	probable phospholip
77	34	45.3	431	2 H84392	O-acetyl homoserin
78	34	45.3	433	2 D75632	probable hemolysin
79	34	45.3	434	2 A69082	coenzyme F390 synt
80	34	45.3	525	2 A02022	hypothetical prote
81	34	45.3	542	2 T46464	hypothetical prote
82	34	45.3	548	2 S56152	H ₂ -transporting tw
83	34	45.3	576	2 A03038	biotin carboxylase
84	34	45.3	576	2 H98247	biotin carboxylase
85	34	45.3	586	1 JC4219	pyruvate kinase (E
86	34	45.3	604	2 T45627	replication factor
87	34	45.3	604	2 T15091	hypothetical prote
88	34	45.3	662	2 T41512	u5 snrnp-like RNA
89	34	45.3	676	2 S74635	protoporphyrin IX
90	34	45.3	676	2 T46870	protoporphyrin IX
91	34	45.3	821	2 T19705	hypothetical prote
92	34	45.3	833	2 A80448	probable insectici
93	34	45.3	838	2 A38172	adenylate cyclase
94	34	45.3	991	2 T25412	hypothetical prote
95	34	45.3	1857	1 S01787	fatty-acid synthas
96	34	45.3	3839	2 T49799	related to TOM1 pr
97	33	44.0	55	2 S33915	hypothetical prote
98	33	44.0	62	2 S37135	class II histocomp
99	33	44.0	102	1 H8504	histone H4 - bovin
100	33	44.0	102	1 H85FG4	histone H4 - pig

A;Accession: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-52 <OH>
A;Cross-references: GB:I03382; NID:G206134; PIDN:AAA1849.1; PID:G206136
R;Hwang, K.S.; Nadal-Ginard, B.
Adv. Exp. Med. Biol. 304, 387-395, 1991
A;Title: Cloning phospholamban cDNA from rat aortic smooth muscle.
A;Reference number: I51840; MUID:92206283; PMID:1725098
A;Accession: I64795
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-52 <HWAL>
A;Cross-references: GB:S95853; NID:G247312; PIDN:MAR21903.1; PID:G247933

QY 1 MEKVOYLTRSAIRRAS 16

DB

RESULT 4

B40424

phospholamban - rabbit

C.Species: *Oryctolagus cuniculus* (domestic rabbit)

C.Date: 28-Feb-1992 #sequence_revision 27-Jun-1994 #text_change 18-Jun-1999

C.Accession: B40424; S00249

J. Biol. Chem. 266, 11663-11675, 1991

A.Title: Structure of the rabbit phospholamban gene, cloning of the human cDNA, and assign

A.Reference number: A40424; MUID:91268032; PMID:1828605

A.Accession: B40424

A.Molecule type: DNA

A.Residues: 1-52 <FUJ>

A.Cross-references: GR:M31601; NID:G165636; PIDN:AAA31445.1; PID:G165639

R; Fujii, J.; Lytton, J.; Tada, M.; MacLennan, D.H.
 FEBS Lett. 227, 51-55, 1988
 A; Title: Rabbit cardiac and slow-twitch muscle express the same phospholamban gene.
 A; Reference number: S00249; MUID:88112222; PMID:2962883
 A; Accession: S00249
 A; Status: not compared with conceptual translation
 A; Molecule type: mRNA
 A; Residues: 1-52 <FU2>
 A; Cross-references: GB:Y00761; NID:G1661; PIDN:CAA68730.1; PID:G1662
 C; Comment: Phospholamban is expressed in cardiac muscle, slow twitch skeletal muscle, and
 C; Comment: Phospholamban is the major phosphorylated protein in cardiac muscle sarcoplasm
 e; after phosphorylation, the Ca++ pump is activated and the rate of muscle relaxation is
 C; Genetics:
 A; Note: only one gene was detected
 A; Note: the single intron is upstream of the coding region
 C; Superfamily: phospholamban
 C; Keywords: acetylated amino end; ATPase inhibitor; muscle; pentamer; phosphoprotein; tr
 F; 31-52/Domain: transmembrane #status predicted <TM>
 F; 1/Modified site: acetylated amino end (Met) #status predicted
 F; 16/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predict
 F; 17/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase) #status p

Query Match 100.0%; Score 75; DB 1; Length 52;
 Best Local Similarity 100.0%; Pred. No. 5.4e-07; Mismatches 0; Indels 0; Gaps 0;
 Matches 16; Conservative 0

QY 1 MEKVQYLTSAIRRAS 16
 Db 1 MEKVQYLTSAIRRAS 16
 |||||

RESULT 5
 phospholamban - dog
 C; Species: Canis lupus familiaris (dog)
 C; Date: 23-Aug-1987 #sequence_revision 27-Jun-1994 #text_change 18-Jun-1999
 C; Accession: A29002; A26805; A25307; A24818; I46227
 R; Fujii, J.; Ueno, A.; Kitano, K.; Tanaka, S.; Kadoya, M.; Tada, M.
 J. Clin. Invest. 79, 301-304, 1987
 A; Title: Complete complementary DNA-derived amino acid sequence of canine cardiac phosph
 A; Reference number: A29002; MUID:87083954; PMID:3793929
 A; Accession: A29002
 A; Molecule type: mRNA
 A; Residues: 1-52 <FUJ>
 A; Cross-references: GB:M16012; NID:G164043; PIDN:AA330884.1; PID:G164044
 R; Uyeda, A.; Kitano, K.; Fujii, J.; Kadoya, M.; Tada, M.; Tanaka, S.
 Nucleic Acids Res. 15, 6738, 1987
 A; Title: The cDNA sequence of the major phospholamban mRNA in canine cardiac ventricular
 A; Reference number: A26805; MUID:87316936; PMID:3628007
 A; Accession: A26805
 A; Molecule type: mRNA
 A; Residues: 1-52 <UYE>
 A; Cross-references: GB:Y00399; NID:G911; PIDN:CAA68461.1; PID:G912
 R; Simmerman, H.K.B.; Collins, J.H.; Theibert, J.L.; Wegener, A.D.; Jones, L.R.
 J. Biol. Chem. 261, 13333-13341, 1986
 A; Title: Sequence analysis of phospholamban. Identification of phosphorylation sites and
 A; Reference number: A25307; MUID:87008549; PMID:3759968
 A; Contents: partial sequence and phosphorylation sites
 A; Accession: A25307
 A; Molecule type: protein
 A; Residues: 10-45 <SIM>
 R; Fujii, J.; Kadoya, M.; Tada, M.; Toda, H.; Sakiyama, F.
 Biochem. Biophys. Res. Commun. 138, 1044-1050, 1986
 A; Title: Characterization of structural unit of phospholamban by amino acid sequencing a
 A; Reference number: A24818; MUID:86323152; PMID:3753485
 A; Contents: partial sequence and acetylation site
 A; Accession: A24818
 A; Molecule type: protein
 A; Residues: 1-35, 'X', 37-40, 'X', 42-45 <FU2>
 R; Uyeda, A.; Kitano, K.; Fujii, J.; Kadoya, M.; Tada, M.; Tanaka, S.
 Nucleic Acids Symp. Ser. 17, 121-124, 1986
 A; Title: Characterization of recombinant cDNA clones for canine cardiac phospholamban.
 A; Reference number: I46227; MUID:87174860; PMID:3562256

A; Accession: I46227
 A; Status: translated from GB/EMBL/DBRJB
 A; Molecule type: mRNA
 A; Residues: 1-52 <UY2>
 A; Cross-references: GB:M35393; NID:G164045; PIDN:AA41618.1; PID:G164046
 C; Comment: Phospholamban is expressed in cardiac muscle, slow twitch skeletal muscle, and
 C; Comment: Phospholamban is the major phosphorylated protein in cardiac muscle sarcoplasm
 e; after phosphorylation, the Ca++ pump is activated and the rate of muscle relaxation is
 C; Superfamily: phospholamban
 C; Keywords: acetylated amino end; ATPase inhibitor; muscle; pentamer; phosphoprotein; tr
 F; 31-52/Domain: transmembrane #status predicted <TM>
 F; 1/Modified site: acetylated amino end (Met) #status experimental
 F; 16/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status experime
 F; 17/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase) #status ex

Query Match 96.0%; Score 72; DB 1; Length 52;
 Best Local Similarity 93.8%; Pred. No. 2e-06; Mismatches 1; Indels 0; Gaps 0;
 Matches 15; Conservative 1

QY 1 MEKVQYLTSAIRRAS 16
 Db 1 MDKVQYLTSAIRRAS 16
 |||||

RESULT 6
 S05540
 phospholamban - pig
 C; Species: Sus scrofa domestica (domestic pig)
 C; Date: 21-Nov-1993 #sequence_revision 27-Jun-1994 #text_change 18-Jun-1999
 C; Accession: S05540
 R; Verboom, H.; Wuytack, F.; Eggermont, J.A.; de Jaegere, S.; Missiaen, L.; Raeymaekers,
 Biochem. J. 262, 353-356, 1989
 A; Title: cDNA cloning and sequencing of phospholamban from pig stomach smooth muscle.
 A; Reference number: S05540; MUID:90056437; PMID:2530978
 A; Accession: S05540
 A; Molecule type: mRNA
 A; Residues: 1-52 <VER>
 A; Cross-references: EMBL:X15075; NID:G2055; PIDN:CAA33171.1; PID:G2056
 C; Comment: Phospholamban is expressed in cardiac muscle, slow twitch skeletal muscle, and
 C; Comment: Phospholamban is the major phosphorylated protein in cardiac muscle sarcoplasm
 e; after phosphorylation, the Ca++ pump is activated and the rate of muscle relaxation is
 C; Superfamily: phospholamban
 C; Keywords: acetylated amino end; ATPase inhibitor; muscle; pentamer; phosphoprotein; tr
 F; 31-52/Domain: transmembrane #status predicted <TM>
 F; 1/Modified site: acetylated amino end (Met) #status predicted
 F; 16/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predict
 F; 17/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase) #status p

Query Match 96.0%; Score 72; DB 1; Length 52;
 Best Local Similarity 93.8%; Pred. No. 2e-06; Mismatches 1; Indels 0; Gaps 0;
 Matches 15; Conservative 1

QY 1 MEKVQYLTSAIRRAS 16
 Db 1 MDKVQYLTSAIRRAS 16
 |||||

RESULT 7
 A39535
 phospholamban - chicken
 C; Species: Gallus gallus (chicken)
 C; Date: 06-Mar-1992 #sequence_revision 27-Jun-1994 #text_change 18-Jun-1999
 C; Accession: A39535; B39535; A44531
 R; Toyofuku, T.; Zak, R.
 J. Biol. Chem. 266, 5375-5383, 1991
 A; Title: Characterization of cDNA and genomic sequences encoding a chicken phospholamban.
 A; Reference number: A39535; MUID:91170195; PMID:1825996
 A; Accession: A39535
 A; Molecule type: mRNA
 A; Residues: 1-17, 'L', 19-52 <TOY>
 A; Cross-references: GB:M59039; NID:G212575; PIDN:AAA62738.1; PID:G212576
 A; Note: the authors translated the codon CTT for residue 18 as lle
 A; Accession: B39535

A:Molecule type: DNA
A:Residues: 1-52 <T02>
A:Cross-references: GB:M59038
A>Note: the sequence of residues 33-52 and the corresponding nucleotide sequence are not submitted to GenBank, April 1991
R:Toyofuku, T.; Zak, R.
A:Reference number: A44531
A:Accession: A44531
A:Molecule type: DNA
A:Residues: 1-52 <T03>
A:Cross-references: GB:M59038
C:Comment: Phospholamban is expressed in cardiac muscle, slow twitch skeletal muscle, and after phosphorylation, the Ca++ pump is activated and the rate of muscle relaxation is increased.
C:Genetics:
A>Note: only one gene was detected
A>Note: the single intron is upstream of the coding region
C:Superfamily: Phospholamban
C:Keywords: acetylated amino end; ATPase inhibitor; muscle; pentamer; phosphoprotein; trypsin; 31-52/Domain: transmembrane #status predicted <MM>
F:1/Modified site: acetylated amino end (Met) #status predicted
F:16/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predicted
F:17/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase) #status predicted

Query Match 94.7%; Score 71; DB 1; Length 52;
Best Local Similarity 87.5%; Pred. No. 3e-06;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKQVLTSAIRRAS 16
DB 1 MEKQVLTSAIRRAS 16
|||||:|||||

RESULT 8
T34780
ribosomal protein l19 - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 21-Jan-2000
C:Accession: T34780
R:Murphy, L.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
A:Reference number: Z21557
A:Accession: T34780
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-116 <MUR>
A:Cross-references: EMBL:AL023797; PIDN:CAA19387.1; GSPDB:GN000070; SCOEDB:SC2E1.12
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: rplS; SCOEDB:SC2E1.12
C:Superfamily: Escherichia coli ribosomal protein l19

Query Match 54.7%; Score 41; DB 2; Length 116;
Best Local Similarity 46.7%; Pred. No. 2.8;
Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 MEKQVLTSAIRRA 15
DB 81 VEKIELVTRGDVRA 95
|||||:|||||

RESULT 9
F75083
phospho-sugar mutase PAB1666 - Pyrococcus abyssi (strain Orsay)
C:Species: Pyrococcus abyssi
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C:Accession: F75083
R:Anonymous, Genoscope
A:Submitted to the EMBL Data Library, July 1999
A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure
A:Reference number: A75001
A:Accession: F75083
A>Status: preliminary

A:Molecule type: DNA
A:Residues: 1-451 <KAW>
A:Cross-references: GB:AJ248286; GB:AL096836; NID:G5458366; PIDN:CAB49971.1; PID:G545848;
A:Experimental source: strain Orsay
C:Genetics:
A:Gene: PAB1666
C:Superfamily: phosphomannomutase

Query Match 54.7%; Score 41; DB 2; Length 451;
Best Local Similarity 50.0%; Pred. No. 12;
Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 MEKQVLTSAIRRAS 16
DB 435 MEKAEKLVKDAIRKAS 450
|||||:|||||

RESULT 10
B70187
ribosomal protein L19 (rplS) - Lyme disease spirochete
C:Species: Borrelia burgdorferi (Lyme disease spirochete)
C:Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 13-Aug-1999
C:Accession: B70187
R:Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White, S.D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, J.; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
A:Authors: Smith, H.O.; Venter, J.C.
A>Title: Genomic sequence of a Lyme disease spirochete, Borrelia burgdorferi.
A:Reference number: A70100; MUID:98065943; PMID:9403685
A:Accession: B70187
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-121 <KLE>
A:Cross-references: GB:AE001170; GB:AE000783; NID:G2688623; PIDN:AAC67044.1; PID:G2688623;
A:Experimental source: strain B31
C:Superfamily: Escherichia coli ribosomal protein L19

Query Match 53.3%; Score 40; DB 2; Length 121;
Best Local Similarity 53.3%; Pred. No. 4.5;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MEKQVLTSAIRRA 15
DB 80 IERVEVLRGKVRRA 94
|||||:|||||

RESULT 11
E71104
probable cell division control protein - Pyrococcus horikoshii
C:Species: Pyrococcus horikoshii
C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 05-Nov-1999
C:Accession: E71104
R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekine, M.; Chikuba, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kishida, N.; Oguchi, DNA Res. 5, 55-76, 1998
A>Title: Complete sequence and gene organization of the genome of a hyper-thermophilic archaeon, Pyrococcus horikoshii.
A:Reference number: A71000; MUID:98344137; PMID:9679194
A:Accession: E71104
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-1108 <KAW>
A:Cross-references: GB:AP000003; NID:G3236130; PIDN:BAA29695.1; PID:dl030638; PID:G325701
A:Experimental source: strain OT3
A>Note: this accession replaces an interim accession for a sequence replaced by GenBank
C:Genetics:
A:Gene: PH0606

Query Match 53.3%; Score 40; DB 2; Length 1108;
Best Local Similarity 53.3%; Pred. No. 47;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 MEKQVLTSAIRRA 15

Db 668 MEVKDYLTREVRKA 682
|||||:|:|

RESULT 12

H75167
hypothetical protein PAB0334 - Pyrococcus abyssi (strain Orsay)
C:Species: Pyrococcus abyssi
C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C:Accession: B75167
R/anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure
A:Reference number: A75001
A:Accession: B75167
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-481 <RAW>
A:Cross-references: GB:AJ248284; GB:AL096836; MID:G5457730; PIDN:CAB49417.1; PID:G545792
A:Experimental source: strain Orsay
C:Genetics:
A:Gene: PAB0334

Query Match 52.0%; Score 39; DB 2; Length 481;
Best Local Similarity 50.0%; Pred. No. 30;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 2 EKVOYLTRSAIRRA 15
||:|:|:|:|
Db 38 EKIKYKRAFERA 51
||:|:|:|:|
RESULT 13
D69155
hypothetical protein MTH425 - Methanobacterium thermoautotrophicum (strain Delta H)
C:Species: Methanobacterium thermoautotrophicum
C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 24-Nov-1999
C:Accession: D69155
R/Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiواني, N.; Ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: functional genome
A:Reference number: A69000; MUID:98037514; PMID:9371463
A:Accession: D69155
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-119 <MTH>
A:Cross-references: GB:AE000827; GB:AE000666; MID:G2621489; PIDN:AAB84931.1; PID:G262149
A:Experimental source: strain Delta H
C:Genetics:
A:Gene: MTH425
A:Start codon: TTG
C:Superfamily: Methanobacterium thermoautotrophicum hypothetical protein MTH425

Query Match 50.7%; Score 38; DB 2; Length 119;
Best Local Similarity 37.5%; Pred. No. 11;
Matches 6; Conservative 6; Mismatches 4; Indels 0; Gaps 0;
QY 1 MEKVQYLTRSAIRAS 16
|:|:|:|:|:|:|
Db 35 MDNIMLTGSTVQSS 50
|:|:|:|:|:|:|
RESULT 14
H69179
conserved hypothetical protein MTH601 - Methanobacterium thermoautotrophicum (strain Delta H)
C:Species: Methanobacterium thermoautotrophicum
C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 17-Mar-2000
C:Accession: H69179
R/Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiواني, N.; Ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.

J. Bacteriol. 179, 7135-7155, 1997
A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: functional genome
A:Reference number: A69000; MUID:98037514; PMID:9371463
A:Accession: H69179
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-283 <MTH>
A:Cross-references: GB:AE000842; GB:AE000666; MID:G2621676; PIDN:AAB85107.1; PID:G262168
A:Experimental source: strain Delta H
C:Genetics:
A:Gene: MTH601
C:Superfamily: hypothetical protein AF1307

Query Match 49.3%; Score 37; DB 2; Length 283;
Best Local Similarity 63.6%; Pred. No. 40;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 6 YLTSAIRRAS 16
|||||:|:|
Db 209 YLTREAFKRAA 219
|||||:|:|
RESULT 15
F70879
hypothetical protein RV2751 - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C:Accession: F70879
R/Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holtroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Nature 393, 537-544, 1998
A:Authors: Scares, R.; Sulistion, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: F70879
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-296 <COL>
A:Cross-references: GB:AL008967; GB:AL123456; MID:G3261491; PIDN:CAA15547.1; PID:ell17388
A:Experimental source: strain H37RV
C:Genetics:
A:Gene: RV2751

Query Match 49.3%; Score 37; DB 2; Length 296;
Best Local Similarity 70.0%; Pred. No. 42;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 5 QYLTRSAIRR 14
|||||:|:|
Db 180 QYLTRSAIRR 189
|||||:|:|
RESULT 16
AC1867
hypothetical protein alr0484 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C:Accession: AC1867
R/Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.; DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AC1867
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-308 <NUR>
A:Cross-references: GB:BA000019; PIDN:BAF72442.1; PID:g17129829; GSPDB:GN00179
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: alr0484

```

Query Match      49.3%; Score 37; DB 2; Length 308;
Best Local Similarity 53.3%; Pred. No. 44;
Matches      8; Conservative      3; Mismatches      4; Indels      0; Gaps      0;

QY      1 MEKVQVLTSAIRRA 15
      :|||:|||:
Db      212 LEEVQNLVRSVMTRA 226

RESULT 17
T05113
hypothetical protein F28M20.240 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 23-Jul-1999
C:Accession: T05113
R:Bevan, M.; Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Hoheisel, J.; Mewes,
submitted to the Protein Sequence Database, November 1998
A:Reference number: Z15398
A:Accession: T05113
A:Molecule type: DNA
A:Residues: 1-2712 <BEV>
A:Cross-references: EMBL:AL031004
A:Experimental source: cultivar Columbia; BAC clone F28M20
C:Genetics:
A:Map position: 4
A:Introns: 17/3; 240/1; 1950/1; 2118/3; 2381/1; 2599/3; 2645/1; 2679/2
A:Note: F28M20.240

Query Match      49.3%; Score 37; DB 2; Length 2712;
Best Local Similarity 63.6%; Pred. No. 4.3e+02;
Matches      7; Conservative      3; Mismatches      1; Indels      0; Gaps      0;

QY      1 MEKVQVLTSA 11
      :|||:|||:
Db      1473 LEKVEWLARS 1483

RESULT 18
D69048
conserved hypothetical protein MTH1364 - Methanobacterium thermoautotrophicum (strain De
C:Species: Methanobacterium thermoautotrophicum
C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
C:Accession: D69048
R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.;
ki S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7138-7155, 1997
A:title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
A:Reference number: A69000; MUID:98037514; PMID:9371463
A:Accession: D69048
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <MTH>
A:Cross-references: GB:AE0000899; GB:AE0000666; NID:G2622468; PIDN:AA85841.1; PID:G262247
A:Experimental source: strain Delta H
C:Genetics:
A:Gene: MTH1364

Query Match      48.0%; Score 36; DB 2; Length 236;
Best Local Similarity 46.7%; Pred. No. 51;
Matches      7; Conservative      4; Mismatches      4; Indels      0; Gaps      0;

QY      1 MEKVQVLTSAIRRA 15
      :|||:|||:
Db      210 VEKLEVLNERAIPRS 224

RESULT 19
T00104
probable dTDP-4-dehydrohannose reductase (EC 1.1.1.133) - Actinobacillus actinomycetemc
N:Alternate names: dTDP-4-keto-L-rhamnose reductase
C:Species: Actinobacillus actinomycetemcomitans

C>Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 21-Jul-2000
C:Accession: T00104
R:Nakano, Y.; Yoshida, Y.; Yamashita, Y.; Koga, T.
Biochim. Biophys. Acta 1442, 409-414, 1998
A:title: A gene cluster for 6-deoxy-L-talan synthesis in Actinobacillus actinomycetemcomi
A:Reference number: Z14111; MUID:99023768; PMID:9805002
A:Accession: T00104
A:Status: translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-294 <NAK>
A:Cross-references: EMBL:AB010415; NID:G3132248; PIDN:BAA28133.1; PID:G3132256
A:Experimental source: strain NCTC 9710
C:Function:
A:Description: probably catalyzes the reaction of dTDP-6-deoxy-L-mannose + NADP(+) to dT
A:Pathway: dTDP-rhamnose biosynthesis
A:Superfamily: dTDP-dihydrostrepase synthase
C:Keywords: oxidoreductase

Query Match      48.0%; Score 36; DB 2; Length 294;
Best Local Similarity 61.5%; Pred. No. 65;
Matches      8; Conservative      1; Mismatches      4; Indels      0; Gaps      0;

QY      4 VOYLTRSAIRRAS 16
      :|||:|||:
Db      84 VOYLAEAIRHNS 96

RESULT 20
A24785
hypothetical protein 335 - slime mold (Dictyostelium discoideum) transposon DIRS-1
C:Species: Dictyostelium discoideum
C>Date: 23-Aug-1987 #sequence_revision 23-Aug-1987 #text_change 18-Jun-1993
C:Accession: A24785
R:Cappello, J.; Handelsman, K.; Lodish, H.F.
Cell 43, 105-115, 1985
A:title: Sequence of Dictyostelium DIRS-1: an apparent retrotransposon with inverted tem
A:Reference number: A94654; MUID:86079481; PMID:2416457
A:Accession: A24785
A:Cross-references:
A:Molecule type: DNA
A:Residues: 1-335 <CAP>

Query Match      48.0%; Score 36; DB 2; Length 335;
Best Local Similarity 58.3%; Pred. No. 74;
Matches      7; Conservative      3; Mismatches      2; Indels      0; Gaps      0;

QY      1 MEKVQVLTSAI 12
      :|||:|||:
Db      188 VELISYLTQSAI 199

RESULT 21
F83493
probable MFS transporter PA1212 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: F83493
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Bri
adman, S.; Yuan, Y.; Brody, L.B.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathoc
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: F83493
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-409 <STO>
A:Cross-references: GB:AE004551; GB:AE004091; NID:G9947135; PIDN:AAG04601.1; GSPDB:GN001;
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA1212

Query Match      48.0%; Score 36; DB 2; Length 409;
Best Local Similarity 77.8%; Pred. No. 91;

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Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 VOYLTRSAI 12
|||||
Db 245 VOYLTRSGI 253
|||||

RESULT 22
T12833
hypothetical protein yonV - Bacillus subtilis phage SPBc2
C:Species: Bacillus subtilis phage SPBc2
C>Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 15-Oct-1999
C:Accession: T12833; E69915
R:Lazarevic, V.; Dueterhoeft, A.; Soldo, B.; Hilbert, H.; Maue, C.; Karamata, D.
submitted to the EMBL Data Library, August 1997
A:Description: The complete nucleotide sequence of the Bacillus subtilis SPBc2 prophage
A:Reference number: Z17583
A:Accession: T12833
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-410 <LAZ>
A:Cross-references: EMBL:AF020713; NID:G3025478; PID:G3025547; PIDN:AAC13042.1
R:Kunst, F.; Ogaewara, N.; Moser, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte
C.; Bron, S.; Bruchli, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gall
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.P.
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A:Authors: Yoshikawa, H.F.; Zumschein, E.; Yoshikawa, H.; Danchin, A.; Yata, K.; Yoshida, K
A:Title: The complete genome sequence of the gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: E69915
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-410 <KUN>
A:Cross-references: GB:Z99115; GB:AL009126; NID:G2634478; PIDN:CAB14016.1; PID:e1183545;
A:Experimental source: strain 168
C:Genetics:
A:Gene: yonV

Query Match 48.0%; Score 36; DB 2; Length 410;
Best Local Similarity 58.3%; Pred. No. 92;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 EKVOYLTRSAIR 13
|:|:|:|
Db 373 EMQWIRSAIR 384
|:|:|:|

RESULT 23
H83370
hydrogen cyanide synthase HcnC PA2195 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: H83370
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim
; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A:Reference number: A82250; MUID:20437337; PMID:10984043
A:Accession: H83370
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-417 <STO>
A:Cross-references: GB:AE004646; GB:AE004091; NID:G9948213; PIDN:AA05583.1; GSPDB:GN001

A:Experimental source: strain PA01
C:Genetics:
A:Gene: hcnC; PA2195

Query Match 48.0%; Score 36; DB 2; Length 417;
Best Local Similarity 50.0%; Pred. No. 93;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 EKVOYLTRSAIRRA 15
|:|:|:|
Db 154 EQVWLDREELARA 167
|:|:|:|

RESULT 24
T04263
phosphoprotein phosphatase (EC 3.1.1.3.16) AB11 - Arabidopsis thaliana
N:Alternate names: protein F20B18.190
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 08-Oct-1999
C:Accession: T04263; A54588
R:Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Hoheisel, J.; Mewes, H.W.; Mayer, K.F.X
submitted to the Protein Sequence Database, March 1999
A:Reference number: Z15263
A:Accession: T04263
A:Molecule type: DNA
A:Residues: 1-434 <BEV>
A:Cross-references: EMBL:AL049483
R:Experimental source: cultivar Columbia; BAC clone F20B18
R:Meyer, K.; Leube, M.F.; Grall, E.
Science 264, 1452-1455, 1994
A:Title: A protein phosphatase 2C involved in ABA signal transduction in Arabidopsis th
A:Reference number: A54588; MUID:94255767; PMID:8197457
A:Accession: A54588
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-104, V', 106-434 <MEY>
A:Cross-references: GB:X78886; NID:G509418; PIDN:CAA55484.1; PID:G509419
C:Genetics:
A:Gene: AB11
A:Map position: 4
A:Introns: 183/3; 280/3; 316/1
A:Note: F20B18.190
C:Keywords: phosphoric monoester hydrolase

Query Match 48.0%; Score 36; DB 2; Length 434;
Best Local Similarity 43.8%; Pred. No. 97;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRA 16
|:|:|:|
Db 396 MSNAEVLKLAIRGS 411
|:|:|:|

RESULT 25
AH1053
probable exported protein STY4756 [imported] - Salmonella enterica subsp. enterica serov
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A:Note: this species has also been called Salmonella typhi
C>Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C:Accession: AH1053
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AH1053
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-462 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD06877.1; PID:G16505525; GSPDB:GN00176
C:Genetics:

A;Gene: STY4756

Query Match 48.0%; Score 36; DB 2; Length 462;
 Best Local Similarity 53.8%; Pred. No. 1e+02;
 Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 EKVOYLTRSAIR 14
 :||:|:|:|
 Db 294 DKVTMTREARR 306

Search completed: October 1, 2004, 12:19:41
 Job time : 15.6 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 1, 2004, 12:04:01 ; Search time 8.8 seconds
(without alignments)
94.673 Million cell updates/sec

Title: US-09-830-779-17_COPY_1_16

Perfect score: 75
Sequence: 1 MEKVQLTSAIRRAS 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	75	100.0	52	1 PPLA_HUMAN	P26678 homo sapien
2	75	100.0	52	1 PPLA_MOUSE	P20006 mus musculus
3	72	96.0	52	1 PPLA_PIG	P07473 sus scrofa
4	71	94.7	52	1 PPLA_CHICK	P26677 gallus gall
5	41	54.7	116	1 RL19_STRAW	Q22jw4 streptomyce
6	41	54.7	116	1 RL19_SIRCO	O69883 streptomyce
7	40	53.3	121	1 RL19_BORBU	O51642 borrelia bu
8	39	52.0	871	1 SYA_THEAC	Q9hjw4 thermoplas
9	38	50.7	115	1 RL19_THETN	Q819x4 thermocae
10	38	50.7	299	1 PSD_CHLCV	Q82113 chlamydophi
11	37	49.3	275	1 APAH_ACTAC	O52655 actinobacil
12	37	49.3	625	1 RPSD_XANAC	Q8p333 xanthomonas
13	36	48.0	47	1 H4Y_BLEJA	P80738 blepharisma
14	36	48.0	97	1 H41_BLEJA	P80737 blepharisma
15	36	48.0	113	1 RL19_COREF	Q8fp56 corynebacte
16	36	48.0	113	1 RL19_CORGL	Q8n20 corynebacte
17	36	48.0	434	1 P2C1_ARATH	Q49597 arabidopsis
18	36	48.0	486	1 2ASA_HUMAN	Q15172 h.sei-ne/th
19	36	48.0	624	1 RPSD_XANCP	Q8p4h2 xanthomonas
20	36	48.0	677	1 CHLD_VSNP7	Q87345 synchococc
21	36	48.0	736	1 DVL2_YENLA	P51142 xenopus lae
22	36	48.0	924	1 HXK3_RAT	P27926 rattus norv
23	36	48.0	1080	1 RPOB_MESVI	Q9mus5 mesostigma
24	35	46.7	144	1 RL28_DROME	Q9vzs5 drosophila
25	35	46.7	196	1 AMIR_PSEAE	P10932 pseudomonas
26	35	46.7	390	1 HEM2_CHLRE	Q42682 chlamydomon
27	35	46.7	423	1 ERG_ANTMA	Q82626 antirrhinum
28	35	46.7	497	1 RPOB_MOUSE	Q9w379 mus musculu
29	35	46.7	506	1 YC46_GUITH	O78439 guillardia
30	35	46.7	515	1 RPB2_METTW	P09844 methanobact
31	35	46.7	516	1 PROD_HUMAN	Q43272 homo sapien
32	35	46.7	626	1 DPO2_SULSO	Q07635 sulfolobus
33	35	46.7	876	1 SYA_THEVO	Q97ah7 thermoplas

RESULT 1

ALIGNMENTS

34	45.3	101	1	YDHD_SCHPO	Q23358 schizosacch
35	45.3	134	1	LRG6_CHICK	P23668 gallus gall
36	45.3	172	1	NUGM_URIAL	P43207 uria aalge
37	45.3	172	1	NUGM_URILO	P43208 uria lomvia
38	45.3	173	1	NUGM_ALCPO	P43193 aica torda
39	45.3	173	1	NUGM_ALCPO	P43192 alle alle
40	45.3	185	1	RM16_MAIZE	P27927 reza mayas
41	45.3	185	1	RM16_ORYSA	P46801 oryza sativ
42	45.3	191	1	YHGI_ECOJI	P46847 escherichia
43	45.3	258	1	SN29_HUMAN	O95721 homo sapien
44	45.3	328	1	GALE_VIBCH	Q56623 vibrio chol
45	45.3	548	1	ATPA_KLULA	P49375 kluyveromyc
46	45.3	586	1	KPYK_BACPY	P51182 bacillus ps
47	45.3	675	1	HPPA_XANCP	Q8p5m6 xanthomonas
48	45.3	676	1	CHLD_SYNY3	P72772 synchocyst
49	45.3	838	1	CYAA_PASMU	Q05766 pasteurella
50	45.3	852	1	RBMA_RAT	P70501 rattus norv
51	45.3	929	1	RBMA_HUMAN	P98175 homo sapien
52	45.3	1857	1	FAS2_PENPA	P15368 p fatty aci
53	44.0	55	1	YCX1_CUSRE	P22035 cuscutea ref
54	44.0	102	1	H41_EBENI	P23750 emericella
55	44.0	102	1	H42_EBENI	P23751 emericella
56	44.0	102	1	H4_ACRFO	P35059 acropora fo
57	44.0	102	1	H4_ARATH	P59259 arabidopsis
58	44.0	102	1	H4_ASCSU	Q27443 ascaris suu
59	44.0	102	1	H4_CAEEL	P02306 caenorhabdi
60	44.0	102	1	H4_CHLRE	P50566 chlamydomon
61	44.0	102	1	H4_DROME	P02307 drosophila
62	44.0	102	1	H4_HUMAN	P02304 homo sapien
63	44.0	102	1	H4_LYCES	P35057 lycopersico
64	44.0	102	1	H4_NEUCR	P04914 neuropept
65	44.0	102	1	H4_OILIU	P82888 olisthodisc
66	44.0	102	1	H4_PHACH	P35058 phanerochae
67	44.0	102	1	H4_PHYPO	P04915 physarum po
68	44.0	102	1	H4_SCHPO	P09322 schizosacch
69	44.0	102	1	H4_SOLST	P27936 solaster st
70	44.0	102	1	H4_VOLCA	P68436 volvox cart
71	44.0	102	1	H4_WHEAT	P59258 triticum ae
72	44.0	102	1	H4_YEAST	P02309 saccharomyc
73	44.0	107	1	H4_MASEA	Q9u740 mastigamoeb
74	44.0	114	1	RL19_BACAA	Q819w6 bacillus an
75	44.0	114	1	RL19_BACOR	Q819w6 bacillus ce
76	44.0	115	1	RL19_THEMA	Q91077 thermotoga
77	44.0	115	1	RL19_TROW8	Q83104 tropheryma
78	44.0	115	1	RL19_TROWT	Q83966 tropheryma
79	44.0	116	1	RL19_STAAM	Q9nu99 staphylococ
80	44.0	116	1	RL19_STAAP	Q8nu95 staphylococ
81	44.0	116	1	RL19_STAEP	Q8csu3 staphylococ
82	44.0	118	1	RL19_GUITH	O78409 guillardia
83	44.0	138	1	HIS3_METHH	Q26347 methanobact
84	44.0	150	1	RS13_AERPE	Q9yb60 aeropyrum p
85	44.0	212	1	NUSB_SYNEL	Q8dk90 synchococc
86	44.0	215	1	YKX1_YEAST	P33144 saccharomyc
87	44.0	252	1	COBS_CLOTE	Q89715 clostridium
88	44.0	257	1	Y123_PYRAB	Q9v2f1 pyrococcus
89	44.0	263	1	YP80_AERPE	Q9y8d3 aeropyrum p
90	44.0	271	1	EUTC_XANAC	Q8pkl1 xanthomonas
91	44.0	272	1	EUTC_XANCP	Q8p810 xanthomonas
92	44.0	286	1	GUB_RHOWR	P45798 rhodothermu
93	44.0	326	1	TMOE_PSEWE	Q00450 pseudomonas
94	44.0	391	1	CAPJ_STAUP	P39859 staphylococ
95	44.0	421	1	ISPG_XANAC	Q8p138 xanthomonas
96	44.0	421	1	ISPG_XANCP	Q8p977 xanthomonas
97	44.0	465	1	TRME_BACTN	Q89236 bacteroides
98	44.0	473	1	AM13_MYCTU	Q10811 mycobacteri
99	44.0	487	1	SYC_CHLTE	Q8kak2 chlorobium
100	44.0	490	1	GLPK_PYRFU	Q8tz18 pyrococcus

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PPLA_HUMAN
ID PPLA_HUMAN STANDARD; PRT; 52 AA.
AC P26678;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cardiac phospholamban (PLB).
GN PLN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
[1]_
SEQUENCE FROM N.A.
RX MEDLINE=91268032; PubMed=128805;
RA Fujii J., Zarain-Herzberg A., Willard H.F., Tada M., MacLennan D.H.;
RT "Structure of the rabbit phospholamban gene, cloning of the human
RT cDNA, and assignment of the gene to human chromosome 6."
RL J. Biol. Chem. 266:11669-11675(1991).
RN [2]
SEQUENCE FROM N.A.
RA Salvatore C.A., Jacobson M.A.;
RL Submitted (XXY-1992) to the EMBL/GenBank/DBSJ databases.
RN [3]
SEQUENCE FROM N.A.
RX MEDLINE=99222499; PubMed=10198197;
RA McTiernan C.F., Frye C.S., Lemster B.H., Kinder E.A.,
RA Ogletree-Hughes M.L., Moravec C.S., Feldman A.M.;
RT "The human phospholamban gene: structure and expression."
RL J. Mol. Cell. Cardiol. 31:679-692(1999).
RN [4]
SEQUENCE FROM N.A.
RX TISSUE=Liver;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan R.A., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marushina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M., Soares K.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.J., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McSwan P.A., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kertanen M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
STRUCTURE BY NMR OF 1-25.
RX MEDLINE=95298769; PubMed=7779806;
RA Northshire-Smith R.J., Pittzenberger S.M., Burke C.J., Middaugh C.R.,
RA Garsky V.M., Johnson R.G.;
RT "Solution structure of the cytoplasmic domain of phospholamban:
RT phosphorylation leads to a local perturbation in secondary
RT structure."
RL Biochemistry 34:7603-7613(1995).
RN [6]
3D-STRUCTURE MODELING.
RX MEDLINE=95269058; PubMed=7749920;
RA Adams P.D., Arkin I.T., Engelman D.M., Bruenger A.T.;
RT "Computational searching and mutagenesis suggest a structure for the
RT pentameric transmembrane domain of phospholamban."
RL Nat. Struct. Biol. 2:154-162(1995).
RN [7]
3D-STRUCTURE MODELING.
RX MEDLINE=98170370; PubMed=9512019;

```

```

RA Herzyk P., Hubbard R.E.;
RT "Using experimental information to produce a model of the
RT transmembrane domain of the ion channel phospholamban."
RL Biophys. J. 74:1203-1214(1998).
CC -!- FUNCTION: Phospholamban has been postulated to regulate the
CC activity of the calcium pump of cardiac sarcoplasmic reticulum.
CC -!- SUBUNIT: Homopentamer.
CC -!- SUBCELLULAR LOCATION: Membrane.
CC -!- TISSUE SPECIFICITY: Heart.
CC -!- SIMILARITY: Belongs to the phospholamban family.
CC -!- SIMILARITY: Belongs to the phospholamban family.
CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M63603; AAA60083.1; --
DR EMBL; M60411; AAA60109.1; --
DR EMBL; AF177764; AAD55950.1; --
DR EMBL; BC005269; AAH05269.1; --
DR FIR; A40424; A40424.
DR PDB; 1K9N; 14-NOV-01.
DR PDB; 1KCH; 28-NOV-01.
DR PDB; 1PLN; 29-DEC-99.
DR PDB; 1PLP; 31-JUL-95.
DR PDB; 1PSL; 03-JUN-95.
DR Gene; HGNC:9080; PLN.
DR MIM; 172405; --
DR InterPro; IPR005984; P_lamban.
DR Pfam; PF04272; Phospholamban; 1.
DR TIGRFAVS; TIGR01294; P_lamban; 1.
KW Transmembrane; Phosphorylation; Acetylation; 3D-structure.
FT DOMAIN 1 31 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 32 52 POTENTIAL.
FT MOD_RES 1 1 ACETYLATION (BY SIMILARITY).
FT MOD_RES 16 16 PHOSPHORYLATION (BY PKA) (BY SIMILARITY).
FT MOD_RES 17 17 PHOSPHORYLATION (BY CMK) (BY
FT TURN 2 3 SIMILARITY).
FT HELIX 4 14
FT TURN 15 15
SQ SEQUENCE 52 AA; 6108 MW; 0766304A76A854D3 CRC64;
Query Match 100.0%; Score 75; DB 1; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEKVYLTRSAIRRAS 16
Db 1 MEKVYLTRSAIRRAS 16
RESULT 2
PPLA_MOUSE STANDARD; PRT; 52 AA.
AC P20006;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cardiac phospholamban (PLB).
GN PLN.
OS Mus musculus (Mouse),
OS Rattus norvegicus (Rat), and
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090, 10116, 9986;
[1]
SEQUENCE FROM N.A.
RP

```

RC SPECIES=Rabbit;
RX MEDLINE=91286032; PubMed=1828805;
RA Fujii J., Zarain-Herzberg A., Willard H.F., Tada M., MacLennan D.H.;
RT "Structure of the rabbit phospholamban gene, cloning of the human
RL cDNA, and assignment of the gene to human chromosome 6.";
RN J. Biol. Chem. 266:11669-11675(1991).
[2]
RN SEQUENCE FROM N.A.
RC SPECIES=Rabbit;
RX MEDLINE=88112222; PubMed=2962883;
RA Fujii J., Lytton J., Tada M., MacLennan D.H.;
RT "Rabbit cardiac and slow-twitch muscle express the same phospholamban
RL gene.";
RN FEBS Lett. 227:51-55(1988).
[3]
RN SEQUENCE FROM N.A.
RC SPECIES=Rat;
RX MEDLINE=93284726; PubMed=8508530;
RA Shanahan C.M., Weissberg P.J., Metcalfe J.C.;
RT "Isolation of gene markers of differentiated and proliferating
RL vascular smooth muscle cells.";
RN Circ. Res. 73:193-204(1993).
[5]
RN SEQUENCE FROM N.A.
RC SPECIES=Rat; TISSUE=Aortic smooth muscle;
RX MEDLINE=92206283; PubMed=1725096;
RA Huang K.S., Nadal-Ginard B.;
RT "Cloning phospholamban cDNA from rat aortic smooth muscle.";
RN Adv. Exp. Med. Biol. 304:387-395(1991).
[6]
RN SEQUENCE FROM N.A.
RC SPECIES=Mouse;
RX MEDLINE=93008802; PubMed=1394867;
RA Ganim J.R., Luo W., Ponniah S., Grupp I., Kim H.W., Ferguson D.G.,
RA Kadambi V., Neumann J.C., Doetschman T., Kranias E.G.;
RT "Mouse phospholamban gene expression during development in vivo and
RL in vitro.";
RN Circ. Res. 71:1021-1030(1992).
CC -1- FUNCTION: Phospholamban has been postulated to regulate the
CC activity of the calcium pump of cardiac sarcoplasmic reticulum.
CC -1- SUBUNIT: Homopentamer.
CC -1- SUBCELLULAR LOCATION: Membrane.
CC -1- TISSUE SPECIFICITY: Heart.
CC -1- PTM: Phosphorylated in response to beta-adrenergic stimulation.
CC -1- SIMILARITY: Belongs to the phospholamban family.
CC -----
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CC -----
DR EMBL; S46792; AAB23706.1; -;
DR EMBL; M63600; -; NOT ANNOTATED_CDS.
DR EMBL; M63601; AAA31445.1; -;
DR EMBL; Y00761; CAA89730.1; -;
DR EMBL; L03382; AAA1849.1; -;
DR EMBL; S95853; AAA21903.1; -;
DR EMBL; S95849; AAN86727.1; -;
DR EMBL; X71068; CAA50394.1; -;
DR PIR; A49057; A49057.
DR PIR; B40424; B40424.
DR PIR; S37638; S37638.

DR HSSP; P26678; 1PLP.
DR MGD; MGI:97622; Pln.
DR InterPro; IPR005984; P.lamban.
DR Pfam; PF04272; Phospholamban; 1.
DR TIGRFAMs; TIGR01294; P.lamban; 1.
KW Transmembrane; Phosphorylation; Acetylation.
FT DOMAIN 1 31 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 32 52 POTENTIAL.
FT MOD_RES 1 1 ACETYLATION (BY SIMILARITY).
FT MOD_RES 16 16 PHOSPHORYLATION (BY PKA) (BY SIMILARITY).
FT MOD_RES 17 17 PHOSPHORYLATION (BY CAMK) (BY
FT SIMILARITY).
SQ SEQUENCE 52 AA; 6094 MW; 0763601F76A854D3 CRC64;
Query Match 100.0%; Score 75; DB 1; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEKVQLTRSAIRRAS 16
DB 1 MEKVQLTRSAIRRAS-16
|||||
RESULT 3
PPLA_PIG STANDARD; PRT; 52 AA.
ID PPLA_PIG
AC P07473;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cardiac phospholamban (PLB).
GN PLN.
OS Sus. scrofa (Pig), and
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Cetartiodactyla; Suina; Suidae; Sus.
CX NCBI_TaxID:9823, 9615;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=C.familiaris;
RX MEDLINE=87083954; PubMed=3793929;
RA Fujii J., Ueno A., Kitano K., Tanaka S., Kadoma M., Tada M.;
RT "Complete complementary DNA-derived amino acid sequence of canine
RL cardiac phospholamban.";
RN J. Clin. Invest. 79:301-304(1987).
[2]
RN SEQUENCE FROM N.A.
RC SPECIES=C.familiaris; TISSUE=Heart ventricle;
RX MEDLINE=8716396; PubMed=3628007;
RA Uyeda A., Kitano K., Fujii J., Kadoma M., Tada M., Tanaka S.;
RT "The cDNA sequence of the major phospholamban mRNA in canine cardiac
RL ventricular muscle.";
RN Nucleic Acids Res. 15:6738-6738(1987).
[3]
RN SEQUENCE OF 1-45.
RC SPECIES=C.familiaris;
RX MEDLINE=86323152; PubMed=3753485;
RA Fujii J., Kadoma M., Tada M., Toda H., Sakiyama F.;
RT "Characterization of structural unit of phospholamban by amino acid
RL sequencing and electrophoretic analysis.";
RN Biochem. Biophys. Res. Commun. 138:1044-1050(1986).
[4]
RN SEQUENCE OF 10-45.
RC SPECIES=C.familiaris;
RX MEDLINE=87008549; PubMed=3759968;
RA Simmerman H.K.B., Collins J.H., Theibert J.L., Wegener A.D.,
RA Jones L.R.;
RT "Sequence analysis of phospholamban. Identification of
RL phosphorylation sites and two major structural domains.";
RN J. Biol. Chem. 261:13333-13341(1986).
[5]
RN PHOSPHORYLATION.
RP SPECIES=C.familiaris;

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CC EMBL; AE001170; AAC67044.1; -
 DR PIR; B70187; B70187.
 DR TIGR; BBO699; -
 DR HAMAP; MF_00402; -; 1.
 DR InterPro; IPR001857; Ribosomal L19.
 DR Pfam; PF01245; Ribosomal L19; 1.
 DR PRINTS; PR00061; RIBOSOMALL19.
 DR ProDom; PD002979; Ribosomal L19; 1.
 DR TIGRFAMs; TIGR01024; rplS_bact; 1.
 DR PROSITE; PS01015; RIBOSOMAL_L19; 1.
 KW Ribosomal protein; Complete proteome.
 SQ SEQUENCE 121 AA; 14011 MW; A33F7B1E4DF24070 CRC64;

Query Match 53.3%; Score 40; DB 1; Length 121;
 Best Local Similarity 53.3%; Pred. No. 1.7;
 Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MEKVYLTRSAIRRA 15
 :|||:|:|:|:
 Db 80 IERVEVLRRGKVERA 94

RESULT 8

SYA-THCAE STANDARD; PRT; 871 AA.
 ID AC Q9HJW4;
 AC Q9HJW4;
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DE Alanyl-tRNA synthetase (EC 6.1.1.7) (Alanine--tRNA ligase) (AlaRS).
 GN ALAS OR TA0849.
 OS Thermoplasma acidophilum.
 OC Archaea; Euryarchaeota; Thermoplasmatia; Thermoplasmatiales;
 OC Thermoplasmataceae; Thermoplasma.
 OX NCBI_TaxID=2303;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DSM 1728;
 RX MEDLINE=20479972; PubMed=11029001;
 RA Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C.,
 EA Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.;
 RT "The genome sequence of the thermophilic scavenger Thermoplasma
 acidophilum.";
 RT Nature 407:508-513 (2000).
 CC -1- CATALYTIC ACTIVITY: ATP + L-alanine + tRNA(Ala) = AMP +
 CC diphosphate + L-alanyl-tRNA(Ala).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.
 CC
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CC EMBL; AL445065; CAC11978.1; -
 DR HAMAP; MF_00036; -; 1.
 DR InterPro; IPR002318; tRNA-synt_2c.
 DR Pfam; PF01411; tRNA-synt_2c; 1.
 DR PRINTS; PR00980; TRNASYNTHALA.
 DR TIGRFAMs; TIGR00344; alaS; 1.
 DR PROSITE; PS00850; AA tRNA LIGASE II ALA; 1.
 KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
 KW Complete proteome.
 SQ SEQUENCE 871 AA; 99907 MW; 6ACB55478463666D CRC64;

Query Match 52.0%; Score 39; DB 1; Length 871;
 Best Local Similarity 59.2%; Pred. No. 22;
 Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 KVOYLTRSAIRRA 15
 :|||:|:|:|:
 Db 353 KVGYLARMLIRRA 365

RESULT 9

RL19-THCAE STANDARD; PRT; 115 AA.
 ID AC Q889X4;
 AC Q889X4;
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DE 50S ribosomal protein L19.
 GN RPLS OR TTE1457.
 OS Thermoplasma acidophilum.
 OC Bacteria; Firmicutes; Clostridia; Thermoplasmatiales;
 OC Thermoplasmataceae; Thermoplasma.
 OX NCBI_TaxID=119072;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MS4 / JCM 11007;
 RX MEDLINE=21992816; PubMed=11997336;
 RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
 RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
 RA Tan H., Chen R., Wang J., Yu J., Yang H.;
 RT "A complete sequence of T. tengcongensis genome.";
 RL Genome Res. 12:689-700 (2002).
 CC -1- FUNCTION: This protein is located at the 30S-50S ribosomal subunit
 CC interface and may play a role in the structure and function of the
 CC aminoacyl-tRNA binding site (By similarity).
 CC -1- SIMILARITY: Belongs to the L19p family of ribosomal proteins.
 CC
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CC EMBL; AE013104; AAM24579.1; -
 DR HAMAP; MF_00402; -; 1.
 DR InterPro; IPR001857; Ribosomal L19.
 DR Pfam; PF01245; Ribosomal L19; 1.
 DR PRINTS; PR00061; RIBOSOMALL19.
 DR ProDom; PD002979; Ribosomal L19; 1.
 DR TIGRFAMs; TIGR01024; rplS_bact; 1.
 DR PROSITE; PS01015; RIBOSOMAL_L19; 1.
 KW Ribosomal protein; Complete proteome.
 SQ SEQUENCE 115 AA; 13395 MW; 9E9E9A1B89D3122B CRC64;

Query Match 50.7%; Score 38; DB 1; Length 115;
 Best Local Similarity 40.0%; Pred. No. 3.8;
 Matches 6; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MEKVYLTRSAIRRA 15
 :|||:|:|:|:
 Db 80 LEKIEVLRRGKVERA 94

RESULT 10

PSD-CHLVC STANDARD; PRT; 299 AA.
 ID AC Q821L3;
 AC Q821L3;
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DE Phosphatidylserine decarboxylase proenzyme (EC 4.1.1.65) [Contains:
 KW Complete proteome.

DE Phosphatidylserine decarboxylase alpha chain; Phosphatidylserine
 DE decarboxylase beta chain)
 GN PSD OR CCA00927.
 OS Chlamydomophila caviae.
 OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydoghila.
 OX NCBI_TaxID=83557;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GPIC;
 RX MEDLINE=22569155; PubMed=12682364;
 RA Read T.D., Myers G.S.A., Brunham R.C., Neilson W.C., Paulsen I.T.,
 RA Heidelberg J., Holtzapfel E., Khouri H., Federova N.B., Carty H.A.,
 RA Umayam L.A., Haft D.H., Petersen J., Beanan M.J., White O.,
 RA Salzberg S.L., Hsia R.-C., McClarty G., Rank R.G., Bavol P.M.,
 RA Fraser C.M.;
 RA "Genome sequence of Chlamydomophila caviae (Chlamydia psittaci GPIC):
 RA examining the role of niche-specific genes in the evolution of the
 RA Chlamydiaceae.";
 RL Nucleic Acids Res. 31:2134-2147(2003).
 CC -!- CATALYTIC ACTIVITY: Phosphatidyl-L-serine =
 CC phosphatidylethanolamine + CO(2).
 CC -!- COFACTOR: Pyruvoyl group (By similarity).
 CC -!- SIMILARITY: Belongs to the phosphatidylserine decarboxylase
 CC family. Subfamily 2.
 CC
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 CC
 CC EMBL; AEO16997; AAP05666.1; -;
 CC TIGR; CCA00927; -;
 CC HAMAP; MF_00563; -; 1.
 CC InterPro; IPR003817; PS Decarboxylase.
 CC InterPro; IPR005221; PS decarb.
 CC Pfam; PF02666; PS Decarboxylase; 1.
 CC TIGRFAMs; TIGR00163; PS decarb; 1.
 CC Phospholipid biosynthesis; Lyase; Decarboxylase; Pyruvate; Zymogen;
 KW Complete proteome.
 FT CHAIN 1 257 PHOSPHATIDYL SERINE DECARBOXYLASE BETA
 FT CHAIN 258 299 CHAIN (BY SIMILARITY).
 FT CHAIN 258 299 PHOSPHATIDYL SERINE DECARBOXYLASE ALPHA
 FT SITE 257 258 CLEAVAGE (NONHYDROLYTIC) (BY SIMILARITY).
 FT MOD_RES 258 258 CONVERTED TO A PYRUVYL GROUP (BY
 FT SIMILARITY).
 SQ SEQUENCE 299 AA; 34223 MW; 6F8EB837D97EE4E0 CRC64;
 Query Match 50.7%; Score 38; DB 1; Length 299;
 Best Local Similarity 43.8%; Pred. No. 11;
 Matches 7; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
 QY 1 MKKQVILTRSAIRAS 16
 DQ 1 MKKQVILTRSTNORVT 16
 RESULT 11
 APAA ACTAC
 ID -APAA ACTAC STANDARD; PRT; 275 AA.
 AC OS2655;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Bis(5'-nucleosyl)-tetraphosphatase, symmetrical
 DE (diadenosine tetraphosphatase) (AP4A hydrolase).
 DE P1,P4-tetraphosphate pyrophosphohydrolase).
 GN APAA.
 OS Actinobacillus actinomycetemcomitans (Haemophilus
 OS actinomycetemcomitans).

OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
 OC Pasteurellaceae; Actinobacillus.
 OX NCBI_TaxID=714;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Y4;
 RA Saarela M., Fives-Taylor P.;
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBSJ databases.
 CC -!- FUNCTION: Hydrolyzes diadenosine 5',5',5',5'-P1,P4-tetraphosphate to
 CC yield ADP (By similarity).
 CC -!- CATALYTIC ACTIVITY: P(1),P(4)-bis(5'-adenosyl)tetraphosphate +
 CC H(2)O = 2 ADP.
 CC -!- SIMILARITY: Belongs to the Ap4A hydrolase family.
 CC
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 CC
 CC EMBL; AF043398; AAC00202.1; -;
 CC HAMAP; MF_00199; -; 1.
 CC InterPro; IPR004617; APAA.
 CC InterPro; IPR004843; M-ppestrase.
 CC Pfam; PF006186; T_phtase apah.
 CC Pfam; PF00149; Metallophos; 1.
 CC ProDom; PD000252; T_phtase apah; 1.
 CC TIGRFAMs; TIGR00668; apah; 1.
 KW Hydrolase.
 SQ SEQUENCE 275 AA; 31480 MW; 0843F4F7E11FF6DAD CRC64;
 Query Match 49.1%; Score 37; DB 1; Length 275;
 Best Local Similarity 40.0%; Pred. No. 15;
 Matches 6; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
 QY 2 EKQVILTRSAIRAS 16
 DQ 259 EDKQVTSQAVKSN 273
 RESULT 12
 RPSP XANAC
 ID -RPSP XANAC STANDARD; PRT; 625 AA.
 AC Q8P33;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE RNA polymerase sigma factor rpoD (Sigma-70).
 GN RPOD OR XAC3788.
 OS Xanthomonas axonopodis (pv. citri).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
 OC Xanthomonadaceae; Xanthomonas.
 OX NCBI_TaxID=92829;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=306 / ATCC 13902 / XV 101;
 RX MEDLINE=22022145; PubMed=12024217;
 RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
 RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
 RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A., L.P.,
 RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,
 RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
 RA Formighieri E.P., Franco M.C., Greggio C.C., Gruber A.,
 RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
 RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
 RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
 RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
 RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
 RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
 RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,

RA Setubal J.C., Kitajima J.P.;
 RT "Comparison of the genomes of two Xanthomonas pathogens with differing
 RL host specificities";
 RL Nature 417:459-463(2002).
 CC -!- FUNCTION: The sigma factor is an initiation factor that promotes
 CC attachment of the RNA polymerase to specific initiation sites and
 CC then is released. This is the primary sigma-factor of this
 CC bacteria (By similarity).
 CC -!- SIMILARITY: Belongs to the sigma-70 factor family.
 CC -----
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 CC -----
 CC EMBL; AE012027; AAM38630.1; ..
 DR InterPro; IPR009043; RNA_dol_sigma.
 DR InterPro; IPR007631; Sigma70_ner.
 DR InterPro; IPR007127; Sigma70_r1_1.
 DR InterPro; IPR009042; Sigma70_r1_2.
 DR InterPro; IPR007627; Sigma70_r2.
 DR InterPro; IPR007624; Sigma70_r3.
 DR InterPro; IPR007630; Sigma70_r4.
 DR InterPro; IPR000943; Sigma70.
 DR Pfam; PF04546; sigma70_ner7_1.
 DR Pfam; PF03979; sigma70_r1_1; 1.
 DR Pfam; PF00140; sigma70_r1_2; 1.
 DR Pfam; PF04542; sigma70_r27_1.
 DR Pfam; PF04539; sigma70_r3; 1.
 DR Pfam; PF04545; sigma70_r4; 1.
 DR PRINTS; PR00046; SIGMA70FCT.
 DR PROSITE; PS00715; SIGMA70_1; 1.
 DR PROSITE; PS00716; SIGMA70_2; 1.
 KW Transcription regulation; Sigma factor; DNA-directed RNA polymerase;
 KW DNA-binding; Complete proteome.
 FT DOMAIN 414 427 POLYMERASE CORE BINDING (POTENTIAL).
 FT H-T-H MOTIF (BY SIMILARITY).
 FT DNA_BIND 584 603
 SQ SEQUENCE 625 AA; 70084 MW; 6B7032460884C850 CRC64;
 Query Match 49.3%; Score 37; DB 1; Length 625;
 Best Local Similarity 50.0%; Pred. No. 37;
 Matches 8; Conservative 1; Mismatches 7; Indels 0; Gaps 0;
 QY 1 MEKVQYLTRSAIRAS 16
 DB 358 MEKAVYLTGELKEIS 373
 RESULT 13
 H4V BLEJA STANDARD; PRT; 47 AA.
 AC P80738;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Histone H4 (Fragment).
 OS Blepharisma japonicum.
 OC Eukaryota; Alveolata; Ciliophora; Heterotricha; Heterotrichida;
 CC Blepharismidae; Blepharisma.
 OX NCBI_TaxID=5961;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=A5-3;
 RX MEDLINE=97257506; PubMed=9103980;
 RA Salvini M., Bini E., Santucci A., Batistoni R.;
 RT "H4 histone in the macronucleus of Blepharisma japonicum (Protozoa,
 RL FEMS Microbiol. Lett. 149:93-98(1997)).
 CC -!- FUNCTION: Histone H4, along with histone H3, plays a central role
 CC in nucleosome formation.
 Query Match 49.3%; Score 37; DB 1; Length 625;
 Best Local Similarity 50.0%; Pred. No. 37;
 Matches 8; Conservative 1; Mismatches 7; Indels 0; Gaps 0;
 QY 1 MEKVQYLTRSAIRAS 16
 DB 358 MEKAVYLTGELKEIS 373

CC -!- SUBUNIT: The nucleosome is an octamer containing two molecules
 CC each of H2A, H2B, H3 and H4. The octamer wraps approximately 146
 CC bp of DNA.
 CC -!- SIMILARITY: Belongs to the histone H4 family.
 DR InterPro; IPR001951; Histone_H4.
 DR PRINTS; PR00623; HISTONEH4.
 DR ProDom; PD001827; HISTONEH4; 1.
 DR PROSITE; PS00047; HISTONE_H4; PARTIAL.
 KW Chromosomal protein; Nucleosome core; Nuclear protein; DNA-binding.
 FT NON_TER 47
 SQ SEQUENCE 47 AA; 4961 MW; D743BBA73B76BADA CRC64;
 Query Match 48.0%; Score 36; DB 1; Length 47;
 Best Local Similarity 53.8%; Pred. No. 35;
 Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 2 EKVQYLTRSAIR 14
 DB 27 ENIQGITKPAIR 39
 RESULT 14
 H41 BLEJA STANDARD; PRT; 97 AA.
 ID H41 BLEJA
 AC P80737; P90515;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Histone H4-1 (Fragment).
 OS Blepharisma japonicum.
 OC Eukaryota; Alveolata; Ciliophora; Heterotricha; Heterotrichida;
 CC Blepharismidae; Blepharisma.
 OX NCBI_TaxID=5961;
 RN [1]
 RP SEQUENCE OF 1-46; AND SEQUENCE OF 9-97 FROM N.A.
 RC STRAIN=A5-3;
 RX MEDLINE=97257506; PubMed=9103980;
 RA Salvini M., Bini E., Santucci A., Batistoni R.;
 RT "H4 histone in the macronucleus of Blepharisma japonicum (Protozoa,
 RL FEMS Microbiol. Lett. 149:93-98(1997)).
 CC -!- FUNCTION: Histone H4, along with histone H3, plays a central role
 CC in nucleosome formation.
 CC -!- SUBUNIT: The nucleosome is an octamer containing two molecules
 CC each of H2A, H2B, H3 and H4. The octamer wraps approximately 146
 CC bp of DNA.
 CC -!- SIMILARITY: Belongs to the histone H4 family.
 CC -----
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 CC -----
 CC EMBL; X97995; CAA56634.1; ..
 DR InterPro; IPR007124; HIST_TAF.
 DR InterPro; IPR007125; Histone_core_D.
 DR InterPro; IPR001951; Histone_H4.
 DR Pfam; PF00125; histone; 1.
 DR PRINTS; PR00623; HISTONEH4.
 DR ProDom; PD001827; HISTONE_H4; 1.
 DR SMART; SM00417; H4; 1.
 DR PROSITE; PS00047; HISTONE_H4; PARTIAL.
 KW Chromosomal protein; Nucleosome core; Nuclear protein; DNA-binding.
 FT NON_TER 97
 SQ SEQUENCE 97 AA; 10722 MW; 64BBB2D85594607C CRC64;
 Query Match 48.0%; Score 36; DB 1; Length 97;
 Best Local Similarity 53.8%; Pred. No. 7.7;
 Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 EKXQYLTRSAIRR 14
| : : : :
Db 26 ENIQGITKPAIR 38

RESULT 15

RL19 CORGL
ID -RL19 CORGL STANDARD; PRT; 113 AA.
AC Q8PFS6; 2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE 50S ribosomal protein L19.
GN RPLS OR CBL932.
OS Corynebacterium efficiens.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=152794;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Y8-314 / AJ 12310 / DSM 44549 / JCM 11189;
RX MEDLINE=2273752; PubMed=12840036;
RA Nishio Y., Nakamura Y., Kawarabayashi Y., Usuda Y., Kimura E.,
RA Sugimoto S., Matsui K., Yamagishi A., Kikuchi H., Ikeo K.,
RA Gotohori T.;
RT "Comparative complete genome sequence analysis of the amino acid
RT replacements responsible for the thermostability of Corynebacterium
RT efficiens.";
RL Genome Res. 13:1572-1579(2003).
CC -|- FUNCTION: This protein is located at the 30S-50S ribosomal subunit
CC interface and may play a role in the structure and function of the
CC aminoacyl-tRNA binding site (By similarity).
CC -|- SIMILARITY: Belongs to the L19P family of ribosomal proteins.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AP005220; BAC18742.1; ALT INIT.
CC DR HAMAP; MF 00402; -; 1.
CC DR InterPro; IPR001857; Ribosomal L19.
CC DR Pfam; PF01245; Ribosomal L19; 1.
CC DR PRINTS; PR00061; RIBOSOMALL19.
CC DR ProDom; PD002979; Ribosomal L19; 1.
CC DR TIGRFAMs; TIGR01024; rplS_bact; 1.
CC DR PROSITE; PS01015; RIBOSOMAL_L19; 1.
CC KW Ribosomal protein; Complete proteome.
CC SQ SEQUENCE 113 AA; 13008 MW; 9BDIC9D25ADA453A CRC64;
Query Match 48.0%; Score 36; DB 1; Length 113;
Best Local Similarity 40.0%; Pred. No. 9.1;
Matches 6; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MEKXQYLTRSAIRR 15
| : : : :
Db 80 LEKIEVVRGQVRR 94

RESULT 16

RL19 CORGL
ID -RL19 CORGL STANDARD; PRT; 113 AA.
AC Q8NNZ0;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 50S ribosomal protein L19.
GN RPLS OR CGL2037.
OS Corynebacterium glutanicum (Brevibacterium flavum).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OX NCBI_TaxID=152794;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. landsberg erecta;
RX MEDLINE=94255767; PubMed=8197457;
RA Meyer K., Leube M.P., Grill E.;
RT "A protein phosphatase 2C involved in ABA signal transduction in
RT Arabidopsis thaliana";
RL Science 264:1452-1455(1994).
RN [2]
RP SEQUENCE FROM N.A. AND VARIANT ASP-180.
RC STRAIN=cv. landsberg erecta;
RX MEDLINE=94255767; PubMed=8197457;
RA Meyer K., Leube M.P., Grill E.;
RT "A protein phosphatase 2C involved in ABA signal transduction in
RT Arabidopsis thaliana";
RL Science 264:1452-1455(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia; TISSUE=Leaf;
RX MEDLINE=95007758; PubMed=7923358;
RA Mindrinos M., Katagiri F., Yu G.L., Ausubel F.M.;
RT "The A. thaliana disease resistance gene RPS2 encodes a protein
RT containing a nucleotide-binding site and leucine-rich repeats.";
RL Cell 78:1089-1099(1994).
RN [3]

RESULT 17

P2C1 ARATH
ID -P2C1 ARATH STANDARD; PRT; 434 AA.
AC P49597; Q43717; Q94C87;
DT 01-FEB-1996 (Rel. 33, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Protein phosphatase 2C ABII (EC 3.1.3.16) (P2C) (Abscisic acid-
DE insensitive 1).
GN ABII OR AT4G26080 OR P20B18.190.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A. AND VARIANT ASP-180.
RC STRAIN=cv. landsberg erecta;
RX MEDLINE=94255767; PubMed=8197457;
RA Meyer K., Leube M.P., Grill E.;
RT "A protein phosphatase 2C involved in ABA signal transduction in
RT Arabidopsis thaliana";
RL Science 264:1452-1455(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia; TISSUE=Leaf;
RX MEDLINE=95007758; PubMed=7923358;
RA Mindrinos M., Katagiri F., Yu G.L., Ausubel F.M.;
RT "The A. thaliana disease resistance gene RPS2 encodes a protein
RT containing a nucleotide-binding site and leucine-rich repeats.";
RL Cell 78:1089-1099(1994).
RN [3]

PP SEQUENCE FROM N.A.
RC STRAIN=cv, Columbia; TISSUE=Leaf;
RX MEDLINE=94255766; PubMed=7910981;
RA Leung J., Bouvier-Durand M., Morris P.C., Guerrier D., Chedid F.,
RA Giraudat J.,
RT "Arabidopsis ABA response gene AB11: features of a calcium-modulated
RL protein phosphatase";
RN Science 264:1448-1452(1994).
[4]
PP SEQUENCE FROM N.A.
RC STRAIN=cv, Columbia;
RX MEDLINE=20083488; PubMed=10617198;
RA Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G.,
RA Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terryn N.,
RA Harris B., Ansgore W., Brandt P., Grivell L.A., Rieger M.,
RA Weichselgartner M., de Simone V., Obermaier B., Mache R., Mueller M.,
RA Kreis M., Delsen M., Puigdomenech P., Watson M., Schmidtheini T.,
RA Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,
RA Vos P., Hohnel J., Zimmermann W., Medler H., Ridley P.,
RA Langham S.-A., McCullagh B., Silham L., Robben J.,
RA Van der Schueren J., Grymonprez B., Chuang Y.-J., Vandenbussche F.,
RA Braeken M., Weijens I., Voet M., Bastiaens I., Aert R., Defoor E.,
RA Weitzenecker T., Bothe G., Rumpelberger U., Hilbert H., Braun M.,
RA Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W.,
RA Moolman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,
RA Berner S., Hempel S., Feldpausch M., Lamberth S., van den Daele H.,
RA De Keyser A., Buyschaert C., Gielen J., Villarroel R., De Clercq R.,
RA Van Montagu M., Rogers J., Cronin A., Quail M.A., Bray-Allen S.,
RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McLaughlin K., Mayes R.,
RA Pettett A., Rajandream M.A., Lyne M., Benes V., Rechmann S.,
RA Borkova D., Bloeker H., Schaefer M., Grimm M., Loehner T.-H.,
RA Dose S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Partmann B., Grandjean K., Dauner D., Hertzl A.,
RA Neumann S., Agirion A., Vitale D., Liguori R., Piravandi E.,
RA Messner O., Quigley F., Clabaud G., Muendlein A., Felber R.,
RA Schnabl S., Hiller R., Schmidt W., Lechman A., Aubourg S.,
RA Gribbons T., Weber N., Vandenberg M., Barges M., Terol J., Torres A.,
RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,
RA Heijnen L., Schwarz S., Scholler P., Heber S., Francis P., Bieleke C.,
RA Frishman D., Haase D., Lemcke K., Meves H.-W., Stocker S.,
RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,
RA Parnell L., Dedia N., Gnoj L., Schutz K., Huang E., Spiegel L.,
RA Saxon M., Murray J., Sheet P., Cordes M., Abu-Frieden J.,
RA Stoneking T., Kalicki J., Graves T., Harmon G., Edwards J.,
RA Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
RA Kramer J., Fulton L., Mardis E., Dente M., Pepin K., Hillier L.W.,
RA Nelson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D.,
RA Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Joshi C.,
RA Antoniou B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
RA Ma P., Zhong J., Preston R., Vli D., Shekher M., Matero A., Shah R.,
RA Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S.,
RA Granat S., Shohdy N., Hasegawa A., Hameed A., Lodhi M., Johnson A.,
RA Chen E., Marra M.A., Martienssen R., McCombie W.R.;
RT "Sequence and analysis of chromosome 4 of the plant Arabidopsis
thaliana";
RL Nature 402:769-777(1999).
[5]
PP SEQUENCE FROM N.A.
RC STRAIN=cv, Columbia;
RX MEDLINE=22954850; PubMed=14593172;
RA Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J.,
RA Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,
RA Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,
RA Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,
RA Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y.,
RA Arakawa T., Bah J., Banno F., Bowser L., Brooks S.Y., Garninci P.,
RA Chao Q., Choy N., Enju A., Goldsmith A.D., Gurjal M., Hansen N.F.,
RA Hayashizaki Y., Johnson-Hopson C., Hsuan V.W., Iida K., Karnes M.,
RA Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J.,
RA Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,
RA Satou M., Tamse R., Vaysberg M., Wallender E.K., Wong C., Yamamura Y.,

Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
RT "Empirical analysis of transcriptional activity in the Arabidopsis
genome";
RL Science 302:842-846(2003).
CC -!- FUNCTION: Involved in abscisic acid (ABA) signaling pathway.
CC -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC phosphate.
CC -!- COFACTOR: Binds 2 magnesium or manganese ions (By similarity).
CC -!- SIMILARITY: Belongs to the PP2C family.
CC
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CC
CC EMBL: X78866; CAA5484.1; -
CC EMBL: U12856; CAA50237.1; -
CC EMBL: X77116; CAA5383.1; -
CC EMBL: AL049483; CAB39673.1; -
CC EMBL: AL161564; CAB79463.1; -
CC EMBL: AY035073; AAK59578.1; -
CC PIR: T04263; T04263.
CC HSP: P35813; I46Q.
CC InterPro: IPR002048; EF-hand.
CC InterPro: IPR001932; PP2C-like.
CC InterPro: IPR002222; PP2C.
CC Pfam: PF0048; PF2C; 1.
CC SMART: SM00331; PP2C_SIG; 1.
CC SMART: SM00332; PP2C; 1.
CC PROSITE: PS00018; EF_HAND; 1.
CC PROSITE: PS01032; PP2C; 1.
CC Hydrolase; Magnesium; Manganese; Multigene family; Calcium-binding.
CC CA_BIND 93 104 EF-HAND (POTENTIAL).
CC DOMAIN 417 420 POLY-VAL
CC VARIANT 180 190
CC
CC CONFLICT 24 24 G->D (WILTY PHENOTYPE AND ABA-
CC CONFLICT 105 105 G->R (IN REF. 5).
CC CONFLICT 105 105 I->V (IN REF. 1).
CC SEQUENCE 434 AA; 47505 MW; 4A4C54F04195F572 CRC64;

Query Match Similarity 48.08; Score 36; DB 1; Length 434;
Best Local Similarity 43.88; Pred. No. 39;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 MERQYLTRSAIRAS 16
DB 396 MSAAEYLSKLAIRGS 411

RESULT 18
2ASA_HUMAN
ID 2ASA_HUMAN STANDARD; PRT; 486 AA.
AC Q15172;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Serine/threonine protein phosphatase 2A, 56 kDa regulatory subunit,
DE alpha isoform (PP2A, B subunit, B' alpha isoform) (PP2A, B subunit,
DE B56 alpha isoform) (PP2A, B subunit, PP61 alpha isoform) (PP2A, B
DE subunit, R5 alpha isoform).
DE PPP2R5A.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Breast cancer;
RX MEDLINE=96064678; PubMed=7592815;
RA McCright B., Virshup D.M.;

RT subunits.",
 RN J. Biol. Chem. 270:26123-26128(1995).
 RP SEQUENCE OF 47-56; 129-132; 347-354; 448-462 AND 471-480.
 RX MEDLINE=96276417; PubMed=8694763;
 RA Zolnierowicz S., van Hoof C., Andjelkovic N., Cron P., Stevens I.,
 RA Merlevede W., Goris J., Hemmings B.A.;
 RT "The variable subunit associated with protein phosphatase 2A defines
 RT a novel multimer family of regulatory subunits.",
 RN Biochem. J. 317:187-194(1996).
 RP PHOSPHORYLATION, AND SUBCELLULAR LOCATION.
 RX MEDLINE=96355607; PubMed=8703017;
 RA McCright B., Rivers A.M., Audlin S., Virshup D.M.;
 RT "The B56 family of protein phosphatase 2A (PP2A) regulatory subunits
 RT encodes differentiation-induced phosphoproteins that target PP2A to
 RT both nucleus and cytoplasm.",
 RL J. Biol. Chem. 271:22081-22089(1996).
 CC -!- FUNCTION: The B regulatory subunit might modulate substrate
 CC selectivity and catalytic activity, and also might direct the
 CC localization of the catalytic enzyme to a particular subcellular
 CC compartment.
 CC -!- SUBUNIT: PP2A consists of a common heterodimeric core enzyme,
 CC composed of a 36 kDa catalytic subunit (subunit C) and a 65 kDa
 CC constant regulatory subunit (PR65 or subunit A), that associates
 CC with a variety of regulatory subunits. Proteins that associate
 CC with the core dimer include three families of regulatory subunits
 CC B (the R2/B/PR55/B56, R3/B'/PR72/PR130/PR59 and R5/B'/B56
 CC families), the 48 kDa variable regulatory subunit, viral proteins,
 CC and cell signaling molecules.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- TISSUE SPECIFICITY: Widely expressed with the highest expression
 CC in heart and skeletal muscle.
 CC -!- PMW: Phosphorylated on serine residues.
 CC -!- SIMILARITY: Belongs to the phosphatase 2A regulatory subunit B
 CC family.
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 CC EMBL; L42373; AAC37601.1; -
 DR PIR; I55449; I55449.
 DR Genbank; HGNC:9309; PPRK5A.
 DR MIM; 601643; -
 DR GO; GO:0005737; Cytoplasm; TAS.
 DR GO; GO:0008601; F:protein phosphatase type 2A, intrinsic regu. . .; TAS.
 DR InterPro; IPR008938; ARM.
 DR InterPro; IPR002554; B56.
 DR Pfam; PF01603; B56; 1.
 DR Phosphorylation; Multigene family.
 KW DOMAIN 2 5 POLY-SER.
 FT CONFLICT 52 52 E -> F (IN REF. 2; AA SEQUENCE).
 FT CONFLICT 54 54 H -> S (IN REF. 2; AA SEQUENCE).
 FT CONFLICT 451 451 R -> E (IN REF. 2; AA SEQUENCE).
 SQ SEQUENCE 486 AA; 56193 MW; D314077032A6D44 CRC64;
 Query Match 48.0%; Score 36; DB 1; Length 486;
 Best Local Similarity 50.0%; Pred. No. 44;
 Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 Oy 2 EKQVLTSAIRRA 15
 Db 19 EKVDGFTKSVKRA 32

RESULT 19

RPD XANCP
 ID RPSD_XANCP STANDARD; PRT; 624 AA.
 AC Q9P4H2;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DE RNA polymerase sigma factor rpoD (sigma-70).
 GN RPOD OR XCC3736.
 OS Xanthomonas campestris (pv. campestris).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
 OC Xanthomonadaceae; Xanthomonas.
 OX NCBI_TaxID=340;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=ATCC 33913 / NCPPB 538;
 RC MEDLINE=22022145; PubMed=12024217;
 RA da Silva A.C.R., Ferto J.A., Reinach F.C., Farah C.S., Furlan L.R.,
 RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
 RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
 RA Camarotte G., Cannavan P., Cardozo J., Chamberg F., Ciapina L.P.,
 RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,
 RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferto M.I.T.,
 RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
 RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
 RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
 RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
 RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
 RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
 RA Spindola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
 RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
 RA Setubal J.C., Kitajima J.P.;
 RT "Comparison of the genomes of two Xanthomonas pathogens with differing
 RT host specificities.",
 RL Nature 417:459-463(2002).
 CC -!- FUNCTION: The sigma factor is an initiation factor that promotes
 CC attachment of the RNA polymerase to specific initiation sites and
 CC then is released. This is the primary sigma-factor of this
 CC bacteria (by similarity).
 CC -!- SIMILARITY: Belongs to the sigma-70 factor family.
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 CC EMBL; AE012494; AAM42993.1; -
 DR InterPro; IPR009043; RNA_pol_sigma.
 DR InterPro; IPR007631; Sigma70_ner.
 DR InterPro; IPR007127; Sigma70_r1.
 DR InterPro; IPR009042; Sigma70_r1_2.
 DR InterPro; IPR007627; Sigma70_r2.
 DR InterPro; IPR007624; Sigma70_r3.
 DR InterPro; IPR007630; Sigma70_r4.
 DR InterPro; IPR000943; Sigma70.
 DR Pfam; PF04546; sigma70_ner; 1.
 DR Pfam; PF03979; sigma70_r1; 1.
 DR Pfam; PF00140; sigma70_r1_2; 1.
 DR Pfam; PF04542; sigma70_r2; 1.
 DR Pfam; PF04539; sigma70_r3; 1.
 DR Pfam; PF04545; sigma70_r4; 1.
 DR PRINTS; PR00046; SIGMA70PFT.
 DR PROSITE; PS00715; SIGMA70_1; 1.
 DR PROSITE; PS00716; SIGMA70_2; 1.
 KW Transcription regulation; Sigma factor; DNA-directed RNA polymerase;
 KW DNA-binding; Complete proteome.
 FT DOMAIN 413 426 POLYMERASE CORE BINDING (POTENTIAL).
 FT DNA_BIND 583 602 H-T-H MOTIF (BY SIMILARITY).
 SQ SEQUENCE 624 AA; 69947 MW; 1F6C8CA093F7E1AF CRC64;
 Query Match 48.0%; Score 36; DB 1; Length 624;

```

Best Local Similarity 50.0%; Pred. No. 57;
Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 MEKVQVLTSAIRRAS 16
    ||| ||| : : |
DB 357 MEKANYLTIAEKDIS 372

RESULT 20
CHLD_SYN7P7
ID CHLD_SYN7P7 STANDARD; PRT; 677 AA.
AC O07345;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Magnesium-chelatase subunit chld (Mg-protoporphyrin IX chelatase) (Mg-
  chelatase subunit D).
GN CHLD.
OS Synecococcus sp. (strain PCC 7942) (Anacystis nidulans R2).
OC Bacteria; Cyanobacteria; Chroococcales; Synecococcus.
CX NCBI_TaxID=1140;
RN [1]
RP SEQUENCE FROM N.A.
RA Masuda T., Nakayama M., Ohta H., Takayama K.-I.;
RT "Cloning and sequencing of a chid gene encoding a subunit of
  magnesium-chelatase from the cyanobacterium Synecococcus sp. PCC
  7942."
RL (in) Plant Gene Register PGR97-094.
CC -!- FUNCTION: Involved in chlorophyll biosynthesis; introduces a
  magnesium ion into protoporphyrin IX to yield Mg-protoporphyrin
  IX.
CC -!- PATHWAY: Chlorophyll biosynthesis.
CC -!- SIMILARITY: BELONGS TO THE MG-CHELATASE SUBUNITS D/I FAMILY.
CC -!- SIMILARITY: Contains 1 VWFA domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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  or send an email to license@isb-sib.ch).
CC EMBL; AB003135; BAA20346.1; -
CC InterPro; IPR003593; AAA ATPase.
CC InterPro; IPR000523; Mg_chelatase_chII.
CC InterPro; IPR002035; VWF A.
CC Pfam; PF01078; Mg_chelatase; 1.
CC Pfam; PF00092; vwa; 1.
CC SMART; SM00382; AAA; 1.
CC SMART; SN00327; VWFA; 1.
CC PROSITE; PS0234; VWFA; 1.
KW Photosynthesis; Chlorophyll biosynthesis; ATP-binding.
FT DOMAIN 329 383
FT DOMAIN 481 676
FT SEQUENCE 677 AA; 73367 MW; 7E2988E096DF5506 CRC64;
SQ SEQUENCE 677 AA; 73367 MW; 7E2988E096DF5506 CRC64;

Query Match 48.0%; Score 36; DB 1; Length 677;
Best Local Similarity 58.3%; Pred. No. 63;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 ERKVQVLTSAIR 13
    ||| ||| |||
DB 267 EQIGLVREAIR 278

RESULT 21
DVL2_XENLA
ID DVL2_XENLA STANDARD; PRT; 736 AA.
AC P51142;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)

```

```

DE (DSH homolog 2) (Xdsh).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=83355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Oocyte;
RX MEDLINE=95324391; PubMed=7600981;
RA Sokol S.Y., Klingensmith J., Perrimon N., Itoh K.;
RT "Dorsalizing and neuralizing properties of Xdsh, a maternally
  expressed Xenopus homolog of Dishevelled."
RL Development 121:1637-1647(1995).
RN [2]
RP ERRATUM.
RX MEDLINE=96017659; PubMed=7598081;
RA Sokol S.Y., Klingensmith J., Perrimon N., Itoh K.;
RL Development 121:3487-3487(1995).
CC -!- FUNCTION: May play a role in the signal transduction pathway
  mediated by multiple Wnt genes. Plays a role in dorsal axis
  formation and in neural induction.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -!- TISSUE SPECIFICITY: Ubiquitous protein found equally distributed
  in both animal-vegetal and dorsal-ventral directions.
CC -!- DEVELOPMENTAL STAGE: Maternal gene detected in different
  developmental stages being most abundant in eggs.
CC -!- SIMILARITY: Belongs to the DSH family.
CC -!- SIMILARITY: Contains 1 DEP domain.
CC -!- SIMILARITY: Contains 1 PDZ/DHR domain.
CC -!- SIMILARITY: Contains 1 DIX domain.
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CC EMBL; U31552; AB006688.1; -
CC PIR; I51691; I51691.
CC HSP; Q12323; 3PDZ.
CC InterPro; IPR000591; DEP.
CC InterPro; IPR008339; Dishevelled.
CC InterPro; IPR003351; Dishevelled.
CC InterPro; IPR008341; Dishevelled_2.
CC InterPro; IPR001158; DIX.
CC InterPro; IPR001478; PDZ.
CC Pfam; PF00610; DEP; 1.
CC Pfam; PF02377; Dishevelled; 1.
CC Pfam; PF00778; DIX; 1.
CC Pfam; PF00595; PDZ; 1.
CC PRINTS; PR01760; DISHEVELLED.
CC PRINTS; PR01762; DISHEVELLED2.
CC PRODOM; PD003639; DIX; 1.
CC SMART; SM00021; DAX; 1.
CC SMART; SM00049; DEP; 1.
CC SMART; SM00228; PDZ; 1.
CC PROSITE; PS0186; DEP; 1.
CC PROSITE; PS00841; DIX; 1.
CC PROSITE; PS0106; PDZ; 1.
KW Wnt signaling pathway; Developmental protein.
FT DOMAIN 1 82
FT DOMAIN 99 113
FT DOMAIN 222 227
FT DOMAIN 254 326
FT DOMAIN 428 502
FT DOMAIN 680 687
FT SEQUENCE 736 AA; 79787 MW; AF6C9A1662DD7CEB CRC64;
SQ SEQUENCE 736 AA; 79787 MW; AF6C9A1662DD7CEB CRC64;

Query Match 48.0%; Score 36; DB 1; Length 736;

```

Best Local Similarity 70.0%; Pred. No. 69;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 5 QYLTRSAIRR 14
: |||||:
Db 624 EYSTRSSIRR 633

RESULT 22

HXK3 RAT STANDARD; PRT; 924 AA.
AC P27926;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hexokinase type III (EC 2.7.1.1) (HK III).
GN HK3
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=91378267; PubMed=1897938;
RA Schwab D.A., Wilson J.E.,
RT "Complete amino acid sequence of the type III isozyme of rat
hexokinase, deduced from the cloned cDNA.";
RL Arch. Biochem. Biophys. 285:365-370(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA White J.A.;
RL Submitted (Oct-1996) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ATP + D-hexose = ADP + D-hexose 6-phosphate.
CC -1- ENZYME REGULATION: Hexokinase is an allosteric enzyme inhibited by
its product Glc-6-P.
CC -1- PATHWAY: First step of several metabolic pathways.
CC -1- SUBUNIT: Monomer.
CC -1- DOMAIN: THE N- AND C-TERMINAL HALVES OF THIS HEXOKINASE SHOW
EXTENSIVE SEQUENCE SIMILARITY TO EACH OTHER. THE CATALYTIC
ACTIVITY IS ASSOCIATED WITH THE C-TERMINUS WHILE REGULATORY
FUNCTION IS ASSOCIATED WITH THE N-TERMINUS.
CC -1- MISCELLANEOUS: In vertebrates there are four major glucose-
phosphorylating isoenzymes, designated hexokinase I, II, III and
IV (glucokinase).
CC -1- SIMILARITY: Belongs to the hexokinase family.
CC
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CC
CC EMBL; U73859; AAB18253.1; --
CC PR; S13913; S13913.
CC HSP; P05708; IKG3.
CC InterPro; IPR001312; Hexokinase.
CC Pfam; PF03727; hexokinase2; 2.
CC Pfam; PF00349; hexokinase; 2.
CC PRINTS; PR00475; HEXOKINASE.
CC ProDom; PD001109; Hexokinase; 2.
CC PROSITE; PS00378; HEXOKINASES; 2.
CC Transferrase; Kinase; Glycolysis; Allosteric enzyme; Repeat;
KW ATP-binding; Membrane.
FT DOMAIN 1 488 REGULATORY.
FT DOMAIN 489 924 CATALYTIC.
FT DOMAIN 162 188 GLUCOSE-BINDING (POTENTIAL).
FT DOMAIN 604 630 GLUCOSE-BINDING (POTENTIAL).
FT NP_BIND 95 100 ATP (POTENTIAL).
FT NP_BIND 542 547 ATP (POTENTIAL).

SQ SEQUENCE 924 AA; 100253 MW; 0162C1591AF040AC CRC64;

Query Match 48.0%; Score 36; DB 1; Length 924;
Best Local Similarity 61.5%; Pred. No. 88;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 EKQVLTSAIRR 14

Db 638 QDVVLLREAIR 650

RESULT 23

RPOB MESVI STANDARD; PRT; 1080 AA.
AC QSMUS3;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE DNA-directed RNA polymerase beta chain (EC 2.7.7.6).
GN RPOB.
OS Mesostigma viride.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Mesostigmatophyceae;
OC Mesostigmatales; Mesostigmataceae; Mesostigma.
OX NCBI_TaxID=41882;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NIES-296;
RX MEDLINE=20150907; PubMed=10688199;
RA Lemieux C., Otis C., Turmel M.;
RT "Ancestral chloroplast genome in Mesostigma viride reveals an early
branch of green plant evolution.";
RL Nature 403:649-652(2000).
CC -1- FUNCTION: DNA-dependent RNA polymerase catalyzes the transcription
of DNA into RNA using the four ribonucleoside triphosphates as
substrates.
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
(RNA)(N).
CC -1- SUBUNIT: In chloroplasts, the RNA polymerase is composed of four
subunits: alpha, beta, beta', and beta".
CC -1- SUBCELLULAR LOCATION: Chloroplast.
CC -1- SIMILARITY: Belongs to the RNA polymerase beta chain family.
CC
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CC
CC EMBL; AF166114; AAF43826.1; --
CC HSP; Q9KMU7; IHW6.
CC InterPro; IPR007121; RNA pol B.
CC InterPro; IPR007644; RNA_pol_Rpb2_1.
CC InterPro; IPR007642; RNA_pol_Rpb2_2.
CC InterPro; IPR007645; RNA_pol_Rpb2_3.
CC InterPro; IPR007120; RNA_pol_Rpb2_6.
CC InterPro; IPR007641; RNA_pol_Rpb2_7.
CC Pfam; PF04563; RNA_pol_Rpb2_1; 1.
CC Pfam; PF04561; RNA_pol_Rpb2_2; 1.
CC Pfam; PF04565; RNA_pol_Rpb2_3; 1.
CC Pfam; PF00562; RNA_pol_Rpb2_6; 1.
CC Pfam; PF04560; RNA_pol_Rpb2_7; 1.
CC PROSITE; PS01166; RNA_POL_BETA; 1.
CC Transferrase; DNA-directed RNA polymerase; Transcription; Chloroplast.
KW
SQ SEQUENCE 1080 AA; 121910 MW; 6FEC1BDB547422A CRC64;

Query Match 48.0%; Score 36; DB 1; Length 1080;
Best Local Similarity 43.8%; Pred. No. 1e+02;
Matches 7; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MEKVQLTRSAIRR 16

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CC -----
CC DR EMBL; AE003477; AAF47742.1; -.
CC DR EMBL; AY071444; AAL49066.1; -.
CC DR FlyBase; FBgn0035422; CG12740.
CC DR GO; GO:0005842; Cytosolic large ribosomal subunit (sensu Eu. . .; ISS.
CC DR GO; GO:0003735; P: structural constituent of ribosome; ISS.
CC DR GO; GO:0006412; P: protein biosynthesis; ISS.
CC DR InterPro; IPR002672; Ribosomal_L28e.
CC DR Pfam; PF01778; Ribosomal_L28e; 1.
CC DR ProDom; PD010767; Ribosomal_L28e; 1.
CC KW Ribosomal protein.
CC SQ SEQUENCE 144 AA; 16029 MW; 14D5C7866P585113 CRC64;
CC -----
Query Match 46.7%; Score 35; DB 1; Length 144;
Best Local Similarity 70.0%; Pred. No. 18;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
CC -----
CC QY 7 LTRSAIRAS 16
CC DB 110 LTRSAIRAS 119
CC -----
RESULT 25
AMIR_PSEAE
ID AMIR_PSEAE STANDARD; PRT; 196 AA.
AC P10932;
DC 01-JUL-1999 (Rel. 11, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Alphatic amidase regulator.
GN AMIR OR PA3363.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PA433;
RX MEDLINE=89211409; PubMed=2495988;
RA Lowe N., Rice P.M., Drew R.E.;
RT "Nucleotide sequence of the alphatic amidase regulator gene (amir)
RT of Pseudomonas aeruginosa."
RL FEBS Lett. 246:39-43(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 1562 / PA01;
RX MEDLINE=2043733; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman P.S.I., Huynh W.O., Kowalik D.J., Lagrou M.,
RA Gabor R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA Brady L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen."
RL Nature 406:959-964(2000).
RN [3]
RP CHARACTERIZATION.
RX MEDLINE=95286483; PubMed=7539417;
RA Wilson S.A., Drew R.E.;
RT "Transcriptional analysis of the amidase operon from Pseudomonas
RT aeruginosa."
RN [4]
RP J. Bacteriol. 177:3052-3057(1995).
CC -----
CC X-RAY-CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF COMPLEX WITH AMIC.
CC STRAIN=PA01;
CC MEDLINE=99437995; PubMed=10508151;
CC O'Hara B.P., Norman R.A., Wan P.T., Roe S.M., Barrett T.E., Drew R.E.,

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RA Pearl L.H.;
RT "Crystal structure and induction mechanism of AmiC-AmiR: a
RL ligand-regulated transcription antitermination complex.";
CC EMBL J. 18:5175-5186(1999)
CC
CC -!- FUNCTION: Positive controlling element of amiE, the gene for
CC aliphatic amidase. Acts as a transcriptional antitermination
CC factor. It is thought to allow RNA polymerase read through a rho-
CC independent transcription terminator between the amiE promoter and
CC gene.
CC
CC -!- SUBUNIT: Forms a complex with amiC.
CC
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CC
CC -----
CC EMBL: X13776; CAA32023.1; -.
CC EMBL: AE004758; AAC06751.1; -.
CC PIR: B83226; B83226.
CC PIR: S03884; S03884.
CC PDB: 1Q00; 23-DEC-99.
CC InterPro: IPR005561; ANTAAR.
CC Pfam: PF03861; ANTAAR; 1.
CC PIRSF: PIRSF036382; Res_reg_antiterm.
CC Transcription regulation; Transcription antitermination; 3D-structure;
CC Complete proteome.
CC
CC CONFLICT 48 48 S -> A (IN REF. 1).
CC CONFLICT 64 64 R -> G (IN REF. 1).
CC CONFLICT 141 141 E -> D (IN REF. 1).
CC CONFLICT 154 154 A -> V (IN REF. 1).
CC CONFLICT 170 170 Y -> H (IN REF. 1).
CC
CC HELIX 3 9
CC HELIX 10 12
CC STRAND 14 18
CC TURN 23 35
CC TURN 36 36
CC STRAND 38 42
CC STRAND 55 59
CC TURN 64 64
CC HELIX 65 75
CC TURN 78 79
CC STRAND 81 86
CC HELIX 91 100
CC TURN 101 101
CC STRAND 104 107
CC HELIX 112 114
CC HELIX 115 160
CC TURN 161 161
CC HELIX 164 176
CC TURN 177 179
CC HELIX 182 189
CC
CC SEQUENCE 196 AA; 21903 MW; 306A4F308E4C6C0 CRC64;

```

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Query Match 46.7%; Score 35; DB 1; Length 196;
Best Local Similarity 53.8%; Pred. No. 26;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

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Qy 2 EKQVYLTSAIRR 14
Db 166 EAHQYLSREAMKR 178

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Search completed: October 1, 2004, 12:18:16
Job time : 8.8 secs

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OM protein - protein search, using sw model

Run on: October 1, 2004, 11:56:56 ; Search time 50.8 Seconds

(without alignments)
99.376 Million cell updates/sec

Title: US-09-830-779-17_COPY_1_16

Perfect score: 75

Sequence: 1 MEKVQYLTRSAIRAS 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

1: SPREMEL 25:*

2: SP_Archea:*

3: SP_Fungi:*

4: SP_Human:*

5: SP_Invertebrate:*

6: SP_Mammal:*

7: SP_Mhc:*

8: SP_Organelle:*

9: SP_Phage:*

10: SP_Plant:*

11: SP_Rodent:*

12: SP_Virus:*

13: SP_Vertebrate:*

14: SP_Unclassified:*

15: SP_Rvirus:*

16: SP_Bacteriophage:*

17: SP_Archea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	54.7	116	16	Q82JW4
2	41	54.7	451	17	Q9U2T5
3	40	53.3	527	12	Q9G6Q3
4	40	53.3	998	11	Q8CFM4
5	40	53.3	1104	16	Q87GQ3
6	40	53.3	1108	17	O58310
7	39	52.0	364	16	Q9A0Y9
8	39	52.0	406	16	Q8BLL1
9	39	52.0	421	2	Q9AM36
10	39	52.0	481	17	Q9V1D2
11	39	52.0	644	5	O868U8
12	38	50.7	119	17	O26525
13	38	50.7	122	17	Q974N9
14	38	50.7	268	16	Q85J03
15	38	50.7	211	16	Q7UFR1
16	38	50.7	252	3	Q9HF62

17	38	50.7	376	16	Q99ZW6
18	38	50.7	376	16	Q8P177
19	38	50.7	398	16	Q878L1
20	38	50.7	408	16	Q8K7R5
21	38	50.7	578	2	Q9F8B7
22	38	50.7	882	10	Q84SQ7
23	38	50.7	1223	5	Q8WVG5
24	38	50.7	1541	16	Q8DJ60
25	37.5	50.0	68	16	Q7UWM3
26	37	49.3	163	16	Q8G4I3
27	37	49.3	283	17	O26701
28	37	49.3	296	16	O33293
29	37	49.3	296	16	O7TXV8
30	37	49.3	302	16	O92RES
31	37	49.3	308	16	O8YZH6
32	37	49.3	376	16	Q8E5S3
33	37	49.3	376	16	Q8E046
34	37	49.3	527	16	Q8DBN7
35	37	49.3	707	16	Q7VDP9
36	37	49.3	755	3	Q9HDM2
37	37	49.3	1698	5	Q9V8I5
38	37	49.3	1701	5	Q9V8I6
39	37	49.3	1922	5	Q8MLH7
40	37	49.3	2112	10	Q9SB74
41	36	48.0	71	5	O61185
42	36	48.0	71	5	O61184
43	36	48.0	71	5	O61183
44	36	48.0	71	5	O61182
45	36	48.0	72	5	O62614
46	36	48.0	74	5	O62586
47	36	48.0	79	7	Q8WM34
48	36	48.0	89	16	Q82VU6
49	36	48.0	101	5	Q27875
50	36	48.0	111	2	O07154
51	36	48.0	128	16	Q8FP56
52	36	48.0	220	17	Q97BD7
53	36	48.0	230	11	Q8CF99
54	36	48.0	236	17	O27417
55	36	48.0	237	16	Q87Q89
56	36	48.0	273	5	Q8R2B4
57	36	48.0	279	16	Q89VDS
58	36	48.0	294	2	O66251
59	36	48.0	335	5	O96847
60	36	48.0	335	5	Q23896
61	36	48.0	368	16	Q92P72
62	36	48.0	387	5	Q9VZC7
63	36	48.0	401	16	Q82RM1
64	36	48.0	409	16	Q914C6
65	36	48.0	410	9	O64082
66	36	48.0	410	16	O31939
67	36	48.0	417	16	Q9REV7
68	36	48.0	422	16	Q8F7A1
69	36	48.0	454	10	O7XZV4
70	36	48.0	462	16	Q82158
71	36	48.0	466	4	Q82B19
72	36	48.0	549	17	Q97ZB3
73	36	48.0	622	2	O08348
74	36	48.0	633	2	Q9E221
75	36	48.0	765	4	Q8NFD2
76	36	48.0	780	3	Q9UVJ6
77	36	48.0	784	10	O7XNF3
78	36	48.0	861	16	Q82HP5
79	36	48.0	886	5	Q851F1
80	36	48.0	936	6	Q9TR68
81	36	48.0	1040	12	Q9WSX6
82	36	48.0	1148	16	Q8X8E7
83	36	48.0	1199	12	Q83859
84	36	48.0	1330	16	Q8XRI4
85	36	48.0	1508	10	Q8S6W4
86	36	48.0	1844	10	Q8LM84
87	36	48.0	3020	12	Q9E160
88	35.5	47.3	319	5	Q9VGW4
89	35	46.7	59	16	Q8PBI5

Q99ZW6	streptococ
Q8P177	streptococ
Q878L1	streptococ
Q8K7R5	streptococ
Q9F8B7	streptococ
Q84SQ7	oryza sativ
Q8WVG5	dictyosteli
Q8DJ60	synchococ
Q7UWM3	rhodospirell
Q8G4I3	bifidobacte
O26701	methanobact
O33293	mycobacteri
O7TXV8	mycobacteri
O92RES	rhizobium m
O8YZH6	anabaena sp
Q8E5S3	streptococ
Q8E046	streptococ
Q8DBN7	vibrio vuln
Q7VDP9	prochloroco
Q9HDM2	schizosacch
Q9V8I5	drosophila
Q9V8I6	drosophila
Q8MLH7	drosophila
Q9SB74	arabidopsis
O61185	blepharisma
O61184	blepharisma
O61183	blepharisma
O61182	blepharisma
O62614	protocruzia
O62586	blepharisma
Q8WM34	ursus marit
Q82VU6	nitrosomona
Q27875	trichomonas
O07154	mycobacteri
Q8FP56	corynebacte
Q97BD7	thermoplasm
Q8CF99	rattus norv
O27417	methanobact
Q87Q89	vibrio para
Q8R2B4	drosophila
Q89VDS	bradyrhizob
O66251	actinobacti
O96847	dictyosteli
Q23896	dictyosteli
Q92P72	rhizobium m
Q9VZC7	drosophila
Q82RM1	streptomyce
Q914C6	pseudomonas
O64082	bacterioph
O31939	bacillus su
Q9REV7	pseudomonas
Q8F7A1	leptospiro
O7XZV4	oryza sativ
Q82158	salmonella
Q82B19	homocapten
Q97ZB3	sulfolobus
O08348	xanthomonas
Q9E221	sodalis glo
Q8NFD2	homo sapien
Q9UVJ6	botrytis ci
O7XNF3	oryza sativ
Q82HP5	streptomyce
Q851F1	dictyosteli
Q9TR68	myotis daub
Q9WSX6	marek s dis
Q8X8E7	escherichia
Q83859	niilaparvata
Q8XRI4	talstonia s
Q8S6W4	oryza sativ
Q8LM84	oryza sativ
Q9E160	wheat stria
Q9VGW4	drosophila
Q8PBI5	xanthomonas

90 35 46.7 60 16 Q8PN39
 91 35 46.7 81 7 Q30735
 92 35 46.7 165 4 Q81Y90
 93 35 46.7 185 16 Q8YWS1
 94 35 46.7 188 16 Q92RY5
 95 35 46.7 190 4 Q9NWF6
 96 35 46.7 207 16 Q8CS49
 97 35 46.7 212 10 Q9ARS3
 98 35 46.7 220 10 Q9LVU1
 99 35 46.7 227 16 Q82C01
 100 35 46.7 234 16 Q832P8

Q8PN39 xanthomonas
 Q30735 macaca neme
 Q81Y90 homo sapien
 Q8YWS1 anabaena sp
 Q92RY5 rhizobium m
 Q9NWF6 homo sapien
 Q8CS49 staphylococ
 Q9ARS3 volvox cart
 Q9LVU1 arabidopsis
 Q82C01 streptomyces
 Q832P8 enterococcus

ALIGNMENTS

RESULT 1
 Q82JW4 PRELIMINARY; PRT; 116 AA.
 AC Q82JW4
 DT 01-JUN-2003 (TRENBLrel. 24, Created)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE Putative ribosomal protein L19.
 GN RPLS OR SAV2640.
 OS Streptomyces avermitilis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycineae; Streptomycetaceae; Streptomycetes.
 OX NCBI_TaxID=33903;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MA-4580 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
 RX MEDLINE=2147403; PubMed=11572948;
 RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
 RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osone T.,
 RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
 RT "Genome sequence of an industrial microorganism Streptomyces
 RT avermitilis: deducing the ability of producing secondary
 RT metabolites.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
 RN [2]

RP SEQUENCE FROM N.A.
 RC STRAIN=MA-4580 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
 RX MEDLINE=22608306; PubMed=1292562;
 RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
 RA Sakaki Y., Hattori M., Omura S.;
 RT "Complete genome sequence and comparative analysis of the industrial
 RT microorganism Streptomyces avermitilis.";
 RL Nat. Biotechnol. 21:526-531(2003).
 DR EMBL; AP005031; BAC70351.1; -
 DR GO; GO:0005822; C:intracellular; IEA.
 DR GO; GO:0005840; C:ribosome; IEA.
 DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
 DR GO; GO:0006412; P:protein biosynthesis; IEA.
 DR InterPro; IPR001857; Ribosomal L19.
 DR Pfam; PF01245; Ribosomal L19; 1.
 DR PRINTS; PR00061; RIBOSOMAL_L19.
 DR ProDom; PD002979; Ribosomal L19; 1.
 DR TIGRfam; TIGR01024; rplS bact; 1.
 DR PROSITE; PS01015; RIBOSOMAL_L19; 1.
 DR Ribosomal protein; Complete proteome.
 SK SEQUENCE 116 AA; 13186 MW; 47081773B07F5EB6 CRC64;

Query Match 54.7%; Score 41; DB 16; Length 116;
 Best Local Similarity 46.7%; Pred. No. 7.5;
 Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 MEKVOYLTSATRR 15
 DB 81 VEKIELVTRGDVRR 95

RESULT 2

Q9UZT5 PRELIMINARY; PRT; 451 AA.
 AC Q9UZT5
 DT 01-MAY-2000 (TRENBLrel. 13, Created)
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
 DE Phospho-sugar mutase.
 GN PYRAB10610 OR PAB1666.
 OS Pyrococcus abyssi.
 OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
 OC Pyrococcus.
 OX NCBI_TaxID=29292;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GES / Orsay;
 RA Heilig R.;
 RT "Pyrococcus abyssi genome sequence: insights into archaeal chromosome
 RT structure and evolution.";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ248286; CAB49971.1; -
 DR FIR; F75083; F75083.
 DR GO; GO:0006868; P:intramolecular transferase activity, phosph. . .; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro; IPR005841; PG_PMM mutase.
 DR InterPro; IPR005844; PG_PMM ABAIL.
 DR InterPro; IPR005845; PG_PMM ABAIL.
 DR InterPro; IPR005846; PG_PMM ABAIL.
 DR InterPro; IPR005843; PG_PMM_C.
 DR Pfam; PF00408; PGM_PMM; 1.
 DR Pfam; PF02878; PGM_PMM_I; 1.
 DR Pfam; PF02879; PGM_PMM_II; 1.
 DR Pfam; PF02880; PGM_PMM_III; 1.
 DR PRINTS; PR00509; PGMPMM.
 DR PROSITE; PS00710; PGM_PMM; 1.
 KW Complete proteome.
 SQ SEQUENCE 451 AA; 49786 MW; F337BA57645E7269 CRC64;

Query Match 54.7%; Score 41; DB 17; Length 451;
 Best Local Similarity 50.0%; Pred. No. 32;
 Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 MEKVOYLTSATRRAS 16
 DB 435 MEKAEKLVDAIKKAS 450

RESULT 3
 Q9O6Q3 PRELIMINARY; PRT; 527 AA.
 AC Q9O6Q3
 DT 01-MAY-2000 (TRENBLrel. 13, Created)
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE RNA-dependent RNA polymerase (fragment).
 GN POL.
 OS Grapevine leafroll-associated virus 1.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Closteroviridae;
 OC Ampelovirus.
 OX NCBI_TaxID=47985;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20141373; PubMed=10675398;
 RA Fazeli C.F., Rezaian M.A.;
 RT "Nucleotide sequence and organization of ten open reading frames in
 RT the genome of Grapevine leafroll-associated virus 1 and identification
 RT of three subgenomic RNAs.";
 RL J. Gen. Virol. 81:605-615(2000).
 DR EMBL; AF195822; RAF22738.1; -
 DR GO; GO:0003723; F:RNA binding; IEA.
 DR GO; GO:0003568; F:RNA-directed RNA polymerase activity; IEA.
 DR GO; GO:0006350; P:transcription; IEA.
 DR GO; GO:0019079; P:viral genome replication; IEA.
 DR InterPro; IPR001788; RNA_dep_RNApol2.

```
DR InterPro; IPR007095; RNA_pol_DS_PS.
DR InterPro; IPR007094; RNA_pol_PSVir.
DR Pfam; PF00978; RNA_dep_RNAPolI2; 1.
KW RNA-directed RNA polymerase.
FT NON_TER 1
SQ SEQUENCE 527 AA; 53276 MW; C445CE1169946132 CRC64;
Query Match 53.3%; Score 40; DB 12; Length 527;
Best Local Similarity 80.0%; Pred. No. 59;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 5 QYVRSAIR 14
Db 95 QYVRSAIR 104
RESULT 4
Q8CFM4 PRELIMINARY; PRT; 998 AA.
AC Q8CFM4;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Breast tumor;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013626; AAH3626.1; -.
DR InterPro; IPR008160; Collagen.
DR Pfam; PF01391; Collagen; 12.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 998 AA; 95451 MW; 2AB4BA953B7084A6 CRC64;
Query Match 53.3%; Score 40; DB 11; Length 998;
Best Local Similarity 42.9%; Pred. No. 1.2e+02;
Matches 6; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
QY 1 MEKVQLTRSAIR 14
Db 974 METIOWISRTIKR 987
RESULT 5
Q87GQ3 PRELIMINARY; PRT; 1104 AA.
AC Q87GQ3;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN VPA1262.
OS Vibrio parahaemolyticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=670;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RIMD 2210633 / Serotype O3:K6;
RA Makino K., Oshina K., Kurokawa K., Yokoyama K., Uda T., Tagemori K.,
RA Iijima Y., Nejima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
RT "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
distinct from that of V. cholerae."
RL Lancet 361:743-749(2003).
DR EMBL; AP005088; BAC62605.1; -.
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KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 1104 AA; 125574 MW; 61C89EB3AB30C5DD CRC64;
Query Match 53.3%; Score 40; DB 16; Length 1104;
Best Local Similarity 42.9%; Pred. No. 1.3e+02;
Matches 6; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
QY 1 MEKVQLTRSAIR 14
Db 853 LSKIEHTPSAVRR 866
RESULT 6
O58310 PRELIMINARY; PRT; 1108 AA.
AC O58310;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-JAN-1999 (TrEMBLrel. 09, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 1108AA long hypothetical cell division control protein.
GN PH0606.
OS Pyrococcus horikoshii.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=33953;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OT3;
RA Kawarabayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
RA Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
RA Masuchi Y., Shizuwa H., Kikuchi H.;
RT "Complete sequence and gene organization of the genome of a hyper-
thermophilic archaeobacterium, Pyrococcus horikoshii OT3."
RL DNA Res. 5:55-76(1998).
DR EMBL; AP000003; BAA29695.1; -.
DR PIR; E71104; E71104.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003877; F:DNA binding; IEA.
DR GO; GO:0008094; F:DNA dependent ATPase activity; IEA.
DR GO; GO:0000910; P:cytokinesis; IEA.
DR GO; GO:0006270; P:DNA replication initiation; IEA.
DR InterPro; IPR003586; Hedgehog_hintC.
DR InterPro; IPR003587; Hedgehog_hintC.
DR InterPro; IPR06142; INTEIN.
DR InterPro; IPR06141; Intein_S.
DR InterPro; IPR01208; MCM.
DR Pfam; PF00493; MCM; 1.
DR PRINTS; PR00379; INTEIN.
DR PRINTS; PR01657; MCMFAMILY.
DR PRINTS; PR01658; MCMFAMILY.
DR ProDom; PD001041; MCM; 2.
DR SMART; SM00305; HintC; 2.
DR SMART; SM00306; HintN; 2.
DR SMART; SM00350; MCM; 1.
DR TIGFAMS; TIGR01443; intein_Cterm; 2.
DR TIGFAMS; TIGR01445; intein_Nterm; 2.
DR PROSITE; PS50818; INTEIN_C_TERM; 2.
DR PROSITE; PS50817; INTEIN_N_TERM; 2.
DR PROSITE; PS50051; MCM 2; 3.
KW Cell division; Complete proteome.
SQ SEQUENCE 1108 AA; 125967 MW; 92D2578B31351F75 CRC64;
Query Match 53.3%; Score 40; DB 17; Length 1108;
Best Local Similarity 53.3%; Pred. No. 1.3e+02;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
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QY 1 MEKVQYLTRSAIRRA 15
||| ||| :||
668 MEVKDYLTREVRKA 682

Db

RESULT 7

Q9A0Y9 PRELIMINARY; PRT; 364 AA.

AC Q9A0Y9; 17, Created)

DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)

DT 01-JUN-2001 (TRENBLrel. 19, Last annotation update)

DE Hypothetical protein SPY0549.

GN SPY0549.

OS Streptococcus pyogenes.

OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;

OC Streptococcus.

OX NCBI_TaxID=1314;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=SF370 / ATCC 700294 / Serotype M1;

RX MEDLINE=21192684; PubMed=1296296;

RA Ferreretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K., Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P., Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J., Yuan X., Clifton S.W., Roe B.A., McLaughlin R., "Complete genome sequence of an M1 strain of Streptococcus pyogenes.";

RT Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).

RL EMBL; AE006512; AAK33542.1; -

DR Hypothetical protein; Complete proteome.

KW Hypothetical protein; Complete proteome.

SQ SEQUENCE 364 AA; 41754 MW; 038B8D36F4234020 CRC64;

Query Match 52.0%; Score 39; DB 16; Length 364;
Best Local Similarity 53.8%; Pred. No. 62;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 EKQVYLTSAIRR 14
||| ||| :||
307 EKIQYTRSMYVK 319

Db

RESULT 8

Q88LL1 PRELIMINARY; PRT; 406 AA.

AC Q88LL1; 24, Created)

DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)

DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)

DE Hypothetical protein.

GN PP1920.

OS Pseudomonas putida (strain KT2440).

OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;

OC Pseudomonadaceae; Pseudomonas.

OX NCBI_TaxID=160488;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=22423060; PubMed=12534463;

RA Nelson K.E., Weiner C., Paulsen I.T., Dodson R.J., Hilbert H., Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M., Brinkac L., Beanan M., DeBoy R.T., Daugherty S., Kolonay J., Madupu R., Nelson W., White O., Peterson J., Khouri H., Hance I., Chris Lee P., Holtzapple E., Scanlan D., Tran K., Moazzes A., H., Uterback T., Rizzo M., Lee K., Kesack D., Moesti D., Wedler H., Lauber J., Stjepandic D., Hohseil J., Straetz M., Heim S., Kiewitz C., Eisen J., Tammis K.N., Duesterhoft A., Tummeler B., Fraser C.M.;

RT "Complete genome sequence and comparative analysis of the metabolically versatile Pseudomonas putida KT2440.";

RL Environ. Microbiol. 4:799-808(2002).

DR EMBL; AS016781; AAN67537.1; -

DR TIGR; PP1920; -

KW Hypothetical protein; Complete proteome.

SQ SEQUENCE 406 AA; 47318 MW; 7CDB8C30DFD0D3C6E2 CRC64;

Query Match 52.0%; Score 39; DB 16; Length 406;
Best Local Similarity 50.0%; Pred. No. 73;
Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRA 16
||| ||| :||
6 MEKIQYVDQSDPRAN 21

Db

RESULT 10

Q9VID2 PRELIMINARY; PRT; 481 AA.

AC Q9VID2; 13, Created)

DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)

DT 01-MAY-2000 (TRENBLrel. 13, Last annotation update)

DE Hypothetical protein PYRAB04950.

GN PYRAB04950 OR PAB0334.

OS Pyrococcus abyssi.

OC Archaea; Euryarchaeota; Thermococci; Thermococcaceae;

OC Pyrococcus.

OX NCBI_TaxID=29292;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CE5 / Orsay;

RA Helling R.;

RT "Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure and evolution.";

RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ248284; CAB49417.1; -

DR PIR; B75167; B75167.

QY 3 KQVYLTSAIRR 14
||| ||| :||
273 KKQVLTSAIRR 284

Db

RESULT 9

Q9AM36 PRELIMINARY; PRT; 421 AA.

AC Q9AM36; 17, Created)

DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)

DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)

DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)

DE [Fe] hydrogenase large subunit.

GN HYDA.

OS Desulfovibrio desulfuricans.

OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales;

OC Desulfovibrionaceae; Desulfovibrio.

OX NCBI_TaxID=876;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=G20;

RA Ringbauer J.A. Jr., Wall J.D.;

RT "[Fe] hydrogenase of Desulfovibrio desulfuricans G20.";

RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF31719; AAK11625.1; -

DR HSSP; P00193; 1DUR.

DR GO; GO:0005489; F:electron transporter activity; IEA.

DR GO; GO:0005118; F:electron transport; IEA.

DR InterPro; IPR001450; 4Fe4S_ferredoxin.

DR InterPro; IPR009016; Fe_hydrog.

DR InterPro; IPR004108; Fe_hyd_lg_C.

DR Pfam; PF00037; fer4; 2.

DR Pfam; PF02906; Fe_hyd_lg_C; 1.

DR PROSITE; PS00198; 4Fe4S_FERREDOXIN; 2.

DR 4Fe-4S; Iron; Iron-sulfur.

KW SEQUENCE 421 AA; 46120 MW; 1116557AB0C94219 CRC64;

Query Match 52.0%; Score 39; DB 2; Length 421;
Best Local Similarity 50.0%; Pred. No. 73;
Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRA 16
||| ||| :||
6 MEKIQYVDQSDPRAN 21

Db

RESULT 10

Q9VID2 PRELIMINARY; PRT; 481 AA.

AC Q9VID2; 13, Created)

DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)

DT 01-MAY-2000 (TRENBLrel. 13, Last annotation update)

DE Hypothetical protein PYRAB04950.

GN PYRAB04950 OR PAB0334.

OS Pyrococcus abyssi.

OC Archaea; Euryarchaeota; Thermococci; Thermococcaceae;

OC Pyrococcus.

OX NCBI_TaxID=29292;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CE5 / Orsay;

RA Helling R.;

RT "Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure and evolution.";

RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ248284; CAB49417.1; -

DR PIR; B75167; B75167.

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DR GO: GO:0016020; C-membrane; IEA.
DR GO: GO:0005267; F:potassium channel activity; IEA.
DR GO: GO:0006813; P:potassium ion transport; IEA.
DR InterPro: IPR001622; K-channel_pore.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 481 AA; 55655 MW; 685FE30056A45259 CRC64;

Query Match 52.0%; Score 39; DB 17; Length 481;
Best Local Similarity 50.8%; Pred. No. 84;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 EKQVYLTRSAIRRA 15
||:|:|:|:|:|
Db 38 EKIKYIKRAFERA 51

RESULT 11
Q86808 PRELIMINARY; PRT; 644 AA.
AC Q86808;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Beta/gamma-platein precursor.
OS Euplotes adiculatus.
OC Eukaryota; Alveolata; Ciliophora; Spirotrichea; Hypotrichia;
OC Euplotida; Euplotidae; Euplotes.
OX NCBI_TaxID=5940;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=12615971;
RA Kioetzel J.A., Baroin-Tourancheau A., Miceli C., Barchetta S.,
RA Farmer J., Banerjee D., Fleury-Aubusson A.;
RT "Cytoskeletal proteins with N-terminal signal peptides: plateins in
RT the ciliate Euplotes define a new family of articulins.";
RL J. Cell Sci. 116:1291-1303(2003).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22559397; PubMed=12674476;
RA Kioetzel J.A., Baroin-Tourancheau A., Miceli C., Barchetta S.,
RA Farmer J., Banerjee D., Fleury-Aubusson A.;
RT "Plateins: a novel family of signal peptide-containing articulins in
RT euplotid ciliates.";
RL J. Eukaryot. Microbiol. 50:19-33(2003).
DR EMBL; AF14991; AM94464.1; -.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 644 AA; 74972 MW; 7298E314EFB7417A CRC64;

Query Match 52.0%; Score 39; DB 5; Length 644;
Best Local Similarity 54.5%; Pred. No. 11e+02;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 3 KQVYLTRSAIR 13
||:|:|:|:|
Db 395 EIQVYTREAVR 405

RESULT 12
Q26525 PRELIMINARY; PRT; 119 AA.
AC Q26525;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein MTH425.
GN MTH425.
OS Methanobacterium thermoautotrophicum.
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
OC Methanobacteriaceae; Methanothermobacter.
CX NCBI_TaxID=167420;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN=Delta H;
RX MEDLINE=98037514; PubMed=9371463;
RA Smith D.R., Doucette-Stamm L.A., DeLoughery C., Lee H.-M., Dubois J.,
RA Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
RA Harrison D., Hoang L., Kestle P., Lum W., Pochier B., Qiu D.,
RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
RA Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
RA McDougall S., Shimer G., Goyal A., Pietrowski S., Church G.M.,
RA Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
RT "Complete genome sequence of Methanobacterium thermoautotrophicum
RT deltaH: functional analysis and comparative genomics.";
RL J. Bacteriol. 179:7135-7155(1997).
DR EMBL; AE000827; AAB84931.1; -.
DR FIR; D69155; D69155.
DR GO: GO:0005874; C:microtubule; IEA.
DR GO: GO:0005525; F:GTP binding; IEA.
DR GO: GO:0005198; F:structural molecule activity; IEA.
DR GO: GO:0007018; P:microtubule-based movement; IEA.
DR PROSITE; PS002453; Beta tubulin.
DR InterPro; IPR002228; TUBULIN_B_AUTOREG; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 119 AA; 13045 MW; DB5119ED7630F098 CRC64;

Query Match 50.7%; Score 38; DB 17; Length 119;
Best Local Similarity 37.5%; Pred. No. 29;
Matches 6; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 MEKVQLTRSAIRAS 16
||:|:|:|:|
Db 35 MDNIMYLTQSTVQSS 50

RESULT 13
Q974N9 PRELIMINARY; PRT; 122 AA.
ID Q974N9;
AC Q974N9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein SF0620.
GN SF0620.
OS Sulfolobus tokodaii.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OX NCBI_TaxID=111955;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=JCM 10545 / 7;
RX MEDLINE=21456156; PubMed=11572479;
RA Kawarabayashi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
RA Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.,
RA Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
RA Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
RA Aoki K.-I., Masuda S., Yanagi M., Nishimura M., Yamagishi A.,
RA Oshima T., Kikuchi H.;
RT "Complete genome sequence of an aerobic thermoacidophilic
RT Crenarchaeon, Sulfolobus tokodaii strain7.";
RL DNA Res. 8:123-140(2001).
DR EMBL; AP000983; BAB565618.1; -.
DR InterPro; IPR008301; UCP016498.
DR PIRSF; PIRSF016498; UCP016498; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 122 AA; 14467 MW; 988A31A274842EB3 CRC64;

Query Match 50.7%; Score 38; DB 17; Length 122;
Best Local Similarity 42.9%; Pred. No. 30;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 MEKVQLTRSAIRR 14
||:|:|:|:|
Db 26 MKKIKYLTEALMK 39

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RESULT 14
Q89J03 PRELIMINARY; PRT; 208 AA.
ID Q89J03
AC Q89J03
DT 01-JUN-2003 (TREMELrel. 24, Created)
DT 01-JUN-2003 (TREMELrel. 24, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE BL15481 protein.
GN BL15481
OS Bradyrhizobium japonicum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Bradyrhizobium.
OX NCBI_TaxID=375;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=USDA 110;
RX MEDLINE=22484998; PubMed=12597275;
RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
RA Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
RA Kohara M., Matsumoto M., Shimpou S., Tsuruoka H., Wada T., Yamada M.,
RA Tabata S.;
RA "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
Bradyrhizobium japonicum USDA110.";
RL DNA Res. 9:189-197(2002).
DR EMBL; AP005955; BAC50746.1; -.
KW Complete proteome.
SQ SEQUENCE 208 AA; 22494 MW; E461C88B14793C7A CRC64;

Query Match 50.7%; Score 38; DB 16; Length 208;
Best Local Similarity 72.7%; Pred. No. 53;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 QYLTRSAIRRA 15
Db 74 QELTRALRRA 84

RESULT 15
Q7UFR1 PRELIMINARY; PRT; 211 AA.
ID Q7UFR1
AC Q7UFR1
DT 01-OCT-2003 (TREMELrel. 25, Created)
DT 01-OCT-2003 (TREMELrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Thymidine kinase Tdk (EC 2.7.1.21).
DR TDK OR RB9399.
GN Rhodospirillum rubrum.
OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
OC Planctomycetaceae; Fireillula.
OX NCBI_TaxID=117;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1;
RX MEDLINE=22735913; PubMed=12835416;
RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
RA Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,
RA Schlesner H., Amann R., Reinhardt R.;
RA "Complete genome sequence of the marine planctomycete Fireillula sp.
strain 1.";
RT Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
RL EMBL; BX294147; CAD7862.1; -.
KW Kinase; Transferase; Complete proteome.
SQ SEQUENCE 211 AA; 23976 MW; 2FF54BF16F094376 CRC64;

Query Match 50.7%; Score 38; DB 16; Length 211;
Best Local Similarity 37.5%; Pred. No. 54;
Matches 6; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 1 MEKQYLTRSAIRRAS 16
Db 86 VDEAQFLTRQVRLS 101

RESULT 16
Q9HF62 PRELIMINARY; PRT; 252 AA.
ID Q9HF62
AC Q9HF62
DT 01-MAR-2001 (TREMELrel. 16, Created)
DT 01-MAR-2001 (TREMELrel. 16, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE YC1016C (Fragment).
GN YC1016C.
OS Ashbya gossypii (Yeast) (Bremothecium gossypii).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Ashbya.
OX NCBI_TaxID=33169;
RN [1]
RP SEQUENCE FROM N.A.
RC Wendlend J., Philippsen P.;
RX "Isolation and characterization of the Ashbya gossypii BUD3 gene.";
RT Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF210625; AAG41241.1; -.
FT NON TER. 252 252
SQ SEQUENCE 252 AA; 27793 MW; 20B2C7F284042B76 CRC64;

Query Match 50.7%; Score 38; DB 3; Length 252;
Best Local Similarity 54.5%; Pred. No. 66;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 EKQYLTSAIRSAI 12
Db 228 ERIQYLSRSTL 238

RESULT 17
Q99ZW6 PRELIMINARY; PRT; 376 AA.
ID Q99ZW6
AC Q99ZW6
DT 01-JUN-2001 (TREMELrel. 17, Created)
DT 01-JUN-2001 (TREMELrel. 17, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE Putative coproporphyrinogen III oxidase (EC 1.3.3.3).
GN HEMN OR SPV1040.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SF370 / ATCC 700294 / Serotype M1;
RX MEDLINE=21192684; PubMed=11296296;
RA Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,
RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
RA "Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
DR EMBL; AB006549; AAK33932.1; -.
DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:0004109; F:coproporphyrinogen oxidase activity; IEA.
DR GO; GO:0018491; F:oxidoreductase activity; IEA.
DR GO; GO:0006779; P:porphyrin biosynthesis; IEA.
DR InterPro; IPR006638; EIP3.
DR InterPro; IPR004559; HemN rel.
DR InterPro; IPR007197; Radical SAM.
DR Pfam; PF04055; Radical SAM; I.
DR SMART; SM00729; EIP3; I.
DR TIGRfams; TIGR00539; hemN rel; I.
KW Oxidoreductase; Complete proteome.
SQ SEQUENCE 376 AA; 43111 MW; 737548C68DB358E3 CRC64;

Query Match 50.7%; Score 38; DB 16; Length 376;
Best Local Similarity 53.3%; Pred. No. 1e+02;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 EKQYLTSAIRRAS 16

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Db      102 EKIAVLQSAVNRIIS 116
      |||:|||||:|
RESULT 18
Q8P177 PRELIMINARY; PRT; 376 AA.
ID Q8P177
AC Q8P177
DT 01-OCT-2002 (TREMELrel. 22, Created)
DT 01-OCT-2002 (TREMELrel. 22, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE Putative coproporphyrinogen III oxidase.
GN HEMN OR SPYM18 1022.
OS Streptococcus pyogenes (serotype M18).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=186103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS8232 / Serotype M18;
RX MEDLINE=21927593; PubMed=11917108;
RA Smoot J.C., Barbican K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S.,
RA Sylva G.L., Sturdevant D.E., Rickielfs S.M., Porcella S.F.,
RA Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,
RA Kapur V., Daly J.A., Veasy L.G., Musser J.M.;
RT "Genome sequence and comparative microarray analysis of serotype M18
RT group A Streptococcus strains associated with acute rheumatic fever
RT outbreaks.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002).
DR EMBL; AE010030; AAL9657.1; -
DR GO; GO:0005733; C:cytoplasm; IEA.
DR GO; GO:0004109; F:coproporphyrinogen oxidase activity; IEA.
DR GO; GO:0006779; F:porphyrin biosynthesis; IEA.
DR InterPro; IPR004559; HemN rel.
DR Pfam; PF04055; Radical SAM; I.
DR TIGRFAMs; TIGR00539; hemN_rel; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 376 AA; 43093 MW; 7236F821EE82EE5 CRC64;

Query Match 50.7%; Score 38; DB 16; Length 376;
Best Local Similarity 53.3%; Pred. No. 1e+02;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 EKQVYLTRSAIRRAS 16
Db 102 EKIAVLQSAVNRIIS 116
      |||:|||||:|

RESULT 19
Q878L1 PRELIMINARY; PRT; 398 AA.
ID Q878L1
AC Q878L1
DT 01-JUN-2003 (TREMELrel. 24, Created)
DT 01-JUN-2003 (TREMELrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Putative coproporphyrinogen III oxidase.
GN SPS1180.
OS Streptococcus pyogenes (serotype M3).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=198466;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SSI-1 / Serotype M3;
RA Nakagawa I., Kurokawa K., Nakata M., Tomiyasu Y., Yanashita A.,
RA Yamazaki K., Okahashi N., Kawabata S., Yasunaga T., Hattori M.,
RA Hayashi H., Kamada S.;
RT "The genome of invasive Streptococcus pyogenes; a comparative analysis
RT of S. pyogenes SSI-1, SF370 and MGAS8232."
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF005144; BAC64275.1; -
DR InterPro; IPR007197; Radical SAM.

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DR Pfam; PF04055; Radical SAM; 1.
SQ SEQUENCE 398 AA; 45941 MW; 669A0563D1206261 CRC64;

Query Match 50.7%; Score 38; DB 16; Length 398;
Best Local Similarity 53.3%; Pred. No. 1e+02;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 EKQVYLTRSAIRRAS 16
Db 124 EKIAVLQSAVNRIIS 138
      |||:|||||:|

RESULT 20
Q8K7R5 PRELIMINARY; PRT; 408 AA.
ID Q8K7R5
AC Q8K7R5
DT 01-OCT-2002 (TREMELrel. 22, Created)
DT 01-OCT-2002 (TREMELrel. 22, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE Putative coproporphyrinogen III oxidase.
GN HEMN OR SPYM3 0673.
OS Streptococcus pyogenes (serotype M3).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=198466;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS315 / Serotype M3;
RX MEDLINE=22133808; PubMed=12122206;
RA Beres S.B., Sylva G.L., Barbican K.D., Lei B., Hoff J.S.,
RA Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D.,
RA Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
RA Schlievert P.M., Musser J.M.;
RT "Genome sequence of a serotype M3 strain of group A Streptococcus;
RT phage-encoded toxins, the high-virulence phenotype, and clone
RT emergence.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083(2002).
DR EMBL; AE014150; AAM79280.1; -
DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:0004109; F:coproporphyrinogen oxidase activity; IEA.
DR GO; GO:0006779; F:porphyrin biosynthesis; IEA.
DR InterPro; IPR006638; Elp3.
DR InterPro; IPR004559; HemN rel.
DR InterPro; IPR007197; Radical SAM.
DR Pfam; PF04055; Radical SAM; I.
DR SMART; SM00729; Elp3; I.
DR TIGRFAMs; TIGR00539; hemN_rel; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 408 AA; 46987 MW; C3113FEA0B1A5AD CRC64;

Query Match 50.7%; Score 38; DB 16; Length 408;
Best Local Similarity 53.3%; Pred. No. 1e+02;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 EKQVYLTRSAIRRAS 16
Db 134 EKIAVLQSAVNRIIS 148
      |||:|||||:|

RESULT 21
Q9F8B7 PRELIMINARY; PRT; 578 AA.
ID Q9F8B7
AC Q9F8B7
DT 01-MAR-2001 (TREMELrel. 16, Created)
DT 01-MAR-2001 (TREMELrel. 16, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE DeoR regulator.
OS Streptococcus agalactiae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1311;
RN [1]
RP SEQUENCE FROM N.A.

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RX MEDLINE=20402586; PubMed=10944228;
RA Lachenauer C.S., Creti R., Michel J.L., Madoff L.C.;
RT "Mosaicism in the alpha-like protein genes of group B streptococci.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:9630-9635(2000).
CC -1- SIMILARITY: BELONGS TO THE DEOR FAMILY OF TRANSCRIPTIONAL
CC REGULATORS.
DR EMBL; AF248038; AACG9976.1; -;
DR GO; GO:0005222; C:intracellular; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR InterPro; IPR001034; HTH_Deor.
DR Pfam; PF00455; deor; 1.
DR SMART; SMO0420; HTH_DEOR; 1.
DR PROSITE; PS00894; HTH DEOR FAMILY; 1.
KW DNA-binding; Transcription; Transcription regulation.
SQ SEQUENCE 578 AA; 66770 MW; CIDE74FB5943B8E3 CRC64;

Query Match 50.7%; Score 38; DB 2; Length 578;
Best Local Similarity 50.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 3 KQVLTSAIRRAS 16
DB 306 KIQFLTRQFIKQIS 319

RESULT 22
Q84S07
ID Q84S07 PRELIMINARY; PRT; 882 AA.
AC Q84S07
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein OSJNB0047D08.27.
GN OSJNB0047D08.27.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M.,
RA Overton II L.L., Tsitrin T., Kim M.M., Bera J.J., Jin S.S.,
RA Fadrosch D.W., Tallon L.J., Koo H., Zismann V., Hsiao J., Blunt S.,
RA Vanaken S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V.,
RA Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J.,
RA White O., Salzberg S.L., Fraser C.M.;
RT "Oryza sativa chromosome 3 BAC OSJNB0047D08 genomic sequence.";
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Buell R.;
RA Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
RW Hypothetical protein.
KW Hypothetical protein.
SQ SEQUENCE 882 AA; 96573 MW; 5CDCB01A2569CEC0 CRC64;

Query Match 50.7%; Score 38; DB 10; Length 882;
Best Local Similarity 56.2%; Pred. No. 2.5e+02;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 MEKVLTSAIRRAS 16
DB 300 VEYSQLTRQAAIRAN 315

RESULT 23
Q8MVG5
ID Q8MVG5 PRELIMINARY; PRT; 1223 AA.

AC Q8MVG5;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to Homo sapiens (Human). similar to SWI/SNF related, matrix
DE associated, actin dependent regulator of chromatin, subfamily C,
DE member 1.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AX4;
RX MEDLINE=22092622; PubMed=12097910;
RA Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P.,
RA Lehmann R., Baumgart C., Farra G., Guigo R., Kumpf K.,
RA Tunggal B., Cox B., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.;
RT "Sequence and analysis of chromosome 2 of Dictyostelium discoideum.";
RL Nature 418:79-85(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AX4;
RA Baumgart C.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC116989; AAM43749.2; -;
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001005; Myb_DNA_binding.
DR InterPro; IPR001873; S_mold_repeat.
DR Pfam; PF00526; S_mold_repeat; 13.
DR SMART; SMO0717; SANT; 1.
DR PROSITE; PS00090; MYB_3; 1.
SQ SEQUENCE 1223 AA; 136240 MW; B7D92B2325F39C72 CRC64;

Query Match 50.7%; Score 38; DB 5; Length 1223;
Best Local Similarity 80.0%; Pred. No. 3.6e+02;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 QYLTSAIRR 14
DB 696 QYLTSAIRR 705

RESULT 24
Q8DJ60
ID Q8DJ60 PRELIMINARY; PRT; 1541 AA.
AC Q8DJ60;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Ferredoxin-dependent glutamate synthase.
GN GLSF OR TLH1368.
OS Synechococcus elongatus (Thermosynechococcus elongatus).
OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
OX NCBI_TaxID=32046;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BP-1;
RX MEDLINE=22225144; PubMed=12240834;
RA Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S.,
RA Watanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y.,
RA Kiyokawa C., Kohara M., Matsumoto M., Yamada M., Tabata S.;
RA Shimo S., Sugimoto M., Takeuchi C., Takeuchi C., Yamada S.;
RT "Complete genome structure of the thermophilic cyanobacterium
RT Thermosynechococcus elongatus BP-1.";
RL DNA Res. 9:123-130(2002).
DR EMBL; AP005373; BAC08920.1; -;
DR GO; GO:0015930; F:glutamate synthase activity; IEA.
DR GO; GO:0006537; P:glutamate biosynthesis; IEA.
DR GO; GO:0006807; P:nitrogen metabolism; IEA.
DR InterPro; IPR002489; DUF14.
DR InterPro; IPR002932; Glu_synthase.
DR InterPro; IPR006982; Glu_synth_cent.

DR InterPro; IPR006981; Glu synth NTN.
 DR Pfam; PF01645; Glu synthase; 1
 DR Pfam; PF04897; Glu synth NTN; 1
 DR Pfam; PF04898; Glu synth NTN; 1
 DR Pfam; PF01493; GXGKG; 1
 KW Complete proteome.
 SQ SEQUENCE 1541 AA; 168017 MW; 9CB26077859306A6 CRC64;

Query Match 50.7%; Score 38; DB 16; Length 1541;
 Best Local Similarity 53.3%; Pred. No. 4.6e+02;
 Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 MEKQVLTSAIRRA 15
 DB 162 LERQLYTRKRIERA 176

RESULT 25

Q7UWM3 PRELIMINARY; PRT; 68 AA.
 AC Q7UWM3; 2003 (TREMBLrel. 25, Created)
 DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 GN R51931.
 OS Rhodopirellula baltica.
 OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
 OC Planctomycetaceae; Firellula.
 OX NCBI_TaxID=117;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1;
 RX MEDLINE=2273513; PubMed=12835416;
 RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
 Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,
 Schliesner H., Amann R., Reinhardt R.;
 RT "Complete genome sequence of the marine planctomycete Firellula sp.
 strain 1.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
 DR EMBL; BX294136; CAD72339.1; -;
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 68 AA; 7494 MW; 7EC1DFP98DBSF67C CRC64;

Query Match 50.0%; Score 37.5; DB 16; Length 68;
 Best Local Similarity 66.7%; Pred. NO. 20;
 Matches 10; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

QY 3 KVOYLTRSAI-REAS 16
 DB 44 KLTFLSRSAISRRAS 58

Search completed: October 1, 2004, 12:17:32
 Job time : 51.8 secs

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OM protein - protein search, using sw model

Run on: October 1, 2004, 11:56:15 ; Search time 63.2 Seconds
(without alignments)
71.531 Million cell updates

Title: US-09-830-779-18_COPY_1_16
Perfect score: 76
Sequence: 1 MEKVQYLTRSAIRRAE 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : A Geneseq 29Jan04:*

1: geneseqp1980s:
2: geneseqp1990s:
3: geneseqp2000s:
4: geneseqp2001s:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query		DB	ID	Description
	Score	Match Length			
1	76	100.0	35	3	AAY71014 Penetrati
2	76	100.0	36	3	AAY71013 Penetrati
3	76	100.0	52	5	ABb79404 Human pho
4	76	100.0	79	3	AAY71018 H6 tagged
5	71	93.4	16	3	AAY71009 Human Ph
6	71	93.4	35	3	AAY71012 Penetrati
7	71	93.4	36	3	AAY71011 Penetrati
8	71	93.4	36	8	ADE45175 Human SER
9	71	93.4	52	3	AAY71006 Human mut
10	71	93.4	52	3	AAY71003 Human mut
11	71	93.4	52	3	AAY71002 Human Ph
12	71	93.4	52	5	ABp06592 Human ORP
13	71	93.4	52	8	ADE45172 Mouse SER
14	71	93.4	52	8	ADE45170 Rabbit SE
15	71	93.4	52	8	ADE45171 Rat SERCA
16	71	93.4	52	8	ADE45167 Human SER
17	71	93.4	79	3	AAY71019 H6 tagged
18	71	93.4	79	3	AAY71017 Hexahisti
19	68	89.5	52	8	ADE45168 Pig SERCA
20	68	89.5	52	8	ADE45169 Pig SERCA
21	67	88.2	52	8	ADE45173 Chicken S
22	66	86.8	52	3	AAY71005 Human mut
23	65	85.5	52	3	AAY71004 Human mut
24	62	81.6	52	3	AAY71007 Human mut
25	42	55.3	116	7	ADC87928 Ribosomal

99 35 46.1 361 5 ABG91555
100 35 46.1 387 4 AB965660

ALIGNMENTS

RESULT 1
AA71014
ID AAY71014 standard; peptide; 35 AA.

AC AAY71014;
XX
DT 29-AUG-2000 (first entry)
XX
DE Penetratin-based recombinant phospholamban peptide, TAT-mutant PLB.
XX
KW Phospholamban; PLB; human; sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a;
KW cardiant; cardiomyocyte; transport peptide; penetratin; cargo peptide;
KW contractilin; cardiac contractility; inhibitor; cardiac disease; mutant;
KW treatment; heart failure; myocardial dysfunction; recombinant protein;
KW HIV; TAT protein.
XX

OS Homo sapiens.
OS Human immunodeficiency virus.
XX
FH Key Location/Qualifiers
FT Region 5..15
FT /note= "Corresponds to denatured human immunodeficiency
FT virus (HIV) TAT protein"
FT Region 16..35
FT /note= "Corresponds to mutant human phospholamban (PLB)
FT amino terminal peptide"
FT Misc-difference 31
FT /note= "Wild type Ser replaced with Glu"

PN WO200025804-A2.
XX
PD 11-MAY-2000.
XX
PF 02-NOV-1999; 99WO-US025692.
XX
PR 02-NOV-1998; 98US-0106718P.
PR 27-JUL-1999; 99US-0145883P.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Chien K, Dillman W, Minamisawa S, He H, Hoshijima M, Meyer M;
PI Scott C, Wang Y, Silverman GJ;
XX
DR WPI; 2000-365393/31.
XX

PT Treating cardiac diseases, e.g. heart failure or myocardial dysfunction
PT comprises enhancing cardiac contractility by inhibiting interaction
PT between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine
PT triphosphatase.
XX

PS Example 5; Page 53; 56pp; English.
XX
XX The patent discloses a method for the treatment of heart failure, using
CC small peptide complexes and recombinant proteins, that induces
CC phospholamban (PLB) deficiency and inhibits the interaction between PLB
CC and sarcoplasmic reticulum Ca 2+ ATPase (SERCA2a) within cardiomyocytes.
CC The peptide complex comprises of transport peptide like penetratin and
CC cargo peptide selected from mutant PLB, native PLB or antibody against
CC PLB protein (contractilin). Penetratin-PLB peptide functions as a
CC dominant negative inhibitor of PLB-SERCA2a interaction, enhances cardiac
CC contractility and reduces blood pressure. This method is useful for the
CC treatment of cardiac disease e.g. heart failure and myocardial
CC dysfunction. The present sequence is the penetratin-based recombinant
CC peptide TAT-mutant PLB, comprising the amino terminal end of human PLB
CC mutant (Ser1Glu) protein, attached to the 3' end of denatured human
CC immunodeficiency virus (HIV), TAT protein. Penetratin is a class of

CC peptides, with translocating properties having the ability to carry
CC hydrophilic compounds across the plasma membrane
XX
SQ Sequence 35 AA;

Query Match Similarity 100.0%; Score 76; DS 3; Length 35;
Best Local Similarity 100.0%; Pred. NO. 2.2e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKQYLTRSAIRAE 16
DB 16 MEKQYLTRSAIRAE 31

RESULT 2

AA71013
ID AAY71013 standard; peptide; 36 AA.

AC AAY71013;
XX
DT 29-AUG-2000 (first entry)
XX
DE Penetratin-based recombinant phospholamban peptide, mutant PLB-ANT.
XX
KW Phospholamban; PLB; human; sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a;
KW cardiant; cardiomyocyte; transport peptide; penetratin; cargo peptide;
KW contractilin; cardiac contractility; inhibitor; cardiac disease; mutant;
KW treatment; heart failure; myocardial dysfunction; recombinant protein;
KW fruit fly; ANT; antennapedia.
XX

OS Homo sapiens.
OS Drosophila sp.
XX
FH Key Location/Qualifiers
FT Region 1..20
FT /note= "Corresponds to mutant human phospholamban (PLB)
FT amino terminal peptide"
FT Misc-difference 16
FT /note= "Wild type Ser replaced with Glu"
FT Region 21..36
FT /note= "Corresponds to Drosophila antennapedia (ANT)
FT transport peptide"

PN WO200025804-A2.

XX 11-MAY-2000.

XX 02-NOV-1999; 99WO-US025692.

XX 02-NOV-1998; 98US-0106718P.

XX 27-JUL-1999; 99US-0145883P.

XX (REGC) UNIV CALIFORNIA.

XX Chien K, Dillman W, Minamisawa S, He H, Hoshijima M, Meyer M;

XX Scott C, Wang Y, Silverman GJ;

XX WPI; 2000-365393/31.

XX Treating cardiac diseases, e.g. heart failure or myocardial dysfunction
XX comprises enhancing cardiac contractility by inhibiting interaction
XX between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine
XX triphosphatase.

XX Example 5; Page 53; 56pp; English.

XX The patent discloses a method for the treatment of heart failure, using
CC small peptide complexes and recombinant proteins, that induces
CC phospholamban (PLB) deficiency and inhibits the interaction between PLB
CC and sarcoplasmic reticulum Ca 2+ ATPase (SERCA2a) within cardiomyocytes.
CC The peptide complex comprises of transport peptide like penetratin and
CC cargo peptide selected from mutant PLB, native PLB or antibody against
CC PLB protein (contractilin). Penetratin-PLB peptide functions as a

CC dominant negative inhibitor of PLB-SERCA2a interaction, enhances cardiac
 CC contractility and reduces blood pressure. This method is useful for the
 CC treatment of cardiac disease e.g. heart failure and myocardial
 CC dysfunction. The present sequence is the penetratin-based recombinant
 CC peptide, mutant PLB-ANT, comprising the amino terminal end of human PLB
 CC mutant (Ser16Glu) protein, attached to the 5' end of the Drosophila
 CC antennapedia (ANT) transport peptide. Penetratin is a class of peptides,
 CC with translocating properties having the ability to carry hydrophilic
 CC compounds across the plasma membrane
 XX
 SQ Sequence 36 AA;

Query Match 100.0%; Score 76; DB 3; Length 36;
 Best Local Similarity 100.0%; Pred. No. 2.3e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 MEKVQLTRSAIRRAE 16
 |||||
 DB 1 MEKVQLTRSAIRRAE 16
 |||||

RESULT 3
 ABB79404
 ID ABB79404 standard; peptide; 52 AA.
 AC ABB79404;
 XX
 DT 24-JUN-2002 (first entry)
 XX

DE Human phospholamban pseudophosphorylation mutant S16E PLB.
 XX
 XX Human; phospholamban; PLB; cardiant; heart disease; gene therapy;
 KW cardiac function; mutant; mutein.
 KW
 XX Homo sapiens.
 OS

EH Key Location/Qualifiers
 FT Misc-difference 16 /note= "Wildtype Ser substituted by Glu"
 FT
 XX US2002032167-A1.
 XX 14-MAR-2002.
 XX

PF 11-SEP-2001; 2001US-00954571.
 XX
 PR 11-SEP-2000; 2000US-0231821P.
 XX
 PA (CHIE/) CHIEN K R.
 PA (HOSH/) HOSHJIMA M.
 PA (ROSS/) ROSS J.
 PA (IKED/) IKEDA Y.

XX Chien KR, Hoshijima M, Ross J, Ikeda Y;
 DR WPI; 2002-361185/39.
 XX
 PT Delivering a dose of a gene expression cassette in a fluid selectively to
 PT heart for sustained expression, useful for improving or enhancing cardiac
 PT function, by employing a viral vector together with a vascular
 PT permeabilizing agent.
 XX

PS Example 6; Fig 1; 12pp; English.
 XX
 CC The invention relates to delivering a therapeutic dose of a gene
 CC expression cassette in a fluid selectively to heart for sustained
 CC expression, comprising employing a viral vector together with a vascular
 CC permeabilizing agent. The method is useful for gene therapy delivering
 CC genes for improving or enhancing cardiac function, particularly in
 CC hamster models of heart disease. The present sequence is that of a
 CC pseudophosphorylation mutant of phospholamban (S16EPLB). This point
 CC mutant is among a number of dominant negative mutants identified and
 CC characterised in WO00/25804 and used in the method of the present

CC invention
 XX
 SQ Sequence 52 AA;

Query Match 100.0%; Score 76; DB 5; Length 52;
 Best Local Similarity 100.0%; Pred. No. 3.4e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 MEKVQLTRSAIRRAE 16
 |||||
 DB 1 MEKVQLTRSAIRRAE 16
 |||||

RESULT 4
 AAY71018
 ID AAY71018 standard; protein; 79 AA.

XX AAY71018;

XX 29-AUG-2000 (first entry)

DT H6 tagged penetratin-based recombinant protein, H6-(S16E)mutantPLB-ANT.
 XX
 XX Phospholamban; PLB; human; sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a;
 KW cardiant; cardiomyocyte; transport peptide; penetratin; cargo peptide;
 KW contractilin; cardiac contractility; inhibitor; cardiac disease; mutant;
 KW treatment; heart failure; myocardial dysfunction; recombinant protein;
 KW fruit fly; ANT; antennapedia; H6 tag; hexahistidine.

XX Homo sapiens.
 OS
 OS Drosophila sp.
 OS Synthetic.

EH Key Location/Qualifiers

FT Region 1..52 /note= "Corresponds to mutant human phospholamban (PLB)
 FT protein"
 FT Misc-difference 16
 FT /note= "Wild type Ser replaced with Glu"
 FT Region 53..58 /note= "Corresponds to hexahistidine tag (H6)"
 FT Region 63..78 /note= "Corresponds to Drosophila antennapedia (ANT)
 FT transport peptide"

XX WO2000025804-A2.

XX 11-MAY-2000.

XX 02-NOV-1999; 99WO-US025692.

XX 02-NOV-1998; 98US-0106718P.

XX 27-JUL-1999; 99US-0145883P.

XX (REGC) UNIV CALIFORNIA.

XX Chien K, Dillman W, Minamisawa S, He H, Hoshijima M, Meyer M;
 PI Scott C, Wang Y, Silverman GJ;

XX WPI; 2000-365393/31.

XX Treating cardiac diseases, e.g. heart failure or myocardial dysfunction
 PT comprises enhancing cardiac contractility by inhibiting interaction
 PT between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine
 PT triphosphatase.

XX Example 6; Page 55; 56pp; English.

XX The patent discloses a method for the treatment of heart failure, using
 CC small peptide complexes and recombinant proteins, that induces
 CC phospholamban (PLB) deficiency and inhibits the interaction between PLB
 CC and sarcoplasmic reticulum Ca 2+ ATPase (SERCA2a) within cardiomyocytes.
 CC The peptide complex comprises of transport peptide like penetratin and

CC cargo peptide selected from mutant PLB, native PLB or antibody against
 CC PLB protein (contractilin). Penetratin-PLB peptide functions as a
 CC dominant negative inhibitor of PLB-SERCA2a interaction, enhances cardiac
 CC contractility and reduces blood pressure. This method is useful for the
 CC treatment of cardiac disease e.g. heart failure and myocardial
 CC dysfunction. The present sequence is the hexahistidine (H6) tagged
 CC penetratin-based recombinant protein H6-mutant PLB-ANT, comprising the
 CC human mutant (Ser16Glu) PLB protein and Drosophila antennapedia (ANT)
 CC transport peptide attached by a hexahistidine tag. This sequence is
 CC expressed in *Escherichia coli* cells

XX SQ Sequence 79 AA;

Query Match 100.0%; Score 76; DB 3; Length 79;
 Best Local Similarity 100.0%; Pred. No. 5.2e-06; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 0;

QY 1 MEKVQLTRSAIRRAE 16
 |||||
 Db 1 MEKVQLTRSAIRRAE 16

RESULT 5

AAAY71009 standard; peptide; 16 AA.

XX AC AAY71009;
 XX DT 29-AUG-2000 (first entry)
 XX DE Human Phospholamban (PLB) cargo peptide.
 XX KW Phospholamban; PLB; human; sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a;
 KW cardiant; cardiomyocyte; transport peptide; penetratin; cargo peptide;
 KW contractilin; cardiac contractility; inhibitor; cardiac disease;
 KW treatment; heart failure; myocardial dysfunction.

XX OS Homo sapiens.

XX PN W0200025804-A2.

XX PD 11-MAY-2000.

XX PF 02-NOV-1999; 99WO-US025692.

XX PR 02-NOV-1998; 98US-0106718P.

XX PR 27-JUL-1999; 99US-0145883P.

XX PA (REGC) UNIV CALIFORNIA.

XX PI Chien K, Dillman W, Minamisawa S, He H, Hoshijima M, Meyer M;
 XX PI Scott C, Wang Y, Silverman GJ;

XX DR WPI; 2000-365393/31.

XX PT Treating cardiac diseases, e.g. heart failure or myocardial dysfunction
 PT comprises enhancing cardiac contractility by inhibiting interaction
 PT between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine
 triphosphatase.

XX PS Example 4; Page 50; 56pp; English.

XX PS The patent discloses a method for the treatment of heart failure, using
 CC small peptide complexes and recombinant proteins, that induces
 CC phospholamban (PLB) deficiency and inhibits the interaction between PLB
 CC and sarcoplasmic reticulum Ca 2+ ATPase (SERCA2a) within cardiomyocytes.
 CC The peptide complex comprises of transport peptide like penetratin and
 CC cargo peptide selected from mutant PLB, native PLB or antibody against
 CC PLB protein (contractilin). Penetratin-PLB peptide functions as a
 CC dominant negative inhibitor of PLB-SERCA2a interaction, enhances cardiac
 CC contractility and reduces blood pressure. This method is useful for the
 CC treatment of cardiac disease e.g. heart failure and myocardial
 CC dysfunction. The present amino acid sequence is the cargo peptide from

CC human PLB amino terminal residues 1-16. It could be derived from any
 CC segment of wild type or mutant PLB protein. The cargo peptide is linked
 CC to the transport peptide by a covalent linkage

XX SQ Sequence 16 AA;

Query Match 93.4%; Score 71; DB 3; Length 16;
 Best Local Similarity 100.0%; Pred. No. 7.6e-06; Indels 0; Gaps 0;
 Matches 15; Conservative 0; Mismatches 0;

QY 1 MEKVQLTRSAIRRA 15
 |||||
 Db 1 MEKVQLTRSAIRRA 15

RESULT 6

AAAY71012 standard; peptide; 35 AA.

XX AC AAY71012;

XX DT 29-AUG-2000 (first entry)

XX DE Penetratin-based recombinant phospholamban peptide, TAT-PLB.

XX KW Phospholamban; PLB; human; sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a;
 KW cardiant; cardiomyocyte; transport peptide; penetratin; cargo peptide;
 KW contractilin; cardiac contractility; inhibitor; cardiac disease;
 KW treatment; heart failure; myocardial dysfunction; recombinant peptide;
 KW HIV; TAT protein.

XX OS Homo sapiens.

XX OS Human immunodeficiency virus.

XX FH Key Location/Qualifiers

XX FT Region 5..15

XX FT /note= "Corresponds to denatured human immunodeficiency
 virus (HIV) TAT protein"

XX FT Region 16..35

XX FT /note= "Corresponds to human phospholamban (PLB) amino
 terminal peptide"

XX PN W0200025804-A2.

XX PD 11-MAY-2000.

XX PF 02-NOV-1999; 99WO-US025692.

XX PR 02-NOV-1998; 98US-0106718P.

XX PR 27-JUL-1999; 99US-0145883P.

XX PA (REGC) UNIV CALIFORNIA.

XX PI Chien K, Dillman W, Minamisawa S, He H, Hoshijima M, Meyer M;
 XX PI Scott C, Wang Y, Silverman GJ;

XX DR WPI; 2000-365393/31.

XX PT Treating cardiac diseases, e.g. heart failure or myocardial dysfunction
 PT comprises enhancing cardiac contractility by inhibiting interaction
 PT between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine
 triphosphatase.

XX PS Example 5; Page 52; 56pp; English.

XX PS The patent discloses a method for the treatment of heart failure, using
 CC small peptide complexes and recombinant proteins, that induces
 CC phospholamban (PLB) deficiency and inhibits the interaction between PLB
 CC and sarcoplasmic reticulum Ca 2+ ATPase (SERCA2a) within cardiomyocytes.
 CC The peptide complex comprises of transport peptide like penetratin and
 CC cargo peptide selected from mutant PLB, native PLB or antibody against
 CC PLB protein (contractilin). Penetratin-PLB peptide functions as a
 CC dominant negative inhibitor of PLB-SERCA2a interaction, enhances cardiac

CC contractility and reduces blood pressure. This method is useful for the
 CC treatment of cardiac disease e.g. heart failure and myocardial
 CC dysfunction. The present sequence is the penetratin-based recombinant
 CC peptide TAR-PLB, comprising the amino terminal end of human PLB native
 CC protein, attached to the 3' end of denatured human immunodeficiency virus
 CC (HIV) TAR protein. Penetratin is a class of peptides, with translocating
 CC properties having the ability to carry hydrophilic compounds across the
 CC plasma membrane

XX Sequence 35 AA;

Query Match 93.4%; Score 71; DB 3; Length 35;

Best Local Similarity 100.0%; Pred. No. 1.8e-05;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRA 15

DB 16 MEKVQYLTRSAIRRA 30

RESULT 7

AAAY71011

ID AAY71011 standard; peptide; 36 AA.

XX AAY71011;

AC AAY71011;

DT 29-AUG-2000 (first entry)

DE Penetratin-based recombinant phospholamban peptide, PLB-ANT.

XX Phospholamban; PLB; human; sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a;

XX cadiant; cardiomyocyte; transport peptide; penetratin; cargo peptide;

XX contractilin; cardiac contractility; inhibitor; cardiac disease;

XX treatment; heart failure; myocardial dysfunction; recombinant peptide;

XX fruit fly; antennapedia; ANT.

XX Homo sapiens.

OS Drosophila sp.

XX Key

XX Region

XX Location/Qualifiers

XX 1..20

XX /note= "Corresponds to human phospholamban (PLB) amino

XX terminal peptide"

XX 21..36

XX /note= "Corresponds to Drosophila antennapedia (ANT)

XX transport peptide"

XX WO200025804-A2.

XX 11-MAY-2000.

XX 02-NOV-1999; 99WO-US025692.

XX 02-NOV-1998; 98US-0106718P.

XX 27-JUL-1999; 99US-0145883P.

XX (REGC) UNIV CALIFORNIA.

XX Chien K, Dillman W, Minamisawa S, He H, Hoshijima M, Meyer M;

XX Scott C, Wang Y, Silverman GJ;

XX WPI; 2000-365393/31.

XX Treating cardiac diseases, e.g. heart failure or myocardial dysfunction

XX comprises enhancing cardiac contractility by inhibiting interaction

XX between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine

XX triphosphatase.

XX Example 5; Page 52; 56pp; English.

XX The patent discloses a method for the treatment of heart failure, using

XX small peptide complexes and recombinant proteins, that induces

XX phospholamban (PLB) deficiency and inhibits the interaction between PLB

CC

CC and sarcoplasmic reticulum Ca 2+ ATPase (SERCA2a) within cardiomyocytes.
 CC The peptide complex comprises of transport peptide like penetratin and
 CC cargo peptide selected from mutant PLB, native PLB or antibody against
 CC PLB protein (contractilin). Penetratin-PLB peptide functions as a
 CC dominant negative inhibitor of PLB-SERCA2a interaction, enhances cardiac
 CC contractility and reduces blood pressure. This method is useful for the
 CC treatment of cardiac disease e.g. heart failure and myocardial
 CC dysfunction. The present sequence is the penetratin-based recombinant
 CC peptide PLB-ANT, comprising the amino terminal end of human PLB native
 CC protein, attached to the 5' end of the Drosophila antennapedia (ANT)
 CC transport peptide. Penetratin is a class of peptides, with translocating
 CC properties having the ability to carry hydrophilic compounds across the
 CC plasma membrane

XX Sequence 36 AA;

Query Match 93.4%; Score 71; DB 3; Length 36;

Best Local Similarity 100.0%; Pred. No. 1.8e-05;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRA 15

DB 1 MEKVQYLTRSAIRRA 15

RESULT 8

ADE45175

ID ADE45175 standard; peptide; 36 AA.

XX ADE45175;

AC ADE45175;

XX 29-JAN-2004 (first entry)

XX Human SERCA_2 inhibitor phospholamban, cytosolic domain.

DE Human; SERCA_2; phospholamban; PLB;

XX Ca2+ ATPase of the sarco/endoplasmic reticulum; protein co-ordinate data;

XX cadiant.

XX Homo sapiens.

XX US6538022-B1.

XX 25-MAR-2003.

XX 18-FEB-1999; 99US-00252063.

XX 24-SEP-1997; 97US-00937117.

XX (ORIN) ORION CORP.

XX Pollesello P, Ovaska M, Tenhunen J, Vildgren J;

XX Yliperttula-Ikonen M, Tilgmann C, Lotta T, Kaivola J;

XX WPI; 2004-019625/02.

XX New compound, useful for relieving inhibitory effects of phospholamban on

XX cardiac SR Ca2+-ATPase by deactivating phospholamban and stimulating Ca2+

XX -ATPase.

XX Disclosure; SEQ ID NO 9; 65pp; English.

XX The invention relates to a compound which deactivates, and exhibits

XX affinity for, a phospholamban (PLB) protein (an inhibitor of SERCA_2,

XX Ca2+ ATPase of the sarco/endoplasmic reticulum) appearing as ADE45167-

XX ADE45173. The compound has a structure containing three of the four

XX moieties: an electronegative moiety associating with an S1 binding site

XX of the phospholamban cytosolic domain when the compound is bound to it.

XX the binding site comprises Tyr-6, Arg-9 and/or Arg-13; an electronegative

XX moiety associating with an S2 binding site of the phospholamban cytosolic

XX domain when the compound is bound to it, the S2 binding site comprises

XX Arg-14; a hydrophobic moiety associating with an S3 binding site of the

XX phospholamban cytosolic domain when the compound is bound, the binding

CC

CC site comprises Met-20, Lys-27 and/or Leu-28; and a hydrophobic moiety
 CC associating with an S4 binding site of the phospholamban cytosolic domain
 CC when the compound is bound, the binding site comprises Phe-32 and/or Phe-
 CC 35. The compound is not 3-benzyl-5,7-bis ((1H-tetrazol-5-yl)-methyl-oxo)-4
 CC -methyl-2H-methyl-2H-1-benzopyran-2-one. Also included are deactivating
 CC phospholamban, comprising administering the novel compound to stimulate
 CC the Ca 2+ -ATPase. The compound is useful for relieving the inhibitory
 CC effects of phospholamban on cardiac SERCA 2. The present sequence is the
 CC cytosolic domain of human phospholamban.

XX Sequence 36 AA;

Query Match 93.4%; Score 71; DB 8; Length 36;

Best Local Similarity 100.0%; Pred. No. 1.8e-05;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRA 15

DB 1 MEKVQYLTRSAIRRA 15

RESULT 2

AA71006

ID AA71006 standard; protein; 52 AA.

AC AA71006;

XX AA71006;

DT 29-AUG-2000 (first entry)

DE Human mutant phospholamban (PLB) S16N protein.

XX Phospholamban; PLB; human; sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a;
 XX cation; cardiomyocyte; transport peptide; penetratin; cargo peptide;
 KW contractilin; cardiac contractility; inhibitor; cardiac disease;
 KW treatment; heart failure; myocardial dysfunction; mutant.

XX Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 16 /note= "Wild type Ser replaced with Asn"

FN WO200025804-A2.

XX 11-MAY-2000.

XX 02-NOV-1999; 99WO-US025692.

XX 02-NOV-1998; 98US-0106718P.

XX 27-JUL-1999; 99US-0145883P.

XX (REGC) UNIV CALIFORNIA.

XX Chien K, Dillman W, Minamisawa S, He H, Hoshijima M, Meyer M;

PI Scott C, Wang Y, Silverman GJ;

XX WPI; 2000-365393/31.

XX Treating cardiac diseases, e.g. heart failure or myocardial dysfunction
 PT comprises enhancing cardiac contractility by inhibiting interaction
 PT between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine
 PT triphosphatase.

PS Disclosure; Page 49; 56pp; English.

XX The patent discloses a method for the treatment of heart failure, using
 CC small peptide complexes and recombinant proteins, that induces
 CC phospholamban (PLB) deficiency and inhibits the interaction between PLB
 CC and sarcoplasmic reticulum Ca 2+ ATPase (SERCA2a) within cardiomyocytes.
 CC The peptide complex comprises of transport peptide like penetratin and
 CC cargo peptide selected from mutant PLB, native PLB or antibody against
 CC PLB protein (contractilin). Penetratin-PLB peptide functions as a
 CC PLB protein (contractilin). Penetratin-PLB peptide functions as a

CC dominant negative inhibitor of PLB-SERCA2a interaction, enhances cardiac
 CC contractility and reduces blood pressure. This method is useful for the
 CC treatment of cardiac disease e.g. heart failure and myocardial
 CC dysfunction. The present amino acid sequence is the human mutant PLB
 CC protein, comprising the mutation Ser16Asn. This mutant sequence when
 CC overexpressed in the transformed cardiomyocytes, shows increased
 CC contractility than the wild type PLB sequence

XX Sequence 52 AA;

Query Match 93.4%; Score 71; DB 3; Length 52;

Best Local Similarity 100.0%; Pred. No. 2.7e-05;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRA 15

DB 1 MEKVQYLTRSAIRRA 15

RESULT 10

AA71003

ID AA71003 standard; protein; 52 AA.

AC AA71003;

XX AA71003;

DT 29-AUG-2000 (first entry)

DE Human mutant phospholamban (PLB) V49A protein.

XX Phospholamban; PLB; human; sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a;
 XX cation; cardiomyocyte; transport peptide; penetratin; cargo peptide;
 KW contractilin; cardiac contractility; inhibitor; cardiac disease;
 KW treatment; heart failure; myocardial dysfunction; mutant.

XX Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 49 /note= "Wild type Val replaced with Ala"

FN WO200025804-A2.

XX 11-MAY-2000.

XX 02-NOV-1999; 99WO-US025692.

XX 02-NOV-1998; 98US-0106718P.

XX 27-JUL-1999; 99US-0145883P.

XX (REGC) UNIV CALIFORNIA.

XX Chien K, Dillman W, Minamisawa S, He H, Hoshijima M, Meyer M;

PI Scott C, Wang Y, Silverman GJ;

XX WPI; 2000-365393/31.

XX Treating cardiac diseases, e.g. heart failure or myocardial dysfunction
 PT comprises enhancing cardiac contractility by inhibiting interaction
 PT between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine
 PT triphosphatase.

PS Disclosure; Page 48; 56pp; English.

XX The patent discloses a method for the treatment of heart failure, using
 CC small peptide complexes and recombinant proteins, that induces
 CC phospholamban (PLB) deficiency and inhibits the interaction between PLB
 CC and sarcoplasmic reticulum Ca 2+ ATPase (SERCA2a) within cardiomyocytes.
 CC The peptide complex comprises of transport peptide like penetratin and
 CC cargo peptide selected from mutant PLB, native PLB or antibody against
 CC PLB protein (contractilin). Penetratin-PLB peptide functions as a
 CC dominant negative inhibitor of PLB-SERCA2a interaction, enhances cardiac
 CC contractility and reduces blood pressure. This method is useful for the

CC and sarcoplasmic reticulum Ca 2+ ATPase (SERCA2a) within cardiomyocytes.
CC The peptide complex comprises of transport peptide like penetratin and
CC cargo peptide selected from mutant PLB, native PLB or antibody against
CC PLB protein (contractilin). Penetratin-PLB peptide functions as a
CC dominant negative inhibitor of PLB-SERCA2a interaction, enhances cardiac
CC contractility and reduces blood pressure. This method is useful for the
CC treatment of cardiac disease e.g heart failure and myocardial
CC dysfunction. The present amino acid sequence is the human PLB wild type
CC protein, a potent inhibitor of SERCA2a activity. It primarily exists in a
CC pentameric form. It is a mediator in the regulation of myocardial
CC function by catecholamines through the cAMP cascade
XX
SQ Sequence 52 AA;

Query Match 93.4%; Score 71; DB 3; Length 52;
Best Local Similarity 100.0%; Pred.No. 2.7e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0

OY 1 MEKVQYLFRSAIRRA 15
| | | | |
Db 1 MEKVQYLFRSAIRRA 15
| | | | |

RESULT 12
ABP06592
ID ABP06592 standard; protein; 52 AA.
XX AC
XX AC
XX AC
DT 25-JUN-2002 (first entry)
XX
DE Human ORFX protein sequence SEQ ID NO:13166.
XX
KW Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;
KW hyperproliferative disorder; psoriasis; benign tumour; haemorrhage;
KW degenerative disorder; osteoarthritis; neurodegenerative disorder;
KW cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;
KW hypertension; hypothyroidism; cholesterol ester storage disease;
KW immune deficiency; immune disorder; infectious disease;
KW autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
KW myasthenia gravis.
XX
OS Homo sapiens.
XX
XX
FN WO200192523-A2.
XX
PD 06-DEC-2001.
XX
PP 29-MAY-2001; 2001WO-US010836.
XX
PP 30-MAY-2000; 2000US-0206132P.
PR 29-AUG-2000; 2000US-0228716P.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Shimkets RA, Leach MD;
XX
XX WPI: 2002-106308/14.
DR N-PSDB; AEN22344.
XX
XX Novel human polypeptides and polynucleotides useful for diagnosing,
PT preventing and treating cardiovascular disease, neurodegenerative,
PT hyperproliferative disorders and autoimmune disorders.
PT
XX Disclosure; SEQ ID NO 13166; 1037pp; English.

The present invention describes substantially purified human proteins
(referred to as open reading frame, ORFX, where X is I-I1491 (see table 1
in the specification). AENI5762 to AEN27252 encode the human ORFX
proteins given in ABP00010 to ABP11500. ORFX proteins are useful for
treating or preventing a pathology associated with an ORFX-associated
disorder in humans, and in the manufacture of a medicament for treating
said disorder, associated with ORFX-associated disorder. ORFX polynucleotide
sequences are also provided.

CC sequences can be used in gene therapy. ORFX sequences can be used in the
 CC treatment of cancer, hyperproliferative disorders, cirrhosis of liver,
 CC psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage,
 CC osteoarthritis, neurodegenerative disorders, disorders related to organ
 CC transplantation, cardiovascular diseases, diabetes mellitus, systemic
 CC lupus erythematosus, hypertension, hypothyroidism, cholesterol ester
 CC storage disease, various immune deficiencies and disorders, infectious
 CC diseases, autoimmune disorders such as multiple sclerosis, rheumatoid
 CC arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host
 CC disease and autoimmune inflammatory eye disease. ORFX proteins are also
 CC useful for treating burns, incisions, ulcers, for treating osteoporosis,
 CC bone degenerative disorders, or periodontal disease, and for gut
 CC protection or regeneration and treatment of lung or liver fibrosis,
 CC reperfusion injury in various tissues and conditions resulting from
 CC systemic cytokine damage. N.B. The sequence data for this patent did not
 CC form part of the printed specification, but was obtained in electronic
 CC format directly from WIPO at fip.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 52 AA;

Query Match 93.4%; Score 71; DB 5; Length 52;
 Best Local Similarity 100.0%; Pred. No. 2.7e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRA 15
 |||||
 DB 1 MEKVQYLTRSAIRRA 15

RESULT 13
 ADE45172
 ID ADE45172 standard; protein; 52 AA.

XX AC ADE45172;
 XX DT 29-JAN-2004 (first entry)
 XX DE Mouse SERCA_2 inhibitor phospholamban.
 XX KW Mouse; SERCA_2; phospholamban; PLB;
 XX KW Ca2+ ATPase of the sarco/endoplasmic reticulum; protein co-ordinate data;
 XX KW cardiant.
 XX OS Mus sp.
 XX DN US6538022-B1.
 XX PD 25-MAR-2003.
 XX PF 18-FEB-1999; 99US-00252063.
 XX PR 24-SEP-1997; 97US-00937117.
 XX PA (ORIN) ORION CORP.
 XX PI Pollesello P, Ovaska M, Tenhunen J, Vidgren J;
 XX PI Yliperttula-Ikonen M, Tilgmann C, Lotta T, Kaivola J;
 XX DR WPI; 2004-019625/02.
 XX PT New compound, useful for relieving inhibitory effects of phospholamban on
 XX PT cardiac SR Ca2+-ATPase by deactivating phospholamban and stimulating Ca2+
 XX PT -ATPase.

XX PS Claim 1; SEQ ID NO 6; 65pp; English.
 XX CC The invention relates to a compound which deactivates, and exhibits
 XX CC affinity for, a phospholamban (PLB) protein (an inhibitor of SERCA_2,
 XX CC Ca2+ ATPase of the sarco/endoplasmic reticulum) appearing as ADE45167-
 XX CC ADE45173. The compound has a structure containing three of the four
 XX CC moieties: an electronegative moiety associating with an S1 binding site
 XX CC of the phospholamban cytosolic domain when the compound is bound to it,
 XX CC the binding site comprises Tyr-6, Arg-9 and/or Arg-13; an electronegative
 XX CC moiety associating with an S2 binding site of the phospholamban cytosolic
 XX CC domain when the compound is bound to it, the S2 binding site comprises
 XX CC Arg-14; a hydrophobic moiety associating with an S3 binding site of the
 XX CC phospholamban cytosolic domain when the compound is bound, the binding

CC moiety associating with an S2 binding site of the phospholamban cytosolic
 CC domain when the compound is bound to it, the S2 binding site comprises
 CC Arg-14; a hydrophobic moiety associating with an S3 binding site of the
 CC phospholamban cytosolic domain when the compound is bound, the binding
 CC site comprises Met-20, Lys-27 and/or Leu-28; and a hydrophobic moiety
 CC associating with an S4 binding site of the phospholamban cytosolic domain
 CC when the compound is bound, the binding site comprises Phe-32 and/or Phe-
 CC 35. The compound is not 3-benzyl-5,7-bis ((1H-tetrazol-5-yl)-methoxy)-4-
 CC -methyl-2H-methyl-2H-1-benzopyran-2-one. Also included are deactivating
 CC phospholamban, comprising administering the novel compound to stimulate
 CC the Ca 2+ -ATPase. The compound is useful for relieving the inhibitory
 CC effects of phospholamban on cardiac SERCA_2. The present sequence is a
 CC phospholamban.

SQ Sequence 52 AA;

Query Match 93.4%; Score 71; DB 8; Length 52;
 Best Local Similarity 100.0%; Pred. No. 2.7e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRA 15
 |||||
 DB 1 MEKVQYLTRSAIRRA 15

RESULT 14
 ADE45170
 ID ADE45170 standard; protein; 52 AA.

XX AC ADE45170;
 XX DT 29-JAN-2004 (first entry)
 XX DE Rabbit SERCA_2 inhibitor phospholamban.
 XX KW Rabbit; SERCA_2; phospholamban; PLB;
 XX KW Ca2+ ATPase of the sarco/endoplasmic reticulum; protein co-ordinate data;
 XX KW cardiant.
 XX OS Oryctolagus cuniculus.
 XX PN US6538022-B1.
 XX PD 25-MAR-2003.
 XX PF 18-FEB-1999; 99US-00252063.
 XX PR 24-SEP-1997; 97US-00937117.
 XX PA (ORIN) ORION CORP.
 XX PI Pollesello P, Ovaska M, Tenhunen J, Vidgren J;
 XX PI Yliperttula-Ikonen M, Tilgmann C, Lotta T, Kaivola J;
 XX DR WPI; 2004-019625/02.

XX PT New compound, useful for relieving inhibitory effects of phospholamban on
 XX PT cardiac SR Ca2+-ATPase by deactivating phospholamban and stimulating Ca2+
 XX PT -ATPase.

XX PS Claim 1; SEQ ID NO 4; 65pp; English.

XX CC The invention relates to a compound which deactivates, and exhibits
 XX CC affinity for, a phospholamban (PLB) protein (an inhibitor of SERCA_2,
 XX CC Ca2+ ATPase of the sarco/endoplasmic reticulum) appearing as ADE45167-
 XX CC ADE45173. The compound has a structure containing three of the four
 XX CC moieties: an electronegative moiety associating with an S1 binding site
 XX CC of the phospholamban cytosolic domain when the compound is bound to it,
 XX CC the binding site comprises Tyr-6, Arg-9 and/or Arg-13; an electronegative
 XX CC moiety associating with an S2 binding site of the phospholamban cytosolic
 XX CC domain when the compound is bound to it, the S2 binding site comprises
 XX CC Arg-14; a hydrophobic moiety associating with an S3 binding site of the
 XX CC phospholamban cytosolic domain when the compound is bound, the binding

The invention relates to a compound which deactivates, and exhibits affinity for, a phospholamban (P_{LB}) protein (an inhibitor of SERCA₂, Ca²⁺ ATPase of the sarco/endoplasmic reticulum) appearing as ADE45167-ADE45173. The compound has a structure containing three of the four moieties: an electronegative moiety associating with an S1 binding site of the phospholamban cytosolic domain when the compound is bound to it, the binding site comprises Tyr-6, Arg-9 and/or Arg-13; an electronegative moiety associating with an S2 binding site of the phospholamban cytosolic domain when the compound is bound to it, the S2 binding site comprises Arg-14; a hydrophobic moiety associating with an S3 binding site of the phospholamban cytosolic domain when the compound is bound, the binding site comprises Met-20, Lys-27 and/or Leu-28; and a hydrophobic moiety associating with an S4 binding site of the phospholamban cytosolic domain when the compound is bound, the binding site comprises Phe-32 and/or Phe-35. The compound is not 3-benzyl-5,7-bis ((1H-tetrazol-5-yl)-methyloxy)-4

PS Claim 1; SEQ ID NO 1; 65pp; English.

XX The invention relates to a compound which deactivates, and exhibits
 CC affinity for, a phospholamban (PLB) protein (an inhibitor of SERCA 2
 CC Ca2+ ATPase of the sarco/endoplasmic reticulum) appearing as ADE45167-
 CC ADE45173. The compound has a structure containing three of the four
 CC moieties: an electronegative moiety associating with an S1 binding site
 CC of the phospholamban cytosolic domain when the compound is bound to it,
 CC the binding site comprises Tyr-6, Arg-9 and/or Arg-13; an electronegative
 CC moiety associating with an S2 binding site of the phospholamban cytosolic
 CC domain when the compound is bound to it, the S2 binding site comprises
 CC Arg-14; a hydrophobic moiety associating with an S3 binding site of the
 CC phospholamban cytosolic domain when the compound is bound, the binding
 CC site comprises Met-20, Lys-27 and/or Leu-28; and a hydrophobic moiety
 CC associating with an S4 binding site of the phospholamban cytosolic domain
 CC when the compound is bound, the binding site comprises Phe-32 and/or Phe-
 CC 35. The compound is not 3-benzyl-5,7-bis ((1H-tetrazol-5-yl)-methoxy)-4-
 CC -methyl-2H-methan-2H-1-benzopyran-2-one. Also included are deactivating
 CC phospholamban, comprising administering the novel compound to stimulate
 CC the Ca 2+ -ATPase. The compound is useful for relieving the inhibitory
 CC effects of phospholamban on cardiac SERCA 2. The present sequence is
 CC human phospholamban.

XX Sequence 52 AA;

Query Match 93.4%; Score 71; DB 8; Length 52;
 Best Local Similarity 100.0%; Pred. No. 2.7e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRA 15
 DB 1 MEKVQYLTRSAIRRA 15

RESULT 17
 AAY71019
 ID AAY71019 standard; protein; 79 AA.

XX AAY71019;
 XX 29-AUG-2000 (first entry)
 XX H6 tagged penetratin-based recombinant protein, H6- (V49A) mutant PLB-ANT.
 DE Phospholamban; PLB; human; sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a;
 KW cardiant; cardiomyocyte; transport peptide; penetratin; cargo peptide;
 KW contractilin; cardiac contractility; inhibitor; cardiac disease; mutant;
 KW treatment; heart failure; myocardial dysfunction; recombinant protein;
 KW fruit fly; ANT; antennapedia; H6 tag; hexahistidine.

XX Homo sapiens.
 OS Drosophila sp.
 OS Synthetic.

XX Key Location/Qualifiers
 FT Region 1..52
 FT /note= "Corresponds to mutant human phospholamban (PLB)
 FT protein"
 FT Misc-difference 49
 FT /note= "Wild type Val replaced with Ala"
 FT Region 53..58
 FT /note= "Corresponds to hexahistidine tag (H6)"
 FT Region 63..78
 FT /note= "Corresponds to Drosophila antennapedia (ANT)
 FT transport peptide"

WO200025804-A2.

11-MAY-2000.

02-NOV-1999; 99WO-US025692.

02-NOV-1998; 98US-0106718P.

27-JUL-1999; 99US-0145883P.

XX (REGC) UNIV CALIFORNIA.
 XX Chien K, Dillman W, Minamisawa S, He H, Hoshijima M, Meyer M;
 PI Scott C, Wang Y, Silverman GJ;
 XX MPI; 2000-365393/31.

XX Treating cardiac diseases, e.g. heart failure or myocardial dysfunction
 CC comprises enhancing cardiac contractility by inhibiting interaction
 CC between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine
 CC triphosphatase.

XX Example 6; Page 56; 56pp; English.

XX The patent discloses a method for the treatment of heart failure, using
 CC small peptide complexes and recombinant proteins, that induces
 CC phospholamban (PLB) deficiency and inhibits the interaction between PLB
 CC and sarcoplasmic reticulum Ca 2+ ATPase (SERCA2a) within cardiomyocytes.
 CC The peptide complex comprises of transport peptide like penetratin and
 CC cargo peptide selected from mutant PLB, native PLB or antibody against
 CC PLB protein (contractilin). Penetratin-PLB peptide functions as a
 CC dominant negative inhibitor of PLB-SERCA2a interaction, enhances cardiac
 CC contractility and reduces blood pressure. This method is useful for the
 CC treatment of cardiac disease e.g. heart failure and myocardial
 CC dysfunction. The present sequence is the hexahistidine (H6) tagged
 CC penetratin-based recombinant protein H6-mutant PLB-ANT, comprising the
 CC human mutant (Val49Ala) PLB protein and Drosophila antennapedia (ANT).
 CC transport peptide attached by a hexahistidine tag. This sequence is
 CC expressed in Escherichia coli cells

XX Sequence 79 AA;

Query Match 93.4%; Score 71; DB 3; Length 79;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRA 15
 DB 1 MEKVQYLTRSAIRRA 15

RESULT 18

AAY71017
 ID AAY71017 standard; protein; 79 AA.

XX AAY71017;

XX 29-AUG-2000 (first entry)

XX Hexahistidine tagged penetratin-based recombinant protein, H6-wtPLB-ANT.
 DE Phospholamban; PLB; human; sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a;
 KW cardiant; cardiomyocyte; transport peptide; penetratin; cargo peptide;
 KW contractilin; cardiac contractility; inhibitor; cardiac disease;
 KW treatment; heart failure; myocardial dysfunction; recombinant protein;
 KW fruit fly; ANT; antennapedia; H6 tag; hexahistidine.

XX Homo sapiens.
 OS Drosophila sp.
 OS Synthetic.

XX Key Location/Qualifiers
 FT Region 1..52
 FT /note= "Corresponds to Human phospholamban (PLB) protein"
 FT Region 53..58
 FT /note= "Corresponds to hexahistidine tag (H6)"
 FT Region 63..78
 FT /note= "Corresponds to Drosophila antennapedia (ANT)
 FT transport peptide"

WO200025804-A2.

PD 11-MAY-2000.
 XX 02-NOV-1999; 99WO-US025692.
 XX 02-NOV-1998; 98US-0106718P.
 PR 27-JUL-1999; 99US-0145883P.
 XX (SEGC) UNIV CALIFORNIA.
 XX Chien K, Dillman W, Minamisawa S, He H, Hoshijima M, Meyer M;
 PI Scott C, Wang Y, Silverman GJ;
 XX WPI; 2000-365393/31.
 XX Treating cardiac diseases, e.g. heart failure or myocardial dysfunction
 PT comprises enhancing cardiac contractility by inhibiting interaction
 PT between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine
 PT triphosphatase.
 XX Example 6; Page 54-55; 56pp; English.
 XX The patent discloses a method for the treatment of heart failure, using
 CC small peptide complexes and recombinant proteins, that induces
 CC phospholamban (PLB) deficiency and inhibits the interaction between PLB
 CC and sarcoplasmic reticulum Ca 2+ ATPase (SERCA2a) within cardiomyocytes.
 CC The peptide complex comprises of transport peptide like penetratin and
 CC cargo peptide selected from mutant PLB, native PLB or antibody against
 CC PLB protein (contractilin). Penetratin-PLB peptide functions as a
 CC dominant negative inhibitor of PLB-SERCA2a interaction, enhances cardiac
 CC contractility and reduces blood pressure. This method is useful for the
 CC treatment of cardiac disease e.g. heart failure and myocardial
 CC dysfunction. The present sequence is the hexahistidine (H6) tagged
 CC penetratin-based recombinant protein H6-wPLB-ANT, comprising the wild
 CC type human PLB protein and prosofilla antennapedia (ANT) transport
 CC peptide attached by a hexahistidine tag. This sequence is expressed in
 CC Escherichia coli cells
 XX Sequence 79 AA;
 SQ Query Match 93.4%; Score 71; DB 3; Length 79;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MEKVQLTRSAIRRA 15
 DB 1 MEKVQLTRSAIRRA 15
 RESULT 19
 ADE45168
 ID ADE45168 standard; protein; 52 AA.
 AC ADE45168;
 XX 29-JAN-2004 (first entry)
 DT Pig SERCA_2 inhibitor phospholamban.
 DE Pig; SERCA_2; phospholamban; PLB;
 XX Ca2+ ATPase of the sarco/endoplasmic reticulum; protein co-ordinate data;
 KW cardiant.
 XX Sus sp.
 XX US6538022-B1.
 PN 25-MAR-2003.
 XX 18-FEB-1999;
 PD 99US-00252063.
 XX 18-FEB-1999; 99US-00252063.
 PF 24-SEP-1997; 97US-00937117.
 XX (ORIN) ORION CORP.
 PA Pollesello P, Ovaska M, Tenhunen J, Vildgren J;
 PI Yliperttula-Ikonen M, Tilgmann C, Lotta T, Kaivola J;

XX Pollesello P, Ovaska M, Tenhunen J, Vildgren J;
 PI Yliperttula-Ikonen M, Tilgmann C, Lotta T, Kaivola J;
 XX WPI; 2004-019625/02.
 XX New compound, useful for relieving inhibitory effects of phospholamban on
 PT cardiac SR Ca2+-ATPase by deactivating phospholamban and stimulating Ca2+
 PT -ATPase.
 XX Claim 1; SEQ ID NO 2; 65pp; English.
 XX The invention relates to a compound which deactivates, and exhibits
 CC affinity for, a phospholamban (PLB) protein (an inhibitor of SERCA 2,
 CC Ca2+ ATPase of the sarco/endoplasmic reticulum) appearing as ADE45167-
 CC ADE45173. The compound has a structure containing three of the four
 CC moieties: an electronegative moiety associating with an S1 binding site
 CC of the phospholamban cytosolic domain when the compound is bound to it,
 CC the binding site comprises Tyr-6, Arg-9 and/or Arg-13; an electronegative
 CC moiety associating with an S2 binding site of the phospholamban cytosolic
 CC domain when the compound is bound to it, the S2 binding site comprises
 CC Arg-14; a hydrophobic moiety associating with an S3 binding site of the
 CC phospholamban cytosolic domain when the compound is bound, the binding
 CC site comprises Met-20, Lys-27 and/or Leu-28; and a hydrophobic moiety
 CC associating with an S4 binding site of the phospholamban cytosolic domain
 CC when the compound is bound, the binding site comprises Phe-32 and/or Phe-
 CC 35. The compound is not 3-benzyl-5,7-bis ((1H-tetrazol-5-yl)-methyloxy)-4
 CC -methyl-2H-methyl-2H-1-benzopyran-2-one. Also included are deactivating
 CC phospholamban, comprising administering the novel compound to stimulate
 CC the Ca 2+ -ATPase. The compound is useful for relieving the inhibitory
 CC effects of phospholamban on cardiac SERCA_2. The present sequence is a
 CC phospholamban.
 XX Sequence 52 AA;
 SQ Query Match 89.5%; Score 68; DB 8; Length 52;
 Best Local Similarity 93.3%; Pred. No. 9.3e-05;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MEKVQLTRSAIRRA 15
 DB 1 MDKVQLTRSAIRRA 15
 RESULT 20
 ADE45169
 ID ADE45169 standard; protein; 52 AA.
 AC ADE45169;
 XX 29-JAN-2004 (first entry)
 DT Dog SERCA_2 inhibitor phospholamban.
 DE Dog; SERCA_2; phospholamban; PLB;
 XX Ca2+ ATPase of the sarco/endoplasmic reticulum; protein co-ordinate data;
 KW cardiant.
 XX Canis sp.
 OS US6538022-B1.
 XX 25-MAR-2003.
 PN 18-FEB-1999; 99US-00252063.
 XX 24-SEP-1997; 97US-00937117.
 XX (ORIN) ORION CORP.
 PA Pollesello P, Ovaska M, Tenhunen J, Vildgren J;
 PI Yliperttula-Ikonen M, Tilgmann C, Lotta T, Kaivola J;

DR WPI; 2004-019625/02.

XX New compound, useful for relieving inhibitory effects of phospholamban on

PT cardiac SR Ca2+-ATPase by deactivating phospholamban and stimulating Ca2+

PT -ATPase.

XX

XX Claim 1; SEQ ID NO 3; 65pp; English.

XX

CC The invention relates to a compound which deactivates, and exhibits

CC affinity for, a phospholamban (PLB) protein (an inhibitor of SERCA 2,

CC Ca2+ ATPase of the sarco/endoplasmic reticulum) appearing as ADE45167-

CC ADE45173. The compound has a structure containing three of the four

CC moieties: an electronegative moiety associating with an S1 binding site

CC of the phospholamban cytosolic domain when the compound is bound to it,

CC the binding site comprises Tyr-6, Arg-9 and/or Arg-13; an electronegative

CC moiety associating with an S2 binding site of the phospholamban cytosolic

CC domain when the compound is bound to it, the S2 binding site comprises

CC Arg-14; a hydrophobic moiety associating with an S3 binding site of the

CC phospholamban cytosolic domain when the compound is bound, the binding

CC site comprises Met-20, Lys-27 and/or Leu-28; and a hydrophobic moiety

CC associating with an S4 binding site of the phospholamban cytosolic domain

CC when the compound is bound, the binding site comprises Phe-32 and/or Phe-

CC -methyl-2H-methyl-2H-1-benzopyran-2-one. Also included are deactivating

CC -methyl-2H-methyl-2H-1-benzopyran-2-one. Also included are deactivating

CC phospholamban, comprising administering the novel compound to stimulate

CC effects of phospholamban on cardiac SERCA 2. The present sequence is a

CC phospholamban.

XX

XX Sequence 52 AA;

XX

Query Match 89.5%; Score 68; DB 8; Length 52;

Best Local Similarity 93.3%; Pred. No. 9.3e-05;

Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

XX

Qy 1 MEKVQYLTRSAIRRA 15

Db 1 MDKVQYLTRSAIRRA 15

XX

RESULT 21

ADE45173

ID ADE45173 standard; protein; 52 AA.

XX

XX ADE45173;

XX

XX 29-JAN-2004 (first entry)

XX

XX Chicken SERCA_2 inhibitor phospholamban.

XX

XX Chicken; SERCA 2; phospholamban; PLB;

XX Ca2+ ATPase of the sarco/endoplasmic reticulum; protein co-ordinate data;

XX cardiant.

XX

XX Gallus sp.

XX

XX US6538022-B1.

XX

XX 25-MAR-2003.

XX

XX 18-FEB-1999; 99US-00252063.

XX

XX 24-SEP-1997; 97US-00937117.

XX

XX (ORIN) ORION CORP.

XX

XX Pollesello P, Ovaska M, Tenhunen J, Vidgren J;

XX Yliperttula-Ikonen M, Tilgmann C, Lotta T, Kaivola J;

XX WPI; 2004-019625/02.

XX

XX New compound, useful for relieving inhibitory effects of phospholamban on

PT cardiac SR Ca2+-ATPase by deactivating phospholamban and stimulating Ca2+

PT -ATPase.

XX

XX Claim 1; SEQ ID NO 7; 65pp; English.

XX

CC The invention relates to a compound which deactivates, and exhibits

CC affinity for, a phospholamban (PLB) protein (an inhibitor of SERCA 2,

CC Ca2+ ATPase of the sarco/endoplasmic reticulum) appearing as ADE45167-

CC ADE45173. The compound has a structure containing three of the four

CC moieties: an electronegative moiety associating with an S1 binding site

CC of the phospholamban cytosolic domain when the compound is bound to it,

CC the binding site comprises Tyr-6, Arg-9 and/or Arg-13; an electronegative

CC moiety associating with an S2 binding site of the phospholamban cytosolic

CC domain when the compound is bound to it, the S2 binding site comprises

CC Arg-14; a hydrophobic moiety associating with an S3 binding site of the

CC phospholamban cytosolic domain when the compound is bound, the binding

CC site comprises Met-20, Lys-27 and/or Leu-28; and a hydrophobic moiety

CC associating with an S4 binding site of the phospholamban cytosolic domain

CC when the compound is bound, the binding site comprises Phe-32 and/or Phe-

CC -methyl-2H-methyl-2H-1-benzopyran-2-one. Also included are deactivating

CC -methyl-2H-methyl-2H-1-benzopyran-2-one. Also included are deactivating

CC phospholamban, comprising administering the novel compound to stimulate

CC effects of phospholamban on cardiac SERCA 2. The present sequence is a

CC phospholamban.

XX

XX Sequence 52 AA;

XX

Query Match 88.2%; Score 67; DB 8; Length 52;

Best Local Similarity 86.7%; Pred. No. 0.00014;

Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

XX

Qy 1 MEKVQYLTRSAIRRA 15

Db 1 MEKVQYLTRSAIRRA 15

XX

RESULT 22

AAV71005

ID AAV71005 standard; protein; 52 AA.

XX

XX AAV71005;

XX

XX 29-AUG-2000 (first entry)

XX

XX Human mutant phospholamban (PLB) R14E protein.

XX

XX Phospholamban; PLB; human; sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a;

XX cardiant; cardiomyocyte; transport peptide; penetratin; cargo peptide;

XX contractilin; cardiac contractility; inhibitor; cardiac disease;

XX treatment; heart failure; myocardial dysfunction; mutant.

XX

XX Homo sapiens.

XX

XX Synthetic.

XX

XX Key Location/Qualifiers

XX Misc-difference 14

XX /note= "Wild type Arg replaced with Glu"

XX

XX WC200025804-A2.

XX

XX 11-MAY-2000.

XX

XX 02-NOV-1999; 99WO-US025692.

XX

XX 02-NOV-1998; 98US-0106718P.

XX 27-JUL-1999; 99US-0145883P.

XX

XX (REGC) UNIV CALIFORNIA.

XX

XX Chien K, Dillman W, Minamisawa S, He H, Hoshijima M, Meyer M;

XX Scott C, Wang Y, Silverman GJ;

XX WPI; 2000-365393/31.

comprises enhancing cardiac contractility by inhibiting interaction between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine triphosphatase.

Disclosure; Page 49; 56pp; English.

The patent discloses a method for the treatment of heart failure, using small peptide complexes and recombinant proteins, that induces phospholamban (PLB) deficiency and inhibits the interaction between PLB and sarcoplasmic reticulum Ca 2+ ATPase (SERCA2a) within cardiomyocytes. The peptide complex comprises of transport peptide like penetratin and CARG peptide selected from mutant PLB, native PLB or antibody against PLB protein (conectatin). Penetratin-PLB peptide functions as a dominant negative inhibitor of PLB-SERCA2a interaction, enhances cardiac contractility and reduces blood pressure. This method is useful for the treatment of cardiac disease e.g. heart failure and myocardial dysfunction. The present amino acid sequence is the human mutant PLB protein, comprising the double mutation Lys39Glu and Arg15Glu. This mutant sequence, when overexpressed in the transformed cardiomyocytes, shows increased contractility than the wild type PLB sequence

Sequence 52 AA;

Query Match 81.8%; Score 62; DB 3; Length 52;
Best Local Similarity 86.7%; Pred. No. 0.0011;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MEKVQYLTRSAIRRA 15
|||:|||||
Db 1 MEEVQYLTRSAIRRA 15

RESULT 25

ADC87928

ID ADC87928 standard; protein; 116 AA.

XX AC

ADC87928;

XX DT 01-JAN-2004 (first entry)

XX DE Ribosomal protein similar to FCWP1 #144.

XX KW Antifungal protein; ribosomal protein; FCWP1; AlyAPP;

XX KW plant fungal infection; Alternaria; Ascochyta; Botrytis; Cercospora;

XX KW Colletotrichum; Diplodia; Fusarium; Gaemanomyces; Helminthosporium;

XX KW Macrophomina; Mycosphaerella; Nectria; Peronospora; Phoma;

XX KW Phymatotrichum; Phytophthora; Plasmodia; Podosphaera; Puccinia; Puthium;

XX KW Pyrenophora; Pyricularia; Pythium; Rhizoctonia; Sclerotium; Sclerotinia;

XX KW Septoria; Thielaviopsis; Venturia; Verticillium.

XX OS Unidentified.

XX PN US6573361-B1.

XX PD 03-JUN-2003.

XX PF 07-DEC-2000; 2000US-00732210.

XX PR 07-DEC-1999; 99US-0169340P.

XX PR 07-DEC-1999; 99US-0169513P.

XX PA (MONS) MONSANTO TECHNOLOGY LLC.

XX PI Bunkers GJ, Liang J, Mittanck CA, Seale JW, Wu YS;

XX DR NPT; 2003-754558/71.

XX PT Novel antifungal protein FCWP1, isolated from Fusarium culmorum, useful

XX PT for controlling fungal infections in plants.

XX PS Example 21; SEQ ID NO 181; 27pp; English.

XX CC The invention relates to an isolated antifungal ribosomal protein from

CC fusarium culmorum, FCWP1. Also included is a fusion protein between the
CC signal peptide of the antifungal protein AlyAPP from Alyseum and FCWP1,
CC encoded by the nucleic acid appearing as ADC87758. The FCWP1 proteins are
CC useful for controlling fungal infections in plants, such as those caused
CC by Alternaria (e.g. Alternaria brassicicola, Alternaria solani),
CC Ascochyta (e.g. Ascochyta blight), Botrytis (e.g. Botrytis cinerea),
CC Cercospora (e.g. Cercospora kikuchii, Cercospora zea-maydis),
CC Colletotrichum (e.g. Colletotrichum lindemuthianum), Diplodia (e.g.
CC Diplodia maydis), Fusarium (e.g. Fusarium nivale, Fusarium oxysporum,
CC Fusarium graminearum, Fusarium culmorum, Fusarium solani, Fusarium
CC moniliforme, Fusarium roseum), Gaemanomyces (e.g. Gaemanomyces
CC graminis f.sp. tritici), Helminthosporium (e.g. Helminthosporium turcicum
CC Helminthosporium carbonum, Helminthosporium maydis), Macrophomina
CC (e.g. Macrophomina phaseolina, Magnaporthe grisea), Mycosphaerella
CC (e.g. Mycosphaerella figiensis), Nectria (Nectria haematococca),
CC Peronospora (e.g. Peronospora manshurica, Peronospora tabacina), Phoma
CC (e.g. Phoma betae), Phymatotrichum (e.g. Phymatotrichum omnivorum),
CC Phytophthora (e.g. Phytophthora cinnamomi, Phytophthora cactorum,
CC Phytophthora phaseoli, Phytophthora parasitica, Phytophthora
CC citrophthora, Phytophthora megasperma f.sp. sojae, Phytophthora
CC infestans), Plasmodia (e.g. Plasmodia viticola), Podosphaera (e.g.
CC Podosphaera leucotricha), Puccinia (e.g. Puccinia sorghi, Puccinia
CC striiformis, Puccinia graminis f.sp. tritici, Puccinia asparagi,
CC Puccinia recondita, Puccinia arachidis), Puthium (e.g. Puthium
CC aphanidermatum), Pyrenophora (e.g. Pyrenophora tritici-repentens),
CC Pyricularia (e.g. Pyricularia oryzae), Pythium (e.g. Pythium ultimum),
CC Rhizoctonia (e.g. Rhizoctonia solani, Rhizoctonia cerealis), Sclerotium
CC (e.g. Sclerotium rolfsii), Sclerotinia (e.g. Sclerotinia sclerotiorum),
CC Septoria (e.g. Septoria lycopersici, Septoria glycines, Stagonospora
CC nodorum, Phaeosphaeria nodorum, Septoria tritici), Thielaviopsis (e.g.
CC Thielaviopsis basicola), Uncinula (e.g. Uncinula necator), Venturia
CC (e.g. Venturia inaequalis) or Verticillium (e.g. Verticillium dahliae,
CC Verticillium albo-atrum). Mutations in the proteolytic consensus
CC sequences contained within FCWP1 provides improved stability of its
CC antifungal activity. Also disclosed are ribosomal proteins with similar
CC PI (>71) and molecular weight (<20kDa) to FCWP1, which may act as
CC antifungal proteins. The present sequence represents one of the ribosomal
CC proteins similar to FCWP1. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=6573361B1.

XX SQ

Sequence 116 AA;

Query Match 55.3%; Score 42; DB 7; Length 116;

Best Local Similarity 43.8%; Pred. No. 11;

Matches 7; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MEKVQYLTRSAIRRAE 16

Db 81 VEKIELVTRGDVREAR 96

Search completed: October 1, 2004, 12:13:19

Job time : 67.2 secs

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OM protein - protein search, using sw model

Run on: October 1, 2004, 12:07:51 ; Search time 17 Seconds
(without alignments)
48.589 Million cell updates/sec

Title: US-09-830-779-18_COPY_1_16

Perfect score: 76
Sequence: 1 MEKVQLTRSAIRAE 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Issued_patents_AA.*

1: /cgn2_6/protdata/2/iaa/5A COMB.pep.*
2: /cgn2_6/protdata/2/iaa/5B COMB.pep.*
3: /cgn2_6/protdata/2/iaa/6A COMB.pep.*
4: /cgn2_6/protdata/2/iaa/6B COMB.pep.*
5: /cgn2_6/protdata/2/iaa/PCUTS COMB.pep.*
6: /cgn2_6/protdata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	71	93.4	36	4	US-09-252-063-9
2	71	93.4	52	4	US-09-252-063-1
3	71	93.4	52	4	US-09-252-063-4
4	71	93.4	52	4	US-09-252-063-5
5	71	93.4	52	4	US-09-252-063-6
6	71	93.4	52	4	US-09-549-872B-15
7	68	89.5	52	4	US-09-252-063-2
8	68	89.5	52	4	US-09-252-063-3
9	68	89.5	52	4	US-09-549-872B-14
10	67	88.2	52	4	US-09-252-063-7
11	42	55.3	116	4	US-09-732-210-181
12	41	53.9	765	4	US-09-252-991A-24791
13	39.5	52.0	835	2	US-08-968-751-4
14	39	51.3	210	4	US-09-252-991A-28362
15	38	50.0	235	4	US-09-198-452A-752
16	37	48.7	631	4	US-09-252-991A-18000
17	37	48.7	924	2	US-08-588-983-18
18	37	48.7	924	2	US-08-588-976-18
19	36	47.4	98	4	US-09-489-039A-7319
20	36	47.4	194	4	US-09-489-039A-11071
21	36	47.4	489	1	US-08-489-733-6
22	36	47.4	489	2	US-08-993-581B-6
23	36	47.4	630	4	US-09-342-647-2
24	36	47.4	686	4	US-09-252-991A-19332
25	36	47.4	3567	2	US-07-642-734C-4
26	36	47.4	3567	3	US-08-439-C09A-4
27	35	46.1	357	4	US-09-910-174B-14

357	4	US-09-620-461-14	Sequence 14, Appl
642	4	US-09-489-039A-12434	Sequence 12434, A
864	4	US-09-323-872A-28	Sequence 28, Appl
864	4	US-09-072-433-16	Sequence 16, Appl
77	4	US-09-328-352-4251	Sequence 4251, Ap
104	4	US-09-134-001C-4945	Sequence 4945, Ap
181	4	US-09-198-452A-599	Sequence 599, App
211	4	US-09-134-001C-5136	Sequence 5136, Ap
230	4	US-09-540-236-2466	Sequence 2466, Ap
266	3	US-08-961-083-14	Sequence 14, Appl
266	4	US-09-536-784-14	Sequence 14, Appl
310	4	US-09-107-532A-5580	Sequence 5580, Ap
348	3	US-09-248-528-7	Sequence 7, Appli
348	3	US-09-549-108-7	Sequence 7, Appli
348	3	US-09-549-111-7	Sequence 7, Appli
348	3	US-09-549-106-7	Sequence 7, Appli
348	3	US-09-550-394-7	Sequence 7, Appli
393	2	US-08-977-554-2	Sequence 2, Appli
393	3	US-09-225-967-2	Sequence 2, Appli
393	3	US-09-227-806-2	Sequence 2, Appli
412	4	US-09-252-991A-28034	Sequence 28034, A
491	1	US-08-489-733-5	Sequence 5, Appli
491	2	US-08-993-581B-5	Sequence 5, Appli
495	4	US-09-107-532A-3679	Sequence 3679, Ap
573	4	US-09-328-352-6420	Sequence 2420, Ap
591	4	US-09-252-991A-24904	Sequence 24904, A
784	4	US-09-252-991A-20416	Sequence 20416, A
978	2	US-08-415-593-43	Sequence 43, Appl
3562	4	US-09-679-279-14	Sequence 14, Appl
53	4	US-09-673-395A-511	Sequence 511, App
24	4	US-09-561-490E-3	Sequence 3, Appli
50	6	5169933-31	Patent No. 5169933
71	4	US-09-489-039A-9691	Sequence 9691, A
113	4	US-09-732-210-681	Sequence 681, App
123	4	US-09-252-991A-24837	Sequence 24837, A
172	4	US-09-252-991A-24148	Sequence 24148, A
180	4	US-09-252-991A-18799	Sequence 18799, A
238	4	US-09-328-352-7630	Sequence 7630, Ap
276	2	US-08-713-072C-4	Sequence 4, Appli
313	4	US-09-413-814-9	Sequence 9, Appli
331	4	US-09-328-352-5369	Sequence 5369, Ap
349	4	US-09-161-241-8	Sequence 8, Appli
350	4	US-09-161-241-9	Sequence 9, Appli
350	4	US-08-637-670-39	Sequence 39, Appl
350	4	US-09-907-794A-236	Sequence 236, App
350	4	US-09-905-125A-236	Sequence 236, App
350	4	US-09-502-775A-236	Sequence 236, App
369	4	US-09-252-991A-25533	Sequence 25533, A
374	4	US-09-679-279-6	Sequence 6, Appli
443	4	US-09-134-001C-4211	Sequence 4211, Ap
477	4	US-09-252-991A-16778	Sequence 16778, A
491	4	US-09-134-000C-5331	Sequence 5331, Ap
496	4	US-09-252-991A-22803	Sequence 22803, A
612	4	US-09-489-039A-10702	Sequence 10702, A
666	4	US-09-134-001C-5465	Sequence 5465, Ap
719	4	US-09-252-991A-28768	Sequence 28768, A
804	4	US-09-107-532A-6348	Sequence 6348, Ap
972	3	US-08-335-844A-24	Sequence 24, Appl
972	4	US-09-129-366-24	Sequence 24, Appl
1124	4	US-09-191-786-1	Sequence 1, Appli
59	4	US-09-732-210-877	Sequence 877, App
60	4	US-09-134-001C-3266	Sequence 3266, Ap
97	4	US-09-543-681A-6995	Sequence 6995, Ap
100	4	US-09-732-210-1175	Sequence 1175, Ap
107	4	US-09-489-039A-7438	Sequence 7438, Ap
139	4	US-08-065-844A-8	Sequence 8, Appli
178	4	US-09-489-039A-11531	Sequence 11531, A
287	4	US-09-489-039A-8878	Sequence 8878, Ap
289	4	US-09-395-674B-2	Sequence 2, Appli
295	4	US-09-425-488-8	Sequence 8, Appli
362	4	US-09-134-001C-4466	Sequence 4466, Ap
373	4	US-09-328-352-5753	Sequence 5753, Ap
383	3	US-08-836-261A-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
 US-09-252-063-9
 ; Sequence 9, Application US/09252063
 ; Patent No. 6538022
 ; GENERAL INFORMATION:
 ; APPLICANT: Pollesello, Piero
 ; APPLICANT: Ovaska, Martti
 ; APPLICANT: Tenhunen, Jukka
 ; APPLICANT: Vidgren, Jukka
 ; APPLICANT: Yliperttula-Ikonen, Marjo
 ; APPLICANT: Tilgmann, Carola
 ; APPLICANT: Lotta, Timo
 ; APPLICANT: Kaivola, Juha
 ; TITLE OF INVENTION: Compounds for Deactivating Phospholamban Function on
 ; FILE REFERENCE: 1102.0250001
 ; CURRENT APPLICATION NUMBER: US/09/252,063
 ; CURRENT FILING DATE: 1999-02-18
 ; EARLIER APPLICATION NUMBER: 08/937,117
 ; EARLIER FILING DATE: 1997-09-24
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 9
 ; LENGTH: 36
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: cystolic part
 ; OTHER INFORMATION: of phospholamban peptide
 US-09-252-063-9

Query Match 93.4%; Score 71; DB 4; Length 36;
 Best Local Similarity 100.0%; Pred. No. 1.1e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRA 15
 |||||
 Db 1 MEKVQYLTRSAIRRA 15

RESULT 2
 US-09-252-063-1
 ; Sequence 1, Application US/09252063
 ; Patent No. 6538022
 ; GENERAL INFORMATION:
 ; APPLICANT: Pollesello, Piero
 ; APPLICANT: Ovaska, Martti
 ; APPLICANT: Tenhunen, Jukka
 ; APPLICANT: Vidgren, Jukka
 ; APPLICANT: Yliperttula-Ikonen, Marjo
 ; APPLICANT: Tilgmann, Carola
 ; APPLICANT: Lotta, Timo
 ; APPLICANT: Kaivola, Juha
 ; TITLE OF INVENTION: Compounds for Deactivating Phospholamban Function on
 ; FILE REFERENCE: 1102.0250001
 ; CURRENT APPLICATION NUMBER: US/09/252,063
 ; CURRENT FILING DATE: 1999-02-18
 ; EARLIER APPLICATION NUMBER: 08/937,117
 ; EARLIER FILING DATE: 1997-09-24
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 1
 ; LENGTH: 52
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-252-063-1

Query Match 93.4%; Score 71; DB 4; Length 52;
 Best Local Similarity 100.0%; Pred. No. 1.1e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRA 15
 |||||
 Db 1 MEKVQYLTRSAIRRA 15

RESULT 3
 US-09-252-063-4
 ; Sequence 4, Application US/09252063
 ; Patent No. 6538022
 ; GENERAL INFORMATION:
 ; APPLICANT: Pollesello, Piero
 ; APPLICANT: Ovaska, Martti
 ; APPLICANT: Tenhunen, Jukka
 ; APPLICANT: Vidgren, Jukka
 ; APPLICANT: Yliperttula-Ikonen, Marjo
 ; APPLICANT: Tilgmann, Carola
 ; APPLICANT: Lotta, Timo
 ; APPLICANT: Kaivola, Juha
 ; TITLE OF INVENTION: Compounds for Deactivating Phospholamban Function on
 ; FILE REFERENCE: 1102.0250001
 ; CURRENT APPLICATION NUMBER: US/09/252,063
 ; CURRENT FILING DATE: 1999-02-18
 ; EARLIER APPLICATION NUMBER: 08/937,117
 ; EARLIER FILING DATE: 1997-09-24
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 4
 ; LENGTH: 52
 ; TYPE: PRT
 ; ORGANISM: Oryctolagus cuniculus
 US-09-252-063-4

Query Match 93.4%; Score 71; DB 4; Length 52;
 Best Local Similarity 100.0%; Pred. No. 1.1e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRA 15
 |||||
 Db 1 MEKVQYLTRSAIRRA 15

RESULT 4
 US-09-252-063-5
 ; Sequence 5, Application US/09252063
 ; Patent No. 6538022
 ; GENERAL INFORMATION:
 ; APPLICANT: Pollesello, Piero
 ; APPLICANT: Ovaska, Martti
 ; APPLICANT: Tenhunen, Jukka
 ; APPLICANT: Vidgren, Jukka
 ; APPLICANT: Yliperttula-Ikonen, Marjo
 ; APPLICANT: Tilgmann, Carola
 ; APPLICANT: Lotta, Timo
 ; APPLICANT: Kaivola, Juha
 ; TITLE OF INVENTION: Compounds for Deactivating Phospholamban Function on
 ; FILE REFERENCE: 1102.0250001
 ; CURRENT APPLICATION NUMBER: US/09/252,063
 ; CURRENT FILING DATE: 1999-02-18
 ; EARLIER APPLICATION NUMBER: 08/937,117
 ; EARLIER FILING DATE: 1997-09-24
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 5
 ; LENGTH: 52
 ; TYPE: PRT
 ; ORGANISM: Rattus sp.
 US-09-252-063-5

Query Match 93.4%; Score 71; DB 4; Length 52;
 Best Local Similarity 100.0%; Pred. No. 1.6e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0;

QY 1 MEKVQYLTRSAIRRA 15
 |||||
 Db 1 MEKVQYLTRSAIRRA 15

RESULT 5

US-09-252-063-6
 ; Sequence 6, Application US/09252063
 ; Patent No. 6538022
 ; GENERAL INFORMATION:
 ; APPLICANT: Pollesello, Piero
 ; APPLICANT: Ovaska, Martti
 ; APPLICANT: Tenhunen, Jukka
 ; APPLICANT: Vidgren, Jukka
 ; APPLICANT: Yliperttula-Ikonen, Marjo
 ; APPLICANT: Tilgmann, Carola
 ; APPLICANT: Lotta, Timo
 ; APPLICANT: Kaivola, Juha
 ; TITLE OF INVENTION: Compounds for Deactivating Phospholamban Function on
 ; TITLE OF INVENTION: Ca-ATPase (Phospholamban Inhibitors)
 ; FILE REFERENCE: 1102.0250001
 ; CURRENT APPLICATION NUMBER: US/09/252,063
 ; CURRENT FILING DATE: 1999-02-18
 ; EARLIER APPLICATION NUMBER: 08/937,117
 ; EARLIER FILING DATE: 1997-09-24
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 6
 ; LENGTH: 52
 ; TYPE: PRT
 ; ORGANISM: Mus sp.
 US-09-252-063-6

Query Match 93.4%; Score 71; DB 4; Length 52;
 Best Local Similarity 100.0%; Pred. No. 1.6e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0;

QY 1 MEKVQYLTRSAIRRA 15
 |||||
 Db 1 MEKVQYLTRSAIRRA 15

RESULT 6

US-09-549-872B-15
 ; Sequence 15, Application US/09549872B
 ; Patent No. 6540996
 ; GENERAL INFORMATION:
 ; APPLICANT: Zwaal, Richard
 ; APPLICANT: Groeten, Jose
 ; APPLICANT: Bogaert, Thierry
 ; TITLE OF INVENTION: COMPOUND SCREENING METHODS
 ; FILE REFERENCE: D00590/70008 (JRV/RE)
 ; CURRENT APPLICATION NUMBER: US/09/549,872B
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: GB 9908670.4
 ; PRIOR FILING DATE: 1999-04-15
 ; PRIOR APPLICATION NUMBER: US 60/129,596
 ; PRIOR FILING DATE: 1999-04-15
 ; PRIOR APPLICATION NUMBER: GB 9912736.7
 ; PRIOR FILING DATE: 1999-06-01
 ; NUMBER OF SEQ ID NOS: 39
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 15
 ; LENGTH: 52
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-549-872B-15

Query Match 93.4%; Score 71; DB 4; Length 52;
 Best Local Similarity 100.0%; Pred. No. 1.6e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0;

QY 1 MEKVQYLTRSAIRRA 15
 |||||
 Db 1 MEKVQYLTRSAIRRA 15

RESULT 7

US-09-252-063-2
 ; Sequence 2, Application US/09252063
 ; Patent No. 6538022
 ; GENERAL INFORMATION:
 ; APPLICANT: Pollesello, Piero
 ; APPLICANT: Ovaska, Martti
 ; APPLICANT: Tenhunen, Jukka
 ; APPLICANT: Vidgren, Jukka
 ; APPLICANT: Yliperttula-Ikonen, Marjo
 ; APPLICANT: Tilgmann, Carola
 ; APPLICANT: Lotta, Timo
 ; APPLICANT: Kaivola, Juha
 ; TITLE OF INVENTION: Compounds for Deactivating Phospholamban Function on
 ; TITLE OF INVENTION: Ca-ATPase (Phospholamban Inhibitors)
 ; FILE REFERENCE: 1102.0250001
 ; CURRENT APPLICATION NUMBER: US/09/252,063
 ; CURRENT FILING DATE: 1999-02-18
 ; EARLIER APPLICATION NUMBER: 08/937,117
 ; EARLIER FILING DATE: 1997-09-24
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 52
 ; TYPE: PRT
 ; ORGANISM: Sus sp.
 US-09-252-063-2

Query Match 89.5%; Score 68; DB 4; Length 52;
 Best Local Similarity 93.3%; Pred. No. 6.1e-06;
 Matches 14; Conservative 1; Mismatches 0; Indels 0;

QY 1 MEKVQYLTRSAIRRA 15
 |||||
 Db 1 MEKVQYLTRSAIRRA 15

RESULT 8

US-09-252-063-3
 ; Sequence 3, Application US/09252063
 ; Patent No. 6538022
 ; GENERAL INFORMATION:
 ; APPLICANT: Pollesello, Piero
 ; APPLICANT: Ovaska, Martti
 ; APPLICANT: Tenhunen, Jukka
 ; APPLICANT: Vidgren, Jukka
 ; APPLICANT: Yliperttula-Ikonen, Marjo
 ; APPLICANT: Tilgmann, Carola
 ; APPLICANT: Lotta, Timo
 ; APPLICANT: Kaivola, Juha
 ; TITLE OF INVENTION: Compounds for Deactivating Phospholamban Function on
 ; TITLE OF INVENTION: Ca-ATPase (Phospholamban Inhibitors)
 ; FILE REFERENCE: 1102.0250001
 ; CURRENT APPLICATION NUMBER: US/09/252,063
 ; CURRENT FILING DATE: 1999-02-18
 ; EARLIER APPLICATION NUMBER: 08/937,117
 ; EARLIER FILING DATE: 1997-09-24
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 3
 ; LENGTH: 52
 ; TYPE: PRT
 ; ORGANISM: Canis sp.
 US-09-252-063-3

Query Match 89.5%; Score 68; DB 4; Length 52;
Best Local Similarity 93.3%; Pred. No. 6.1e-06;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQLTRSAIRRA 15
|:|||||:|||||
Db 1 MDKVQLTRSAIRRA 15

RESULT 9
US-09-549-872B-14
; Sequence 14, Application US/09549872B
; Patent No. 6540996
; GENERAL INFORMATION:
; APPLICANT: Zwaal, Richard
; APPLICANT: Groenen, Jose
; APPLICANT: Egebert, Thierry
; TITLE OF INVENTION: COMPOUND SCREENING METHODS
; FILE REFERENCE: D00590/70008 (JRV/RE)
; CURRENT APPLICATION NUMBER: US/09/549,872B
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: GB 9908670.4
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: US 60/129,596
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: GB 9912736.7
; PRIOR FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Sus sp.
US-09-549-872B-14

Query Match 89.5%; Score 68; DB 4; Length 52;
Best Local Similarity 93.3%; Pred. No. 6.1e-06;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQLTRSAIRRA 15
|:|||||:|||||
Db 1 MDKVQLTRSAIRRA 15

RESULT 10
US-09-252-063-7
; Sequence 7, Application US/09252063
; Patent No. 6538022
; GENERAL INFORMATION:
; APPLICANT: Pollesello, Piero
; APPLICANT: Ovaska, Martti
; APPLICANT: Tenhunen, Jukka
; APPLICANT: Viidgren, Jukka
; APPLICANT: Yliperttula-Ikonen, Marjo
; APPLICANT: Tilgmann, Carola
; APPLICANT: Lotta, Timo
; APPLICANT: Kaivola, Juha
; TITLE OF INVENTION: Compounds for Deactivating Phospholamban Function on
; FILE OF INVENTION: Ca-ATPase (Phospholamban Inhibitors)
; FILE REFERENCE: 1102.0250001
; CURRENT APPLICATION NUMBER: US/09/252,063
; CURRENT FILING DATE: 1999-02-18
; EARLIER APPLICATION NUMBER: 08/937,117
; EARLIER FILING DATE: 1997-09-24
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Gallus sp.
US-09-252-063-7

Query Match 89.2%; Score 67; DB 4; Length 52;
Best Local Similarity 86.7%; Pred. No. 9.4e-06;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQLTRSAIRRA 15
|:|||||:|||||
Db 1 MEKVQLTRSAIRRA 15

RESULT 11
US-09-732-210-181
; Sequence 181, Application US/09732210
; Patent No. 6573361
; GENERAL INFORMATION:
; APPLICANT: Bunkers, Greg J.
; APPLICANT: Liang, Jihong
; APPLICANT: Mittauck, Cindy A.
; APPLICANT: Seale, Jeffrey W.
; APPLICANT: Wu, Yonnie S.
; TITLE OF INVENTION: Anti-fungal Proteins and Methods for Their Use
; FILE REFERENCE: 38-21(15036)B
; CURRENT APPLICATION NUMBER: US/09/732,210
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/169,513
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: US 60/169,340
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 1753
; SEQ ID NO 181
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Streptomyces coelicolor
US-09-732-210-181

Query Match 55.3%; Score 42; DB 4; Length 116;
Best Local Similarity 43.8%; Pred. No. 1.3;
Matches 7; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 MEKVQLTRSAIRRAE 16
|:|||||:|||||
Db 81 VEKIELVIRGDEVRAK 96

RESULT 12
US-09-252-991A-24791
; Sequence 24791, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 24791
; LENGTH: 765
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24791

Query Match 53.9%; Score 41; DB 4; Length 765;
Best Local Similarity 53.3%; Pred. No. 17;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 EKQVQLTRSAIRRAE 16
|:|||||:|||||
Db 502 EQVWLDREELRAE 516

RESULT 13

US-08-968-751-4
 ; Sequence 4, Application US/08968751
 ; Patent No. 5948643
 ; GENERAL INFORMATION:
 ; APPLICANT: Rubinfeld, Bonnie
 ; APPLICANT: Polakis, Paul G.
 ; APPLICANT: Ligenfelter, Carol
 ; APPLICANT: Vuong, Terilyn T.
 ; TITLE OF INVENTION: MODULATORS OF BRCA1 ACTIVITY
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: ONIX Pharmaceuticals, Inc.
 ; STREET: 3031 Research Drive
 ; CITY: Richmond
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94806
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/968,751
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Giotta, Gregory
 ; REGISTRATION NUMBER: 32,028
 ; REFERENCE/DOCKET NUMBER: ONYX1024 CG
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (510) 262-8710
 ; TELEFAX: (510) 222-9758
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 835 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-968-751-4

Query Match 52.0%; Score 39.5; DB 2; Length 835;
 Best Local Similarity 56.7%; Pred. No. 36;
 Matches 10; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

Qy 2 EKQVYLTRSAIRRAE 16

Db 712 EEVTHLTRS-LRRAE 725

RESULT 14

US-09-252-991A-28362
 ; Sequence 28362, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 28362
 ; LENGTH: 210
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 ; US-09-252-991A-28362

Query Match 51.3%; Score 39; DB 4; Length 210;
 Best Local Similarity 53.3%; Pred. No. 9,6;
 Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 2 EKQVYLTRSAIRRAE 16

Db 180 EAHQYLSREAMKRRE 194

RESULT 15

US-09-198-452A-752
 ; Sequence 752, Application US/09198452A
 ; Patent No. 6559294
 ; GENERAL INFORMATION:
 ; APPLICANT: Griffiths, R.
 ; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention
 ; TITLE OF INVENTION: and treatment of infection
 ; FILE REFERENCE: 9710-003-999
 ; CURRENT APPLICATION NUMBER: US/09/198,452A
 ; CURRENT FILING DATE: 1998-11-24
 ; NUMBER OF SEQ ID NOS: 6849
 ; SEQ ID NO 752
 ; LENGTH: 235
 ; TYPE: PRT
 ; ORGANISM: Chlamydia pneumoniae
 ; US-09-198-452A-752

Query Match 50.0%; Score 38; DB 4; Length 235;
 Best Local Similarity 57.1%; Pred. No. 17;
 Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 3 KQVYLTRSAIRRAE 16

Db 200 KQYAVQRTQRAE 213

RESULT 16

US-09-252-991A-18000
 ; Sequence 18000, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 18000
 ; LENGTH: 631
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 ; US-09-252-991A-18000

Query Match 48.7%; Score 37; DB 4; Length 631;
 Best Local Similarity 50.0%; Pred. No. 79;
 Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MEKVQYLTRSAIRRAE 14

Db 430 VELLQFLPRSVRR 443

RESULT 17

US-08-588-983-18
 ; Sequence 18, Application US/08588983
 ; Patent No. 5854067

```

GENERAL INFORMATION:
APPLICANT: Christopher B. Newgard, et al.
TITLE OF INVENTION: Methods and Compositions
for Inhibiting Hexokinase
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: US
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/588,983
FILING DATE: Concurrently herewith
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Fussey, Shelley P.M.
REGISTRATION NUMBER: 39,458
REFERENCE/DOCKET NUMBER: UTSD:424/FUS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
TELEX: N/A
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 924 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-588-983-18

Query Match 48.7%; Score 37; DB 2; Length 924;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 EKVOYLTRSAIRRAE 16
Db 638 QDVVLLREAIRRRQ 652

RESULT 18
US-08-588-976-18
; Sequence 18, Application US/08588976
; Patent No. 5891717
; GENERAL INFORMATION:
; APPLICANT: Christopher B. Newgard, et al.
; TITLE OF INVENTION: Methods and Compositions for
; Inhibiting Hexokinase
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: US
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/588,976
; FILING DATE: Concurrently herewith
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Fussey, Shelley P.M.

```

```

GENERAL INFORMATION:
REGISTRATION NUMBER: 39,458
REFERENCE/DOCKET NUMBER: UTSD:481/FUS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
TELEX: N/A
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 924 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-588-976-18

Query Match 48.7%; Score 37; DB 2; Length 924;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 EKVOYLTRSAIRRAE 16
Db 638 QDVVLLREAIRRRQ 652

RESULT 19
US-09-489-039A-7319
; Sequence 7319, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 7319
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-7319

Query Match 47.4%; Score 36; DB 4; Length 98;
Best Local Similarity 58.3%; Pred. No. 15;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 KVOYLTRSAIR 14
Db 51 KPQHLTRSGMRK 62

RESULT 20
US-09-489-039A-11071
; Sequence 11071, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 11071
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11071

Query Match 47.4%; Score 36; DB 4; Length 194;

```

Best Local Similarity 58.3%; Pred. No. 33;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MEKVOYLTRGAI 12
Db 111 MERVYLLQSQI 122

RESULT 21
US-08-489-733-6
; Sequence 6, Application US/08489733
; Patent No. 5744345
; GENERAL INFORMATION:
; APPLICANT: Atsushi SHIMADA et al.
; TITLE OF INVENTION: HYPERTHERMOSTABLE -GALACTOSIDASES GENE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/489,733
; FILING DATE: June 14, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/175,533
; FILING DATE: December 30, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 489 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-489-733-6

Query Match 47.4%; Score 36; DB 1; Length 489;
Best Local Similarity 46.2%; Pred. No. 92;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 4 VOYLTRSAIRAE 16
Db 319 VNYTVTRVXKTE 331

RESULT 22
US-08-993-581B-6
; Sequence 6, Application US/08993581B
; Patent No. 5962326
; GENERAL INFORMATION:
; APPLICANT: Atsushi SHIMADA et al.
; TITLE OF INVENTION: HYPERTHERMOSTABLE -GALACTOSIDASE GENE,
; AND PROCESS FOR PRODUCTION (AS AMENDED)
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
; STREET: 2033 K Street, N.W., Suite 800

Query Match 47.4%; Score 36; DB 4; Length 630;
Best Local Similarity 55.6%; Pred. No. 1.2e+02;
Matches 10; Conservative 2; Mismatches 4; Indels 2; Gaps 1;

Qy 1 MEKVOYL--TRSAIRAE 16
Db 421 MGRVQYLMQCKSAVSAE 438

CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993,581B
FILING DATE: December 18, 1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/489,733
FILING DATE: June 14, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Lee Cheng
REGISTRATION NUMBER: 40,949
REFERENCE/DOCKET NUMBER: 97-7613/LC(WMC)/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250
TELEX:
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 489 amino acid residues
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-993-581B-6

Query Match 47.4%; Score 36; DB 2; Length 489;
Best Local Similarity 46.2%; Pred. No. 92;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 4 VOYLTRSAIRAE 16
Db 319 VNYTVTRVXKTE 331

RESULT 23
US-09-342-647-2
; Sequence 2, Application US/09342647A
; Patent No. 6368840
; GENERAL INFORMATION:
; APPLICANT: Caboon, Edgar B.
; APPLICANT: Hitz, William D.
; APPLICANT: Kinney, Anthony J.
; TITLE OF INVENTION: ACYL-COA Oxidase Homologs
; FILE REFERENCE: BB-1175
; CURRENT APPLICATION NUMBER: US/09/342,647A
; CURRENT FILING DATE: 1999-06-29
; EARLIER APPLICATION NUMBER: 60/092,482
; EARLIER FILING DATE: 1998-07-10
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 2
; LENGTH: 630
; TYPE: PRT
; ORGANISM: Zea mays
US-09-342-647-2

Query Match 47.4%; Score 36; DB 4; Length 630;
Best Local Similarity 55.6%; Pred. No. 1.2e+02;
Matches 10; Conservative 2; Mismatches 4; Indels 2; Gaps 1;

Qy 1 MEKVOYL--TRSAIRAE 16
Db 421 MGRVQYLMQCKSAVSAE 438

RESULT 24

US-09-252-991A-19332
 ; Sequence 19332, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 19332
 ; LENGTH: 686
 ; TYPE: PRI
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-19332

Query Match 47.4%; Score 36; DB 4; Length 686;
 Best Local Similarity 77.8%; Pred. No. 1.3e+02;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 VQYLRSAL 12
 Db 522 VQYLRSGL 530

RESULT 25

US-07-642-734C-4
 ; Sequence 4, Application US/07642734C
 ; Patent No. 5824513
 ; GENERAL INFORMATION:
 ; APPLICANT: Katz, L
 ; APPLICANT: Donadio, S
 ; APPLICANT: Mcalpine, J B
 ; TITLE OF INVENTION: Recombinant DNA Method for Producing
 ; TITLE OF INVENTION: Erythromycin Analogs
 ; NUMBER OF SEQUENCES: 27
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Edward H. Gortan
 ; STREET: Abbott Laboratories D377/AP6D-2 One Abbott
 ; STREET: Park Rd
 ; CITY: Abbott Park
 ; STATE: IL
 ; COUNTRY: US
 ; ZIP: 60064-3500
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/642,734C
 ; FILING DATE: 17-JAN-91
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Dancakers, Andreas M
 ; REGISTRATION NUMBER: 32652
 ; REFERENCE/DOCKET NUMBER: 4952.US.01
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 708-937-9396
 ; TELEFAX: 708-938-2623
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 3567 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein

US-07-642-734C-4

Query Match 47.4%; Score 36; DB 2; Length 3567;
 Best Local Similarity 70.0%; Pred. No. 8.5e+02;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 7 LTRSAIRPAE 16
 Db 3363 INRSALRPAE 3372

Search completed: October 1, 2004, 12:21:11
 Job time : 18 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 1, 2004, 12:18:23 ; Search time 63.4 Seconds
(without alignments)
81.211 Million call updates/sec

Title: US-09-830-779-18_COPY_1_16

Perfect score: 76
Sequence: 1 MEKVYUYSAIRRAE 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1351062 seqs, 321799191 residues

Total number of hits satisfying chosen parameters: 1351062

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

Published Applications AA:*
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18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	76	100.0	35	16	US-10-705-791-13
2	76	100.0	36	16	US-10-705-791-12
3	76	100.0	52	12	US-09-954-571-1
4	76	100.0	79	16	US-10-705-791-18
5	71	93.4	16	16	US-10-705-791-8
6	71	93.4	35	16	US-10-705-791-11
7	71	93.4	36	16	US-10-705-791-10
8	71	93.4	52	12	US-09-954-571-2
9	71	93.4	52	12	US-09-954-571-5
10	71	93.4	52	14	US-10-371-101-15
11	71	93.4	52	16	US-10-408-765A-478
12	71	93.4	52	16	US-10-705-791-1
13	71	93.4	52	16	US-10-705-791-2
14	71	93.4	52	16	US-10-705-791-3
15	71	93.4	52	16	US-10-705-791-5

Sequence 17, Appl
Sequence 19, Appl
Sequence 3, Appl
Sequence 14, Appl
Sequence 4, Appl
Sequence 3, Appl
Sequence 6, Appl
Sequence 10177, A
Sequence 238702, A
Sequence 46161, A
Sequence 47242, A
Sequence 494, App
Sequence 1447, App
Sequence 20314, A
Sequence 95, Appl
Sequence 53984, A
Sequence 3817, A
Sequence 201301, A
Sequence 176057, A
Sequence 43, Appl
Sequence 43, Appl
Sequence 45, Appl
Sequence 45, Appl
Sequence 752, App
Sequence 177, App
Sequence 176056, A
Sequence 175485, A
Sequence 5733, App
Sequence 53593, A
Sequence 3, Appl
Sequence 21630, A
Sequence 21552, A
Sequence 177006, A
Sequence 13951, A
Sequence 50, Appl
Sequence 188757, A
Sequence 170920, A
Sequence 195661, A
Sequence 61911, A
Sequence 13091, A
Sequence 55916, A
Sequence 3096, App
Sequence 13101, A
Sequence 66259, A
Sequence 48867, A
Sequence 56690, A
Sequence 410, App
Sequence 75204, A
Sequence 76042, A
Sequence 10036, A
Sequence 42898, A
Sequence 701, App
Sequence 60094, A
Sequence 20, Appl
Sequence 56, Appl
Sequence 3, Appl
Sequence 34, Appl
Sequence 36, Appl
Sequence 36, Appl
Sequence 38, Appl
Sequence 39, Appl
Sequence 40, Appl
Sequence 41, Appl
Sequence 41, Appl
Sequence 11000, A
Sequence 453, App
Sequence 453, App
Sequence 3012, App
Sequence 179, App
Sequence 144511, A

Sequence 4858, Ap
Sequence 152503,
Sequence 147002,
Sequence 442, App
Sequence 464, App
Sequence 222332,
Sequence 71415, A
Sequence 164, App
Sequence 38, Appl
Sequence 52269, A
Sequence 11067, A

ALIGNMENTS

RESULT 1
US-10-705-791-13
; Sequence 13, Application US/10705791
; Publication No. US20040121942A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; APPLICANT: Chien, Kenneth
; APPLICANT: Dillmann, Wolfgang
; APPLICANT: Minamisawa, Susanne
; APPLICANT: He, Huaping
; APPLICANT: Hoshijima, Masahiko
; APPLICANT: Meyer, Markus
; APPLICANT: Scott, Christopher
; APPLICANT: Wang, Yibin
; APPLICANT: Silverman, Gregg J.
; TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
; TITLE OF INVENTION: OF CARDIAC DISEASE
; FILE REFERENCE: 6627-PA9025
; CURRENT APPLICATION NUMBER: US/10/705,791
; CURRENT FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: 60/106,718
; PRIOR FILING DATE: 1998-11-02
; PRIOR APPLICATION NUMBER: PCT/US99/25692
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 13
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-705-791-13

Query Match 100.0%; Score 76; DB 16; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRAE 16
Db 16 MEKVQYLTRSAIRRAE 31

RESULT 2
US-10-705-791-12
; Sequence 12, Application US/10705791
; Publication No. US20040121942A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; APPLICANT: Chien, Kenneth
; APPLICANT: Dillmann, Wolfgang
; APPLICANT: Minamisawa, Susanne
; APPLICANT: He, Huaping
; APPLICANT: Hoshijima, Masahiko
; APPLICANT: Meyer, Markus
; APPLICANT: Scott, Christopher
; APPLICANT: Wang, Yibin
; APPLICANT: Silverman, Gregg J.

; TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
; TITLE OF INVENTION: OF CARDIAC DISEASE
; FILE REFERENCE: 6627-PA9025
; CURRENT APPLICATION NUMBER: US/10/705,791
; CURRENT FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: 60/106,718
; PRIOR FILING DATE: 1998-11-02
; PRIOR APPLICATION NUMBER: PCT/US99/25692
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 12
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-705-791-12

Query Match 100.0%; Score 76; DB 16; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRAE 16
Db 1 MEKVQYLTRSAIRRAE 16

RESULT 3
US-09-954-571-1
; Sequence 1, Application US/09954571
; Publication No. US20020032167A1
; GENERAL INFORMATION:
; APPLICANT: Chien, Kenneth R
; APPLICANT: Hoshijima, Masahiko
; APPLICANT: Ross, John
; APPLICANT: Ikeda, Yasuhiro
; TITLE OF INVENTION: HIGH EFFICIENCY CARDIAC GENE TRANSFER
; FILE REFERENCE: 6627-PA0123
; CURRENT APPLICATION NUMBER: US/09/954,571
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: 60/231,821
; PRIOR FILING DATE: 2000-11-09
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 1
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Mutant form of human protein sequence
US-09-954-571-1

Query Match 100.0%; Score 76; DB 12; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRAE 16
Db 1 MEKVQYLTRSAIRRAE 16

RESULT 4
US-10-705-791-18
; Sequence 18, Application US/10705791
; Publication No. US20040121942A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; APPLICANT: Chien, Kenneth
; APPLICANT: Dillmann, Wolfgang
; APPLICANT: Minamisawa, Susanne
; APPLICANT: He, Huaping
; APPLICANT: Hoshijima, Masahiko
; APPLICANT: Meyer, Markus
; APPLICANT: Scott, Christopher

```

; APPLICANT: Wang, Yibin
; APPLICANT: Silverman, Gregg J.
; TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
; TITLE OF INVENTION: OF CARDIAC DISEASE
; FILE REFERENCE: 6627-PA9025
; CURRENT APPLICATION NUMBER: US/10/705,791
; CURRENT FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: 60/106,718
; PRIOR FILING DATE: 1998-11-02
; PRIOR APPLICATION NUMBER: PCT/US99/25692
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 18
; LENGTH: 79
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-705-791-18

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Query Match          100.0%; Score 76; DB 16; Length 79;
Best Local Similarity 100.0%; Pred. No. 2.6e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 MEKVQYLTRSAIRAE 15
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Db 1 MEKVQYLTRSAIRAE 16
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RESULT 5
US-10-705-791-8
; Sequence 8, Application US/10705791
; Publication No. US20040121942A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; APPLICANT: Chien, Kenneth
; APPLICANT: Dillmann, Wolfgang
; APPLICANT: Minamisawa, Susanne
; APPLICANT: He, Huaping
; APPLICANT: Hoshijima, Masahiko
; APPLICANT: Meyer, Markus
; APPLICANT: Scott, Christopher
; APPLICANT: Wang, Yibin
; APPLICANT: Silverman, Gregg J.
; TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
; TITLE OF INVENTION: OF CARDIAC DISEASE
; FILE REFERENCE: 6627-PA9025
; CURRENT APPLICATION NUMBER: US/10/705,791
; CURRENT FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: 60/106,718
; PRIOR FILING DATE: 1998-11-02
; PRIOR APPLICATION NUMBER: PCT/US99/25692
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 8
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-705-791-8

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Query Match          93.4%; Score 71; DB 16; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 MEKVQYLTRSAIRRA 15
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Db 1 MEKVQYLTRSAIRRA 15
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```

RESULT 6
US-10-705-791-11
; Sequence 11, Application US/10705791
; Publication No. US20040121942A1

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; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; APPLICANT: Chien, Kenneth
; APPLICANT: Dillmann, Wolfgang
; APPLICANT: Minamisawa, Susanne
; APPLICANT: He, Huaping
; APPLICANT: Hoshijima, Masahiko
; APPLICANT: Meyer, Markus
; APPLICANT: Scott, Christopher
; APPLICANT: Wang, Yibin
; APPLICANT: Silverman, Gregg J.
; TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
; TITLE OF INVENTION: OF CARDIAC DISEASE
; FILE REFERENCE: 6627-PA9025
; CURRENT APPLICATION NUMBER: US/10/705,791
; CURRENT FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: 60/106,718
; PRIOR FILING DATE: 1998-11-02
; PRIOR APPLICATION NUMBER: PCT/US99/25692
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 11
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-705-791-11

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Query Match          93.4%; Score 71; DB 16; Length 35;
Best Local Similarity 100.0%; Pred. No. 9.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 MEKVQYLTRSAIRRA 15
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Db 16 MEKVQYLTRSAIRRA 30
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RESULT 7
US-10-705-791-10
; Sequence 10, Application US/10705791
; Publication No. US20040121942A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; APPLICANT: Chien, Kenneth
; APPLICANT: Dillmann, Wolfgang
; APPLICANT: Minamisawa, Susanne
; APPLICANT: He, Huaping
; APPLICANT: Hoshijima, Masahiko
; APPLICANT: Meyer, Markus
; APPLICANT: Scott, Christopher
; APPLICANT: Wang, Yibin
; APPLICANT: Silverman, Gregg J.
; TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
; TITLE OF INVENTION: OF CARDIAC DISEASE
; FILE REFERENCE: 6627-PA9025
; CURRENT APPLICATION NUMBER: US/10/705,791
; CURRENT FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: 60/106,718
; PRIOR FILING DATE: 1998-11-02
; PRIOR APPLICATION NUMBER: PCT/US99/25692
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 10
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-705-791-10

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Query Match          93.4%; Score 71; DB 16; Length 36;
Best Local Similarity 100.0%; Pred. No. 9.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MEKVQYLTRSAIRRA 15
 Db 1 MEKVQYLTRSAIRRA 15

RESULT 8

US-09-954-571-2
 ; Sequence 2, Application US/09954571
 ; Publication No. US20020032167A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Chien, Kenneth R
 ; APPLICANT: Hoshijima, Masahiko
 ; APPLICANT: Ross, John
 ; APPLICANT: Ikeda, Yasuhiro
 ; TITLE OF INVENTION: HIGH EFFICIENCY CARDIAC GENE TRANSFER
 ; FILE REFERENCE: 6627-PA0123
 ; CURRENT APPLICATION NUMBER: US/09/954,571
 ; CURRENT FILING DATE: 2001-09-11
 ; PRIOR APPLICATION NUMBER: 60/231,821
 ; PRIOR FILING DATE: 2000-11-09
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 2
 ; LENGTH: 52
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-954-571-2

Query Match 93.4%; Score 71; DB 12; Length 52;
 Best Local Similarity 100.0%; Pred. No. 1.4e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRA 15
 Db 1 MEKVQYLTRSAIRRA 15

RESULT 9

US-09-954-571-4
 ; Sequence 4, Application US/09954571
 ; Publication No. US20020032167A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Chien, Kenneth R
 ; APPLICANT: Hoshijima, Masahiko
 ; APPLICANT: Ross, John
 ; APPLICANT: Ikeda, Yasuhiro
 ; TITLE OF INVENTION: HIGH EFFICIENCY CARDIAC GENE TRANSFER
 ; FILE REFERENCE: 6627-PA0123
 ; CURRENT APPLICATION NUMBER: US/09/954,571
 ; CURRENT FILING DATE: 2001-09-11
 ; PRIOR APPLICATION NUMBER: 60/231,821
 ; PRIOR FILING DATE: 2000-11-09
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 4
 ; LENGTH: 52
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-09-954-571-4

Query Match 93.4%; Score 71; DB 12; Length 52;
 Best Local Similarity 100.0%; Pred. No. 1.4e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRA 15
 Db 1 MEKVQYLTRSAIRRA 15

RESULT 10

US-09-954-571-5
 ; Sequence 5, Application US/09954571
 ; Publication No. US20020032167A1

; GENERAL INFORMATION:
 ; APPLICANT: Chien, Kenneth R
 ; APPLICANT: Hoshijima, Masahiko
 ; APPLICANT: Ross, John
 ; APPLICANT: Ikeda, Yasuhiro
 ; TITLE OF INVENTION: HIGH EFFICIENCY CARDIAC GENE TRANSFER
 ; FILE REFERENCE: 6627-PA0123
 ; CURRENT APPLICATION NUMBER: US/09/954,571
 ; CURRENT FILING DATE: 2001-09-11
 ; PRIOR APPLICATION NUMBER: 60/231,821
 ; PRIOR FILING DATE: 2000-11-09
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 5
 ; LENGTH: 52
 ; TYPE: PRT
 ; ORGANISM: Oryctolagus cuniculus
 US-09-954-571-5

Query Match 93.4%; Score 71; DB 12; Length 52;
 Best Local Similarity 100.0%; Pred. No. 1.4e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRA 15
 Db 1 MEKVQYLTRSAIRRA 15

RESULT 11

US-10-371-101-15
 ; Sequence 15, Application US/10371101
 ; Publication No. US20030149995A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Zwaal, Richard
 ; APPLICANT: Groenert, Jose
 ; APPLICANT: Bogaert, Thierry
 ; TITLE OF INVENTION: COMPOUND SCREENING METHODS
 ; FILE REFERENCE: D00590.70035.US
 ; CURRENT APPLICATION NUMBER: US/10/371,101
 ; CURRENT FILING DATE: 2003-02-21
 ; PRIOR APPLICATION NUMBER: GB 9908670.4
 ; PRIOR FILING DATE: 1999-04-15
 ; PRIOR APPLICATION NUMBER: US 60/129,596
 ; PRIOR FILING DATE: 1999-04-15
 ; PRIOR APPLICATION NUMBER: GB 9912736.7
 ; PRIOR FILING DATE: 1999-06-01
 ; PRIOR APPLICATION NUMBER: 09/549,872
 ; PRIOR FILING DATE: 2000-04-14
 ; NUMBER OF SEQ ID NOS: 39
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 15
 ; LENGTH: 52
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-371-101-15

Query Match 93.4%; Score 71; DB 14; Length 52;
 Best Local Similarity 100.0%; Pred. No. 1.4e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRA 15
 Db 1 MEKVQYLTRSAIRRA 15

RESULT 12

US-10-408-765A-478
 ; Sequence 478, Application US/10408765A
 ; Publication No. US20040101874A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ghosh, Soumitra S.
 ; APPLICANT: Fahy, Eoin D.
 ; APPLICANT: Zhang, Bing

; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 478
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-478

Query Match 93.4%; Score 71; DB 15; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRA 15
Db 1 MEKVQYLTRSAIRRA 15

RESULT 13
US-10-705-791-1
; Sequence 1, Application US/10705791
; Publication No. US20040121942A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; APPLICANT: Chien, Kenneth
; APPLICANT: Dillmann, Wolfgang
; APPLICANT: Minamisawa, Susanne
; APPLICANT: He, Huaping
; APPLICANT: Hoshijima, Masahiko
; APPLICANT: Meyer, Markus
; APPLICANT: Scott, Christopher
; APPLICANT: Wang, Yibin
; APPLICANT: Silverman, Gregg J.
; TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
; FILE REFERENCE: 6627-PA9025
; CURRENT APPLICATION NUMBER: US/10/705,791
; CURRENT FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: 60/106,718
; PRIOR FILING DATE: 1998-11-02
; PRIOR APPLICATION NUMBER: PCT/US99/25692
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-705-791-1

Query Match 93.4%; Score 71; DB 16; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRA 15
Db 1 MEKVQYLTRSAIRRA 15

RESULT 14
US-10-705-791-2
; Sequence 2, Application US/10705791
; Publication No. US20040121942A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California

; APPLICANT: Chien, Kenneth
; APPLICANT: Dillmann, Wolfgang
; APPLICANT: Minamisawa, Susanne
; APPLICANT: He, Huaping
; APPLICANT: Hoshijima, Masahiko
; APPLICANT: Meyer, Markus
; APPLICANT: Scott, Christopher
; APPLICANT: Wang, Yibin
; APPLICANT: Silverman, Gregg J.
; TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
; FILE REFERENCE: 6627-PA9025
; CURRENT APPLICATION NUMBER: US/10/705,791
; CURRENT FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: 60/106,718
; PRIOR FILING DATE: 1998-11-02
; PRIOR APPLICATION NUMBER: PCT/US99/25692
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-705-791-2

Query Match 93.4%; Score 71; DB 16; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRA 15
Db 1 MEKVQYLTRSAIRRA 15

RESULT 15
US-10-705-791-5
; Sequence 5, Application US/10705791
; Publication No. US20040121942A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; APPLICANT: Chien, Kenneth
; APPLICANT: Dillmann, Wolfgang
; APPLICANT: Minamisawa, Susanne
; APPLICANT: He, Huaping
; APPLICANT: Hoshijima, Masahiko
; APPLICANT: Meyer, Markus
; APPLICANT: Scott, Christopher
; APPLICANT: Wang, Yibin
; APPLICANT: Silverman, Gregg J.
; TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
; FILE REFERENCE: 6627-PA9025
; CURRENT APPLICATION NUMBER: US/10/705,791
; CURRENT FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: 60/106,718
; PRIOR FILING DATE: 1998-11-02
; PRIOR APPLICATION NUMBER: PCT/US99/25692
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-705-791-5

Query Match 93.4%; Score 71; DB 16; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRA 15

Db 1 MEKVQYLTRSAIRRA 15

```
RESULT 16
US-10-705-791-17
; Sequence 17, Application US/10705791
; Publication No. US20040121942A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; APPLICANT: Chien, Kenneth
; APPLICANT: Dillmann, Wolfgang
; APPLICANT: Minamisawa, Susanne
; APPLICANT: He, Huaping
; APPLICANT: Hoshijima, Masahiko
; APPLICANT: Meyer, Markus
; APPLICANT: Scott, Christopher
; APPLICANT: Wang, Yibin
; APPLICANT: Silverman, Gregg J.
; TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
; FILE REFERENCE: 6627-PA9025
; CURRENT APPLICATION NUMBER: US/10/705,791
; CURRENT FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: 60/106,718
; PRIOR FILING DATE: 1998-11-02
; PRIOR APPLICATION NUMBER: PCT/US99/25692
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 79
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-705-791-17
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Query Match 93.4%; Score 71; DB 16; Length 79;
Best Local Similarity 100.0%; Pred. No. 2.2e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRA 15
Db 1 MEKVQYLTRSAIRRA 15

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RESULT 17
US-10-705-791-19
; Sequence 19, Application US/10705791
; Publication No. US20040121942A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; APPLICANT: Chien, Kenneth
; APPLICANT: Dillmann, Wolfgang
; APPLICANT: Minamisawa, Susanne
; APPLICANT: He, Huaping
; APPLICANT: Hoshijima, Masahiko
; APPLICANT: Meyer, Markus
; APPLICANT: Scott, Christopher
; APPLICANT: Wang, Yibin
; APPLICANT: Silverman, Gregg J.
; TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
; FILE REFERENCE: 6627-PA9025
; CURRENT APPLICATION NUMBER: US/10/705,791
; CURRENT FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: 60/106,718
; PRIOR FILING DATE: 1998-11-02
; PRIOR APPLICATION NUMBER: PCT/US99/25692
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19
; LENGTH: 79
; TYPE: PRT
; ORGANISM: Escherichia coli
```

; ORGANISM: Escherichia coli
US-10-705-791-19

Query Match 93.4%; Score 71; DB 16; Length 79;
Best Local Similarity 100.0%; Pred. No. 2.2e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRA 15
Db 1 MEKVQYLTRSAIRRA 15

```
RESULT 18
US-09-954-571-3
; Sequence 3, Application US/09954571
; Publication No. US20020032167A1
; GENERAL INFORMATION:
; APPLICANT: Chien, Kenneth R
; APPLICANT: Hoshijima, Masahiko
; APPLICANT: Ross, John
; APPLICANT: Ikeda, Yasuhiro
; TITLE OF INVENTION: HIGH EFFICIENCY CARDIAC GENE TRANSFER
; FILE REFERENCE: 6627-PA0123
; CURRENT APPLICATION NUMBER: US/09/954,571
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: 60/231,821
; PRIOR FILING DATE: 2000-11-09
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-954-571-3
```

Query Match 89.5%; Score 68; DB 12; Length 52;
Best Local Similarity 93.3%; Pred. No. 5e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRA 15
Db 1 MEKVQYLTRSAIRRA 15

```
RESULT 19
US-10-371-101-14
; Sequence 14, Application US/10371101
; Publication No. US20030149995A1
; GENERAL INFORMATION:
; APPLICANT: Zwaal, Richard
; APPLICANT: Groenen, Jose
; APPLICANT: Bogaert, Thierry
; TITLE OF INVENTION: COMPOUND SCREENING METHODS
; FILE REFERENCE: D00590.70035.US
; CURRENT APPLICATION NUMBER: US/10/371,101
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: GB 9908670.4
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: US 60/129,596
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: GB 9912736.7
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: 09/549,872
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Sus sp.
US-10-371-101-14
```

Query Match 89.5%; Score 68; DB 14; Length 52;

Best Local Similarity 93.3%; Pred. No. 5e-05; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MEKVQYLTRSAIRRA 15
Db 1 MDKVQYLTRSAIRRA 15

RESULT 20
US-10-705-791-4
; Sequence 4, Application US/10705791
; Publication No. US20040121942A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; APPLICANT: Chien, Kenneth
; APPLICANT: Dillmann, Wolfgang
; APPLICANT: Minamisawa, Susanne
; APPLICANT: He, Huaping
; APPLICANT: Hoshijima, Masahiko
; APPLICANT: Meyer, Markus
; APPLICANT: Scott, Christopher
; APPLICANT: Wang, Yibin
; APPLICANT: Silverman, Gregg J.
; TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
; FILE REFERENCE: 6627-PA9025
; CURRENT APPLICATION NUMBER: US/10/705,791
; CURRENT FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: 60/106,718
; PRIOR FILING DATE: 1998-11-02
; PRIOR APPLICATION NUMBER: PCT/US99/25692
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-705-791-4

Query Match 86.8%; Score 66; DB 16; Length 52;
Best Local Similarity 93.3%; Pred. No. 0.00012;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MEKVQYLTRSAIRRA 15
Db 1 MEKVQYLTRSAIRRA 15

RESULT 21
US-10-705-791-3
; Sequence 3, Application US/10705791
; Publication No. US20040121942A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; APPLICANT: Chien, Kenneth
; APPLICANT: Dillmann, Wolfgang
; APPLICANT: Minamisawa, Susanne
; APPLICANT: He, Huaping
; APPLICANT: Hoshijima, Masahiko
; APPLICANT: Meyer, Markus
; APPLICANT: Scott, Christopher
; APPLICANT: Wang, Yibin
; APPLICANT: Silverman, Gregg J.
; TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
; FILE REFERENCE: 6627-PA9025
; CURRENT APPLICATION NUMBER: US/10/705,791
; CURRENT FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: 60/106,718
; PRIOR FILING DATE: 1998-11-02
; PRIOR APPLICATION NUMBER: PCT/US99/25692
; PRIOR FILING DATE: 1999-11-02

; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-705-791-3

Query Match 85.5%; Score 65; DB 16; Length 52;
Best Local Similarity 93.3%; Pred. No. 0.00018;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MEKVQYLTRSAIRRA 15
Db 1 MAKVQYLTRSAIRRA 15

RESULT 22
US-10-705-791-6
; Sequence 6, Application US/10705791
; Publication No. US20040121942A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; APPLICANT: Chien, Kenneth
; APPLICANT: Dillmann, Wolfgang
; APPLICANT: Minamisawa, Susanne
; APPLICANT: He, Huaping
; APPLICANT: Hoshijima, Masahiko
; APPLICANT: Meyer, Markus
; APPLICANT: Scott, Christopher
; APPLICANT: Wang, Yibin
; APPLICANT: Silverman, Gregg J.
; TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
; FILE REFERENCE: 6627-PA9025
; CURRENT APPLICATION NUMBER: US/10/705,791
; CURRENT FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: 60/106,718
; PRIOR FILING DATE: 1998-11-02
; PRIOR APPLICATION NUMBER: PCT/US99/25692
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-705-791-6

Query Match 81.6%; Score 62; DB 16; Length 52;
Best Local Similarity 86.7%; Pred. No. 0.00064;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MEKVQYLTRSAIRRA 15
Db 1 MEEVQYLTRSAIRRA 15

RESULT 23
US-10-156-761-10177
; Sequence 10177, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761

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; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 10177
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-10177

Query Match          55.3%; Score 42; DB 14; Length 116;
Best Local Similarity 43.8%; Pred. No. 7.6;
Matches 7; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRAE 16
      :||: :||: :||:
Db 81 VEKIELVTRGDVRRAK 96

RESULT 24
US-10-424-599-238702
; Sequence 238702, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 238702
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_57573C.1.pep
US-10-424-599-238702

Query Match          53.9%; Score 41; DB 12; Length 44;
Best Local Similarity 46.2%; Pred. No. 4.1;
Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIR 13
      :||: :||: :||:
Db 25 LEKIEVITREIRK 37

RESULT 25
US-10-425-114-46161
; Sequence 46161, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 46161
; LENGTH: 88
; TYPE: PRT
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; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 701164165_FLI.pep
US-10-425-114-46161

Query Match          53.9%; Score 41; DB 12; Length 68;
Best Local Similarity 71.4%; Pred. No. 6.5;
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 EKQVYLTRSAIRRA 15
      :||: :||: :||:
Db 51 ETVAYLGRSAIPRA 64

Search completed: October 1, 2004, 12:48:44
Job time : 64.4 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 1, 2004, 12:05:26 ; Search time 15.6 Seconds
(without alignments)
98.658 Million cell updates/sec

Title: US-09-830-779-18_COPY_1_16
Perfect score: 76
Sequence: 1 MEKVQLTRSAIRRAE 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : PIR.78.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	71	93.4	52	1 A40424	phospholamban - hu
2	71	93.4	52	1 S37638	phospholamban - ra
3	71	93.4	52	1 A49057	phospholamban - mo
4	71	93.4	52	1 B40424	phospholamban - ra
5	68	89.5	52	1 A29002	phospholamban - do
6	68	89.5	52	1 S05540	phospholamban - pi
7	67	88.2	52	1 A39535	phospholamban - ch
8	42	55.3	116	2 T34780	ribosomal protein
9	41	53.9	121	2 B70187	ribosomal protein
10	41	53.9	417	2 H83370	hydrogen cyanide s
11	40	52.6	390	2 S53487	porphobilinogen sy
12	40	52.6	1108	2 E71104	probable cell divi
13	39.5	52.0	452	2 T34542	hypothetical prote
14	39.5	52.0	1027	2 T46296	hypothetical prote
15	39.5	52.0	1120	2 JC7765	mitotic spindle as
16	39	51.3	156	2 B83226	aliphatic amides
17	39	51.3	283	2 G83754	transcription regu
18	39	51.3	481	2 B75167	hypothetical prote
19	38	50.0	223	2 H71485	hypothetical prote
20	38	50.0	224	2 D72046	conserved hypothet
21	38	50.0	224	2 A86579	CT668 hypothetical
22	38	50.0	410	2 T12833	hypothetical prote
23	38	50.0	462	2 RH1053	probable exported
24	38	50.0	486	2 T55449	gene PR2A protein
25	38	50.0	2009	2 S49764	SEC7 protein - yea
26	37	48.7	185	2 AG2026	hypothetical prote
27	37	48.7	296	2 F70879	hypothetical prote
28	37	48.7	308	2 AC1867	hypothetical prote
29	37	48.7	451	2 F75083	phospho-sugar muta

30	37	48.7	494	2 H75217	glycerol kinase (E
31	37	48.7	924	1 S13913	hexokinase (EC 2.7
32	37	48.7	2712	2 T05113	hypothetical prote
33	36	47.4	73	2 E95078	conserved hypothet
34	36	47.4	89	2 B37945	conserved hypothet
35	36	47.4	181	2 J05207	EUO protein homolo
36	36	47.4	182	2 C36909	early upstream off
37	36	47.4	236	2 D89048	conserved hypothet
38	36	47.4	274	2 D71032	probable autocontig
39	36	47.4	274	2 F75181	polyribonucleotide
40	36	47.4	283	2 H69179	conserved hypothet
41	36	47.4	335	2 A24785	hypothetical prote
42	36	47.4	409	2 F83493	probable MFS trans
43	36	47.4	444	2 S68122	tubulin beta-4 cha
44	36	47.4	489	2 JQ0767	beta-galactosidase
45	36	47.4	489	2 B90483	beta-galactosidase
46	36	47.4	549	2 A90253	hypothetical prote
47	36	47.4	629	2 AH0521	dihydrolipoamide a
48	36	47.4	630	1 XECPDP	dihydrolipoamide S
49	36	47.4	630	2 G85494	hypothetical prote
50	36	47.4	630	2 G90643	hypothetical prote
51	36	47.4	736	2 I51691	dishevelled homolo
52	36	47.4	966	2 E84053	penicillin-binding
53	36	47.4	1148	2 D90815	transcription-repa
54	36	47.4	1148	2 H85674	hypothetical prote
55	36	47.4	3573	2 S23070	erythronolide synt
56	35	46.1	57	2 H35055	MHC class II histo
57	35	46.1	57	2 A35055	MHC class II histo
58	35	46.1	57	2 A35056	MHC class II histo
59	35	46.1	57	2 C35056	MHC class II histo
60	35	46.1	57	2 D35054	MHC class II histo
61	35	46.1	57	2 H35056	MHC class II histo
62	35	46.1	82	2 I36924	gene MHC DQ-beta 1
63	35	46.1	82	2 I61815	gene MHC DQ-beta 1
64	35	46.1	82	2 I61818	gene MHC DQ-beta 1
65	35	46.1	82	2 I61819	gene MHC DQ-beta 1
66	35	46.1	82	2 I61834	gene MHC DQ-beta 1
67	35	46.1	94	2 F30575	gene MHC DQ-beta 1
68	35	46.1	126	2 I54454	lymphocyte antigen
69	35	46.1	183	2 A32339	MHC class II histo
70	35	46.1	183	2 I54288	MHC class II DQ3.1
71	35	46.1	183	2 I79496	MHC HLA-DQ-beta ch
72	35	46.1	201	2 S74907	hypothetical prote
73	35	46.1	226	2 C81749	conserved hypothet
74	35	46.1	269	2 I54432	MHC class II histo
75	35	46.1	269	2 T16387	hypothetical prote
76	35	46.1	330	2 T08351	hypothetical prote
77	35	46.1	342	2 F98632	hypothetical prote
78	35	46.1	361	2 G75164	mannose-1-phosphat
79	35	46.1	390	2 T09000	cysteine synthase
80	35	46.1	403	2 B69338	conserved hypothet
81	35	46.1	504	1 D69417	probable thymidine
82	35	46.1	515	2 A86143	DNA-directed RNA p
83	35	46.1	515	2 S02194	hypothetical prote
84	35	46.1	522	2 T23705	hypothetical prote
85	35	46.1	535	2 T37189	hypothetical prote
86	35	46.1	561	2 G90303	hypothetical prote
87	35	46.1	622	2 JC5425	transcription init
88	35	46.1	626	1 S34120	DNA-directed DNA p
89	35	46.1	781	2 T50055	C2H2 zinc finger p
90	35	46.1	899	2 H84639	hypothetical prote
91	35	46.1	1102	2 S65235	probable membrane
92	35	46.1	1115	2 S40241	G protein-coupled
93	35	46.1	1385	2 T21706	hypothetical prote
94	35	46.1	1518	2 T28880	hypothetical prote
95	34.5	45.4	421	2 A11112	hypothetical prote
96	34.5	45.4	638	2 T48380	hypothetical prote
97	34.5	45.4	813	2 C97292	ATPases with chape
98	34	44.7	57	2 G35057	MHC class II histo
99	34	44.7	82	2 I61811	gene MHC DQ-beta 1
100	34	44.7	87	2 S38681	major histocompati

ALIGNMENTS

RESULT 1
A40424
Phospholamban - human
C:Species: Homo sapiens (man)
C>Date: 28-Feb-1992 #sequence_revision 27-Jun-1994 #text_change 18-Jun-1999
C:Accession: A40424
R:Fujii, J.; Zarain-Herzberg, A.; Willard, H.F.; Tada, M.; MacLennan, D.H.
J. Biol. Chem. 266, 11669-11675, 1991
A:Title: Structure of the rabbit phospholamban gene, cloning of the human cDNA, and assig
A:Reference number: A40424; MUID:91268032; PMID:1828805
A:Accession: A40424
A:Molecule type: mRNA
A:Residues: 1-52 <FUU>
A:Cross-references: GB:M63603; NID:9189942; PIDN:AAA60083.1; PID:g189943
C:Comment: Phospholamban is expressed in cardiac muscle, slow twitch skeletal muscle, an
C:Comment: Phospholamban is the major phosphorylated protein in cardiac muscle sarcooplasm
e; after phosphorylation, the Ca++ pump is activated and the rate of muscle relaxation i
C:Comment: Helical transmembrane domains of five chains are thought to aggregate in the
C:Genetics:
A:Gene: GDB:PLN; PLB
A:Cross-references: GDB:128300; OMIM:172405
A:Map position: 6q22.1-6q22.1
C:Superfamily: phospholamban
C:Keywords: acetylated amino end; ATPase inhibitor; muscle; pentamer; phosphoprotein; tr
F:31-52/Domain: transmembrane #status predicted <TMM>
F:1/Modified site: acetylated amino end (Met) #status predicted
F:16/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predict
F:17/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase) #status p
Query Match 93.4%; Score 71; DB 1; Length 52;
Best Local Similarity 100.0%; Pred. No. 4.6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEKVQYLTRSAIRRA 15
DB 1 MEKVQYLTRSAIRRA 15
RESULT 2
S37638
phospholamban - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 05-Mar-1994 #sequence_revision 27-Jun-1994 #text_change 18-Jun-1999
C:Accession: S37638; I52270; I64795; I51840
R:Shanahan, C.M.; Weissberg, F.L.; Metcalfe, J.C.
Circ. Res. 73, 193-204, 1993
A:Title: Isolation of gene markers of differentiated and proliferating vascular smooth m
A:Reference number: S37637; MUID:93284726; PMID:8508530
A:Accession: S37638
A:Molecule type: mRNA
A:Residues: 1-52 <SHA>
A:Cross-references: EMBL:X71068; NID:9313809; PIDN:CAA50394.1; PID:g313810
R:Johns, D.C.; Feldman, A.M.
Biochem. Biophys. Res. Commun. 188, 927-933, 1992
A:Title: Identification of a highly conserved region at the 5' flank of the phospholamba
A:Reference number: I52270; MUID:93075183; PMID:1445334
A:Accession: I52270
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 152 <UOH>
A:Cross-references: NID:103382; NID:g206134; PIDN:AAA41849.1; PID:g206136
R:Wang, K.S.; Nadal-Ginard, B.
Adv. Exp. Med. Biol. 304, 387-395, 1991
A:Title: Cloning phospholamban cDNA from rat aortic smooth muscle.
A:Reference number: I51840; MUID:92206263; PMID:1725098
A:Accession: I64795
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-52 <HWAL>
A:Cross-references: GB:S95853; NID:g247932; PIDN:AAE21903.1; PID:g247933

A:Accession: I51840
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-52 <HWA2>
A:Cross-references: GB:S95849; NID:g247934
C:Comment: Phospholamban is expressed in cardiac muscle, slow twitch skeletal muscle, and
C:Comment: Phospholamban is the major phosphorylated protein in cardiac muscle sarcooplasm
ase; after phosphorylation, the calcium pump is activated and the rate of muscle relaxat
C:Superfamily: phospholamban
C:Keywords: acetylated amino end; ATPase inhibitor; cardiac muscle; heart; pentamer; phos
F:31-52/Domain: transmembrane #status predicted <TMM>
F:1/Modified site: acetylated amino end (Met) #status predicted
F:16/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predict
F:17/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase) #status p
Query Match 93.4%; Score 71; DB 1; Length 52;
Best Local Similarity 100.0%; Pred. No. 4.6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEKVQYLTRSAIRRA 15
DB 1 MEKVQYLTRSAIRRA 15
RESULT 3
A49057
phospholamban - mouse
C:Species: Mus musculus (house mouse)
C>Date: 19-Dec-1993 #sequence_revision 27-Jun-1994 #text_change 18-Jun-1999
C:Accession: A49057
R:Sanam, J.R.; Luo, W.; Ponniah, S.; Grupp, I.; Kim, H.W.; Ferguson, D.G.; Kadambi, V.; P
Circ. Res. 71, 1021-1030, 1992
A:Title: Mouse phospholamban gene expression during development in vivo and in vitro.
A:Reference number: A49057; MUID:93008802; PMID:1394867
A:Accession: A49057
A:Molecule type: mRNA
A:Residues: 1-52 <GAN>
A:Cross-references: GB:S46792; NID:g257745; PIDN:AAB23706.1; PID:g257746
A:Experimental source: cardiac muscle
A:Note: sequence extracted from NCBI backbone (NCBI:116999, NCBIP:117001)
C:Comment: Phospholamban is expressed in cardiac muscle, slow twitch skeletal muscle, and
C:Comment: Phospholamban is the major phosphorylated protein in cardiac muscle sarcooplasm
e; after phosphorylation, the Ca++ pump is activated and the rate of muscle relaxation i
C:Superfamily: phospholamban
C:Keywords: acetylated amino end; ATPase inhibitor; muscle; pentamer; phosphoprotein; tra
F:31-52/Domain: transmembrane #status predicted <TMM>
F:1/Modified site: acetylated amino end (Met) #status predicted
F:16/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predict
F:17/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase) #status p
Query Match 93.4%; Score 71; DB 1; Length 52;
Best Local Similarity 100.0%; Pred. No. 4.6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEKVQYLTRSAIRRA 15
DB 1 MEKVQYLTRSAIRRA 15
RESULT 4
B40424
phospholamban - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 28-Feb-1992 #sequence_revision 27-Jun-1994 #text_change 18-Jun-1999
C:Accession: B40424; S00249
R:Fujii, J.; Zarain-Herzberg, A.; Willard, H.F.; Tada, M.; MacLennan, D.H.
J. Biol. Chem. 266, 11669-11675, 1991
A:Title: Structure of the rabbit phospholamban gene, cloning of the human cDNA, and assig
A:Reference number: A40424; MUID:91268032; PMID:1828805
A:Accession: B40424
A:Molecule type: DNA
A:Residues: 1-52 <RUU>
A:Cross-references: GB:M63601; NID:g165636; PIDN:AAA31445.1; PID:g165639

A/Accession: I46227
A:/Status: translated from GB/EMBL/DBDJB
A:/Molecule type: mRNA
A:/Residues: 1-52 <UY2>
A:/Cross-references: GB:M35393; NID:g164045; PIDN:AAC41618.1; PID:g164046
C/Comment: Phospholamban is expressed in cardiac muscle, slow twitch skeletal muscle, and
C/Comment: Phospholamban is the major phosphorylated protein in cardiac muscle sarcoplasm
e; after phosphorylation, the Ca++ pump is activated and the rate of muscle relaxation i
C/Superfamily: phospholamban
C/Keywords: acetylated amino end; ATPase inhibitor; muscle; pentamer; phosphoprotein; tr
F:/1-52/Domain: transmembrane #status predicted <TM>
F:/Modified site: acetylated amino end (Met) #status experimental
F:/16/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status experim
F:/17/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase) #status e;

Query Match 89.5%; Score 68; DB 1; Length 52;
Best Local Similarity 93.3%; Pred. No. 1.6e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRA 15
|:|||||
Db 1 MDKVQYLTRSAIRRA 15
|:|||||

RESULT 6
S05540
phospholamban - pig
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 21-Nov-1993 #sequence_revision 27-Jun-1994 #text_change 18-Jun-1999
C/Accession: S05540
R:/Verboomen, H.; Wuytack, F.; Eggermont, J.A.; de Jaegere, S.; Missiaen, L.; Raeymaekers,
Biochem. J. 262, 353-356, 1989
A/Title: cDNA cloning and sequencing of phospholamban from pig stomach smooth muscle.
A/Reference number: S05540; MUID:90056437; PMID:2530978
A/Accession: S05540
A/Molecule type: mRNA
A/Residues: 1-52 <VER>
A:/Cross-references: EMBL:X15075; NID:g2055; PIDN:CAA3171.1; PID:g2056
C/Comment: Phospholamban is expressed in cardiac muscle, slow twitch skeletal muscle, and
C/Comment: Phospholamban is the major phosphorylated protein in cardiac muscle sarcoplasm
e; after phosphorylation, the Ca++ pump is activated and the rate of muscle relaxation i
C/Superfamily: phospholamban
C/Keywords: acetylated amino end; ATPase inhibitor; muscle; pentamer; phosphoprotein; tr
F:/1-52/Domain: transmembrane #status predicted <TM>
F:/1/Modified site: acetylated amino end (Met) #status predicted
F:/16/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predict
F:/17/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase) #status pi

Query Match 89.5%; Score 68; DB 1; Length 52;
Best Local Similarity 93.3%; Pred. No. 1.6e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRA 15
|:|||||
Db 1 MDKVQYLTRSAIRRA 15
|:|||||

RESULT 7
S05935
phospholamban - chicken
C/Species: Gallus gallus (chicken)
C/Date: 06-Mar-1992 #sequence_revision 27-Jun-1994 #text_change 18-Jun-1999
C/Accession: A39535; R39535; A44531
R:/Toyofuku, T.; Zak, R.
J. Biol. Chem. 266, 5375-5383, 1991
A/Title: Characterization of cDNA and genomic sequences encoding a chicken phospholamban
A/Reference number: A39535; MUID:91170195; PMID:1825996
A/Accession: A39535
A/Molecule type: mRNA
A/Residues: 1-17, 'L', '19-52 <TOY>
A:/Cross-references: GB:M59039; NID:g212575; PIDN:AAA62738.1; PID:g212576
A/Note: the authors translated the codon CTT for residue 18 as Ile
A/Accession: R39535

A;Reference number: A70100; MUID:98065943; PMID:9403685
A;Accession: B70187
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
Molecule type: DNA
Residues: 1-121 <MLE>
Cross-references: GB:AEO001170; GB:AEO000783; NID:g2688623; PIDN:AAC67044.1; PID:g2688623;
Experimental source: strain B31
Superfamily: Escherichia coli ribosomal protein L19

Query Match 53.9%; Score 41; DB 2; Length 121;
Best Local Similarity 50.0%; Pred. No. 3.;
Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

DQ 1 MEKVOYLTRSAIRRAE 16
 :|||: | |: ||:
DB 80 IEKVEVLRGKVRRAK 95
 :|||: | |: ||:

RESULT 10
H83370 hydrogen cyanide synthase HmcC PA2195 [imported] - Pseudomonas aeruginosa (strain PAO1)
Species: Pseudomonas aeruginosa
Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
Accession: H83370
Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, W.J.; Briadman, S.C.; Yuan, Y.; Brady, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen
Reference number: AB2950; MUID:20437337; PMID:10984043
Accession: H83370
Status: preliminary
Molecule type: DNA
Residues: 1-417 <STO>
Cross-references: GB:AEO04646; GB:AEO04091; NID:g9948213; PIDN:AAG05583.1; GSFPB:GN0013;
Experimental source: strain PAOI
Genetics:
Gene: hmcC; PA2195

Query Match 53.9%; Score 41; DB 2; Length 417;
Best Local Similarity 53.3%; Pred. No. 13;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

DQ 2 EKQYVLTRSAIRRAE 16
 |:::||: |||
DB 154 EQRWLDRELRLAE 168
 |:::||: |||

RESULT 11
S53487 porphobilinogen synthase (EC 4.2.1.24) precursor - Chlamydomonas reinhardtii
Alternate names: delta-aminolevulinic acid dehydratase
Species: Chlamydomonas reinhardtii
Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 16-Jul-1999
Accession: S53487
Matters, G.I.; Beale, S.I.
Plant Mol. Biol. 27, 607-617, 1995
Title: Structure and expression of the Chlamydomonas reinhardtii alad gene encoding the
Reference number: S53487; MUID:95201253; PMID:7894023
Accession: S53487
Status: preliminary
Molecule type: mRNA
Residues: 1-390 <MAN>
Cross-references: EMBL,U19876; NID:g642578; PIDN:AAA79515.1; PID:g642579
Superfamily: porphobilinogen synthase
Keywords: carbon-oxygen lyase; hydro-lyase

Query Match 52.6%; Score 40; DB 2; Length 390;
Best Local Similarity 46.7%; Pred. No. 19;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

DQ 2 EKQYVLTRSAIRRAE 16
 |:::||: ||: ||:

Db 199 ETIEYLCQAVSQAE 212

RESULT 12
E71104
C:Species: Pyrococcus horikoshii
C:Probable cell division control protein - Pyrococcus horikoshii
C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 05-Nov-1999
C:Accession: E71104
R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Seki, M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushiida, N.; Oguchi, DNA Res. 5, 55-76, 1998
A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic A:Reference number: A71000; MUID:98344137; PMID:9679194
A:Accession: E71104
A:Status: Preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-1108 <RAW>
A:Cross-references: CB:AP000003; NID:g3236130; PIDN:BAA29695.1; PID:d1030638; PID:g32570
A:Experimental source: strain OT3
A:Note: This accession replaces an interim accession for a sequence replaced by GenBank C:Genetics:
A:Gene: PH0606

Query Match 52.6%; Score 40; DB 2; Length 1108;
Best Local Similarity 53.3%; Pred. No. 57;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRA 15
||| ||| :|:
Db 668 MEVKDYLTRBEVRKA 682

RESULT 13
T34542
hypothetical protein DKFPz434N2421.1 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C:Accession: T34542
R:Blum, H.; Bauersachs, S.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, October 1999
A:Reference number: Z21541
A:Accession: T34542
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-452 <BLU>
A:Cross-references: EMBL:AL122116
A:Experimental source: adult testis; clone DKFPz434N2421
C:Genetics:
A:Note: DKFPz434N2421.1

Query Match 52.0%; Score 39.5; DB 2; Length 452;
Best Local Similarity 66.7%; Pred. No. 27;
Matches 10; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

QY 2 EKQVYLTRSAIRRAE 16
|:|:|:|:|:|:
Db 329 EEVTHLTRS-LRAAE 342

RESULT 14
T46296
hypothetical protein DKFPz434H1210.1 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
C:Accession: T46296
R:Duesterhoeft, A.; Lauber, J.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, January 2000
A:Reference number: Z23035
A:Accession: T46296
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1027 <AAA>

RESULT 17

G83754
transcription regulator BH0839 [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C:Accession: G83754
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: G83754
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-283 <STO>
A:Cross-references: GB:AP001510; GB:BA000004; NID:G10173440; PIDN:BA04558.1; GSPDB:GN00
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH0839

Query Match 51.3%; Score 39; DB 2; Length 283;
Best Local Similarity 46.7%; Pred. No. 21;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 EKQVLTSAIRRAE 16
|||:|:|:|
Db 250 EKRYNTALLARKE 264

RESULT 18

B75167
hypothetical protein PAB0334 - Pyrococcus abyssi (strain Orsay)
C:Species: Pyrococcus abyssi
C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C:Accession: B75167
R:anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome str
A:Reference number: A75001
A:Accession: B75167
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-481 <KAW>
A:Cross-references: GB:AJ248284; GB:AL096836; NID:G5457730; PIDN:CA849417.1; PID:G545792
A:Experimental source: strain Orsay
C:Genetics:
A:Gene: PAB0334

Query Match 51.3%; Score 39; DB 2; Length 481;
Best Local Similarity 50.0%; Pred. No. 36;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 EKQVLTSAIRRA 15
|||:|:|:|
Db 38 EKIKYTKRAPERA 51

RESULT 19

H71485
hypothetical protein CT668 - Chlamydia trachomatis (serotype D, strain UW3/Cx)
C:Species: Chlamydia trachomatis
C>Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 08-Oct-1999
C:Accession: H71485
R:Stephens, R.S.; Kalman, S.; Lamell, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell,
Science 282, 754-759, 1998
A:Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia tra
A:Reference number: A71570; MUID:99000809; PMID:9784136
A:Accession: H71485
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-223 <ARN>
A:Cross-references: GB:AE001337; GB:AE001273; NID:G3329113; PIDN:AA068263.1; PID:G332911

A:Experimental source: serotype D, strain UW-3/Cx
C:Genetics:
A:Gene: CT668

Query Match 50.0%; Score 38; DB 2; Length 223;
Best Local Similarity 57.1%; Pred. No. 25;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 KQVLTSAIRRAE 16
|||:|:|:|
Db 189 KQVAVQRTORAE 201

RESULT 20

D72046
conserved hypothetical protein CP0038 [imported] - Chlamydophila pneumoniae (strains CWL)
N:Alternate names: ct668 hypothetical protein
C:Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000
C:Accession: D72046; E81620
R:Kalman, S.; Mitchell, W.; Marathe, R.; Lamell, C.; Fan, J.; Olinger, L.; Grimwood, J.;
Nature Genet. 21, 385-389, 1999
A:Title: Comparative Genomes of Chlamydia pneumoniae and C. trachomatis.
A:Reference number: A72000; MUID:99206606; PMID:10192388
A:Accession: D72046
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-224 <ARN>
A:Cross-references: GB:AE001652; GB:AE001363; NID:G4376997; PIDN:AA18847.1; PID:G4377011
A:Experimental source: strain CWL029
R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, I
C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A:Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A:Reference number: A81500; MUID:20150255; PMID:10684935
A:Accession: E81620
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-224 <REA>
A:Cross-references: GB:AF002167; GB:AE002161; NID:G7188971; PIDN:AAF37933.1; PID:G7188971
A:Experimental source: strain AR39, HL cells
C:Genetics:
A:Gene: CPN0708; CP0038

Query Match 50.0%; Score 38; DB 2; Length 224;
Best Local Similarity 57.1%; Pred. No. 25;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 KQVLTSAIRRAE 16
|||:|:|:|
Db 189 KQVAVQRTORAE 202

RESULT 21

A86579
CT668 hypothetical protein [imported] - Chlamydophila pneumoniae (strain J138)
C:Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001
C:Accession: A86579
R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Ish
Nucleic Acids Res. 28, 2311-2314, 2000
A:Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A:Reference number: A86491; MUID:20330349; PMID:10871362
A:Accession: A86579
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-224 <STO>
A:Cross-references: GB:BA000008; NID:G8979080; PIDN:BA098915.1; GSPDB:GN00142
A:Experimental source: strain J138
C:Genetics:
A:Gene: CPJ0708

Query Match 50.0%; Score 38; DB 2; Length 224;

Best Local Similarity 57.1%; Pred. No. 25;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 3 KVOYLTRSAIRRAE 16
| | | | |
Db 189 KVQYVQRATQRAE 202

RESULT 22
12833
hypothetical protein yonV - Bacillus subtilis phage SPBc2
C:Species: Bacillus subtilis phage SPBc2
C>Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 15-Oct-1999
R:Lazarevic, V.; Duesterhoeft, A.; Soldo, B.; Hilbert, H.; Maue, C.; Karamata, D.
submitted to the EMBL Data Library, August 1997
A:Description: The complete nucleotide sequence of the Bacillus subtilis SPbetac2 prophage
A:Reference number: Z17583
A:Accession: T12833
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-410 <LAZ>
A:Cross-references: EMBL:AF020713; NID:g3025478; PID:g3025547; PIDN:AAAC13042.1
R:Kunet, F.; Ogasawara, N.; Mosser, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Poulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Funa, S.; Galizzi, A.; Galle
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holtsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maue
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetel
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpestra, P.; Tognoni, A.; Tosato, V.; Uchiyama
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: AG9580; MUID:98044033; PMID:9384377
A:Accession: E69915
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-410 <KUN>
A:Cross-references: GB:Z99115; GB:AL009126; NID:g2634478; PIDN:CAB14016.1; PID:e1183545;
A:Experimental source: strain 168
C:Genetics:
A:Gene: yonV

Query Match 50.0%; Score 38; DB 2; Length 410;
Best Local Similarity 46.7%; Pred. No. 47;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 2 EKVOYLTRSAIRRAE 16
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Db 373 EMQIWNRSALRNGQ 387

RESULT 23
AH1053
probable exported protein STY4756 [imported] - Salmonella enterica subsp. enterica serov
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A:Note: this species has also been called Salmonella typhi
C>Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C:Accession: AH1053
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AH1053
A>Status: preliminary

A:Molecule type: DNA
A:Residues: 1-462 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD06877.1; PID:g16505525; GSPDB:GN00176
C:Genetics:
A:Gene: STY4756

Query Match 50.0%; Score 38; DB 2; Length 462;
Best Local Similarity 46.7%; Pred. No. 53;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 2 EKVOYLTRSAIRRAE 16
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Db 294 DKVTWMTREASRRGD 308

RESULT 24
I55449
gene PP2A protein - human
C:Species: Homo sapiens (man)
C>Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 05-Nov-1999
C:Accession: I55449
R:McCrigh, B.; Virshup, D.M.
J. Biol. Chem. 270, 26123-26128, 1995
A:Title: Identification of a new family of protein phosphatase 2A regulatory subunits.
A:Reference number: I55449; MUID:96084678; PMID:7592815
A:Accession: I55449
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-486 <RES>
A:Cross-references: GB:L42373; NID:g1000887; PIDN:AAAC37601.1; PID:g1000888
C:Genetics:
A:Gene: GDB:PP2B5A
A:Cross-references: GDB:I230485; OMIM:601643
A:Map position: 1q41-1q41

Query Match 50.0%; Score 38; DB 2; Length 486;
Best Local Similarity 46.7%; Pred. No. 56;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 2 EKVOYLTRSAIRRAE 16
| | | | |
Db 19 EKVDGFTKSVRKAQ 33

RESULT 25
S49764
SEC7 protein - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein YD489.05c; protein YDR170c
C:Species: Saccharomyces cerevisiae
C>Date: 13-Jan-1995 #sequence_revision 23-Aug-1996 #text_change 21-Jul-2000
C:Accession: S49764; S50916; A31068; A28784
R:Murphy, L.; Harris, D.E.
Submitted to the EMBL Data Library, November 1994
A:Reference number: S49764
A:Accession: S49764
A:Molecule type: DNA
A:Residues: 1-542 <MUR>
A:Cross-references: EMBL:Z46727; NID:g1289283; PID:g223636; PID:g1204159; MIPS:YDR170c
R:Oliver, K.; Harris, D.
Submitted to the EMBL Data Library, January 1994
A:Reference number: S50912
A:Accession: S50916
A:Molecule type: DNA
A:Residues: 204-2009 <OLI>
A:Cross-references: EMBL:Z47813; NID:g642274; PID:e135579; PID:g1326010; MIPS:YDR170c
R:Achterter, T.; Franzoso, A.; Field, C.; Schekman, R.
J. Biol. Chem. 263, 11711-11717, 1988
A:Title: SEC7 encodes an unusual, high molecular weight protein required for membrane tra
A:Reference number: A31068; MUID:88298841; PMID:3042778
A:Accession: A31068
A:Molecule type: DNA
A:Residues: 1-187, 'S', 189-398, 'LL', 399, 'C', 403-1030, 'PAICF', 1031, 'L', 1038-2009 <ACH1>
A:Cross-references: EMBL:J03918; NID:g1435186; PIDN:AA804031.1; PID:g172570

R;Achstetter, T.; Franzusoff, A.; Field, C.; Schekman, R.
 submitted to the Protein Sequence Database, August 1988
 A;Reference number: A94619
 A;Accession: A28784
 A;Molecule type: DNA
 A;Residues: 1-187, 'S', 189-398, 'LL', 399, 'C', 403-1030, 'PAICF', 1031, 'L', 1038-2009 <ACH2>
 C;Genetics:
 A;Gene: SGD:SEC7
 A;Cross-references: SGD:S0002577; MIPS:YDR170c
 A;Map position: 4R
 C;Keywords: transmembrane protein
 F;582-598/Domain: transmembrane #status predicted <TM1>
 F;728-744/Domain: transmembrane #status predicted <TM2>
 F;1817-1833/Domain: transmembrane #status predicted <TM3>

Query Match 50.0%; Score 38; DB 2; Length 2009;
 Best Local Similarity 61.5%; Pred. No. 2.5e+02;
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 VQYLTRSAIRRAE 16
 Db 668 VDYLTRALTRVE 680

Search completed: October 1, 2004, 12:19:43
 Job time : 17.6 secs

RESULT 1

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PPLA HUMAN
ID PPLA HUMAN STANDARD; PRT; 52 AA.
AC P26678;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cardiac phospholamban (PLB).
GN PLN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=91268032; PubMed=128805;
RA Fujii J., Karain-Herzberg A., Willard H.F., Tada M., MacLennan D.H.;
RT "Structure of the rabbit phospholamban gene, cloning of the human
RT cDNA, and assignment of the gene to human chromosome 6."
RL J. Biol. Chem. 266:11669-11675(1991).
RN [2]
RN SEQUENCE FROM N.A.
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marushina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano P.J., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RN STRUCTURE BY NMR OF 1-25.
RX MEDLINE=95298769; PubMed=7779806;
RA Mortishire-Smith R.J., Fitzberger S.M., Burke C.J., Middaugh C.R.,
RA Garsky V.M., Johnson R.G.;
RT "Solution structure of the cytoplasmic domain of phospholamban:
RT phosphorylation leads to a local perturbation in secondary
RT structure."
RL Biochemistry 34:7603-7613(1995).
RN [6]
RN 3D-STRUCTURE MODELING.
RX MEDLINE=95269058; PubMed=7749920;
RA Adams P.D., Arkin I.T., Engelman D.M., Bruenger A.T.;
RT "Computational searching and mutagenesis suggest a structure for the
RT pentameric transmembrane domain of phospholamban."
RL Nat. Struct. Biol. 2:154-162(1995).
RN [7]
RN 3D-STRUCTURE MODELING.
RX MEDLINE=98170970; PubMed=9512019;

```

```

RA Herzyk P., Hubbard R.E.;
RT "Using experimental information to produce a model of the
RT transmembrane domain of the ion channel phospholamban."
RL Biophys. J. 74:1203-1214(1998).
CC -!- FUNCTION: Phospholamban has been postulated to regulate the
CC activity of the calcium pump of cardiac sarcoplasmic reticulum.
CC -!- SUBUNIT: Homopentamer.
CC -!- SUBCELLULAR LOCATION: Membrane.
CC -!- TISSUE SPECIFICITY: Heart.
CC -!- PTM: Phosphorylated in response to beta-adrenergic stimulation.
CC -!- SIMILARITY: Belongs to the phospholamban family.
CC
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CC
CC EMBL; M63603; AAA60083.1; --
CC EMBL; M60411; AAA60109.1; --
CC EMBL; AF177764; AAD55950.1; --
CC EMBL; BC005269; AAO5269.1; --
CC PIR; A40424; A40424.
CC PDB; 1K9N; 14-NOV-01.
CC PDB; 1KCH; 28-NOV-01.
CC PDB; 1PLN; 29-DEC-99.
CC PDB; 1PLP; 31-JUL-95.
CC PDB; 1PSL; 03-JUN-95.
CC Genew; HGNC:9080; PLN.
CC
CC MIX; 172405; --
CC InterPro; IPR005984; P_lamban.
CC Pfam; PF04272; Phospholamban; 1.
CC TIGRFAMs; TIGR01294; P_lamban; 1.
CC Transmembrane; Phosphorylation; Acetylation; 3D-structure.
FT DOMAIN 1 31 CYTOPLASMIC (POTENTIAL).
FT TRANSVM 32 52
FT MOD_RES 1 1 ACETYLATION (BY SIMILARITY).
FT MOD_RES 16 16 PHOSPHORYLATION (BY PKA) (BY SIMILARITY).
FT MOD_RES 17 17 PHOSPHORYLATION (BY CAMK) (BY
FT TURN 2 3 SIMILARITY).
FT TURN 4 14
FT TURN 15 15
FT TURN 15 15
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Query Match 93.4%; Score 71; DB 1; Length 52;
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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEKVQYLTRSAIRRA 15
Dy 1 MEKVQYLTRSAIRRA 15
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PPLA MOUSE
ID PPLA MOUSE STANDARD; PRT; 52 AA.
AC P20006;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cardiac phospholamban (PLB).
GN PLN.
OS Mus musculus (Mouse).
OS Rattus norvegicus (Rat), and
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090, 10116, 9986;
RN [1]
RN SEQUENCE FROM N.A.

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RC SPECIES=Rabbit;
RA MEDLINE=91268032; PubMed=1828805;
RX Fujii J., Zarain-Herzberg A., Willard H.F., Tada M., MacLennan D.H.;
RT "Structure of the rabbit phospholamban gene, cloning of the human
RT cDNA, and assignment of the gene to human chromosome 6.";
RL J. Biol. Chem. 266:11569-11675(1991).
[2]
RC SEQUENCE FROM N.A.
RP SPECIES=Rabbit;
RX MEDLINE=89112222; PubMed=2962883;
RA Fujii J., Lytton J., Tada M., MacLennan D.H.;
RT "Rabbit cardiac and slow-twitch muscle express the same phospholamban
RT gene.";
RL FEBS Lett. 227:51-55(1988).
[3]
RC SEQUENCE FROM N.A.
RP SPECIES=Rat;
RX MEDLINE=93075183; PubMed=1445334;
RA Johns D.C., Feldman A.M.;
RT "Identification of a highly conserved region at the 5' flank of the
RT phospholamban gene.";
RL Biochem. Biophys. Res. Commun. 188:927-933(1992).
[4]
RC SEQUENCE FROM N.A.
RP SPECIES=Rat;
RX MEDLINE=93284726; PubMed=8508530;
RA Shanahan C.M., Weissberg P.L., Metcalfe J.C.;
RT "Isolation of gene markers of differentiated and proliferating
RT vascular smooth muscle cells.";
RL Circ. Res. 73:193-204(1993).
[5]
RC SEQUENCE FROM N.A.
RP SPECIES=Rat; TISSUE=Aortic smooth muscle;
RX MEDLINE=92206263; PubMed=1725098;
RA Hwang X.S., Nadal-Ginard B.;
RT "Cloning phospholamban cDNA from rat aortic smooth muscle.";
RL Adv. Exp. Med. Biol. 304:387-395(1991).
[6]
RC SEQUENCE FROM N.A.
RP SPECIES=Mouse;
RX MEDLINE=93008802; PubMed=1394867;
RA Garin J.R., Luo W., Ponniah S., Grupp I., Kim H.W., Ferguson D.G.,
RA Kadambi V., Neumann J.C., Doetschman T., Kravits E.G.;
RT "Mouse phospholamban gene expression during development in vivo and
RT in vitro.";
RL Circ. Res. 71:1021-1030(1992).
-!- FUNCTION: Phospholamban has been postulated to regulate the
-!- activity of the calcium pump of cardiac sarcoplasmic reticulum.
-!- SUBUNIT: Homopentamer.
-!- SUBCELLULAR LOCATION: Membrane.
-!- TISSUE SPECIFICITY: Heart.
-!- PTM: Phosphorylated in response to beta-adrenergic stimulation.
-!- SIMILARITY: Belongs to the phospholamban family.
-----
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or send an email to license@isb-sib.ch).
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RC EMBL; S46792; AAB23706.1; -
DR EMBL; M63600; -; NOT ANNOTATED_CDS.
RX EMBL; M63601; AAA31445.1; -
DR EMBL; Y00761; CRA68730.1; -
RX EMBL; L03382; AAA41849.1; -
DR EMBL; S95853; AAB21903.1; -
RX EMBL; S95849; AAB86727.1; -
DR EMBL; X71068; CAA50394.1; -
RX EMBL; A49057; A49057.
DR PIR; B40424; B40424.
RX PIR; B37638; S37638.

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DR	HSP; P26578; IPLP.
DR	MGD; MGI:97622; Pln.
DR	InterPro; IPR005984; P_lamban.
DR	Pfam; PF04272; Phospholamban; 1.
DR	TIGRFAMs; TIGR01294; P_lamban; 1.
DR	Transmembrane; Phosphorylation; Acetylation.
KW	DOMAIN 1 31 CYTOPLASMIC (POTENTIAL).
FT	POTENTIAL
FT	TRANSMEM 32 52
FT	MOD_RES 1 1 ACETYLATION (BY SIMILARITY).
FT	MOD_RES 16 16 PHOSPHORYLATION (BY PKA) (BY SIMILARITY)
FT	MOD_RES 17 17 PHOSPHORYLATION (BY CAMK) (BY SIMILARITY).
FT	
SQ	SEQUENCE 52 AA; 6094 MW; 0763601F76A854D3 CRC64;
Query Match	
Best Local Similarity 93.4%; Score 71; DB 1; Length 52;	
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps	
QY	1 MEKVQYLTRSAIRRA 15
DB	1 MEKVQYLTRSAIRRA 15
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ID	EPLA_PIG STANDARD; PRT; 52 AA.
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DT	01-APR-1988 (Rel. 07, Created)
DT	01-APR-1988 (Rel. 07, Last sequence update)
DT	10-OCT-2003 (Rel. 42, Last annotation update)
DE	Cardiac phospholamban (PLB).
GN	PLN.
OS	Sus scrofa (Pig), and
OS	Canis familiaris (Dog).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OC	NCBI_TaxID=9823, 9615;
RN	[1]
RN	SEQUENCE FROM N.A.
RP	SPECIES=C.familiaris;
RC	MEDLINE=87083954; PubMed=3793929;
RC	Fujii J., Ueno A., Kitano K., Tanaka S., Kadoma M., Tada M.;
RA	"Complete complementary DNA-derived amino acid sequence of canine
RT	cardiac phospholamban.";
RT	J. Clin. Invest. 79:301-304 (1987).
RL	[2]
RN	SEQUENCE FROM N.A.
RP	SPECIES=C.familiaris; TISSUE=Heart ventricle;
RC	MEDLINE=87316936; PubMed=3628007;
RC	Uyeda A., Kitano K., Fujii J., Kadoma M., Tada M., Tanaka S.;
RA	"The cDNA sequence of the major phospholamban mRNA in canine cardiac
RT	ventricular muscle.";
RT	Nucleic Acids Res. 15:6738-6738 (1987).
RL	[3]
RN	SEQUENCE OF 1-45.
RP	SPECIES=C.familiaris;
RC	MEDLINE=86323152; PubMed=3753485;
RC	Fujii J., Kadoma M., Tada M., Toda H., Sakiyama F.;
RA	"Characterization of structural unit of phospholamban by amino acid
RT	sequencing and electrophoretic analysis.";
RT	Biochem. Biophys. Res. Commun. 138:1044-1050 (1986).
RL	[4]
RN	SEQUENCE OF 10-45.
RP	SPECIES=C.familiaris;
RC	MEDLINE=87008549; PubMed=3759968;
RC	Simmerman H.K.B., Collins J.H., Theibert J.L., Wegener A.D.,
RA	"Jones L.R.;"
RT	"Sequence analysis of phospholamban. Identification of
RT	phosphorylation sites and two major structural domains.";
RT	J. Biol. Chem. 261:13333-13341 (1986).
RL	[5]
RN	PHOSPHORYLATION.
RP	SPECIES=C.familiaris;

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RX MEDLINE=89291905; PubMed=2544595;
RA Wegener A.D., Simmerman H.K.B., Lindemann J.P., Jones L.R.;
RT "Phospholamban phosphorylation in intact ventricles. Phosphorylation
RT of serine 16 and threonine 17 in response to beta-adrenergic
RT stimulation."
RL J. Biol. Chem. 264:11468-11474 (1989).
RN [6]
RP SEQUENCE FROM N.A.
RC SPECIES=PIG; TISSUE=Smooth muscle;
RA MEDLINE=90056437; PubMed=2530978;
RA Verboomen H., Wuytack F., Eggermont J.A., de Jaegere S.,
RA Misset L., Raeymaekers L., Casteels R.;
RT "cDNA cloning and sequencing of phospholamban from pig stomach smooth
RT muscle."
RL Biochem. J. 262:353-356 (1989).
RC FUNCTION: Phospholamban has been postulated to regulate the
CC activity of the calcium pump of cardiac sarcoplasmic reticulum.
CC -1- SUBUNIT: Homopentamer.
CC -1- SUBCELLULAR LOCATION: Membrane.
CC -1- TISSUE SPECIFICITY: Heart.
CC -1- PTM: Phosphorylated in response to beta-adrenergic stimulation.
CC -1- SIMILARITY: Belongs to the phospholamban family.
CC
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CC
CC -----
CC EMBL; M16012; AAA30884.1; -
CC EMBL; Y00395; CAA8461.1; -
CC EMBL; M35393; AAC41618.1; -
CC EMBL; X15075; CAA33171.1; -
CC PIR; A29002; A29002.
CC PIR; S05540; S05540.
CC PDB; 1FJK; 06-SEP-00.
CC InterPro; IPR005984; P.lamban.
CC TIGRfam; TIGR01294; P.lamban; 1.
CC Transmembrane, Phosphorylation; Acetylation; 3D-structure.
KW DOMAIN 1 31 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 32 52 POTENTIAL.
FT MOD_RES 1 1 ACETYLATION.
FT MOD_RES 16 16 PHOSPHORYLATION (BY PKA).
FT MOD_RES 17 17 PHOSPHORYLATION (BY CAMK1).
SQ SEQUENCE 52 AA; 6080 MW; 076361D9ADC424D3 CRC64;
Query Match 89.5%; Score 69; DB 1; Length 52;
Best Local Similarity 93.3%; Pred. No. 4.6e-06;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEKVQYLTRSAIRRA 15
Db 1 MDRVQYLTRSAIRRA 15
RESULT 4
PFLA_CHICK STANDARD; PRT; 52 AA.
AC P26677;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cardiac phospholamban (PLB).
GN PLN.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
CC Gallus.
OX NCBI_TaxID=9031;
RN [1]

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RP SEQUENCE FROM N.A.
RX MEDLINE=91170195; PubMed=1825996;
RA Toyofuku T., Zak R.;
RT "Characterization of cDNA and genomic sequences encoding a chicken
RT phospholamban."
RL J. Biol. Chem. 266:5375-5383 (1991).
RC FUNCTION: Phospholamban has been postulated to regulate the
CC activity of the calcium pump of cardiac sarcoplasmic reticulum.
CC -1- SUBUNIT: Homopentamer.
CC -1- SUBCELLULAR LOCATION: Membrane.
CC -1- TISSUE SPECIFICITY: Heart.
CC -1- PTM: Phosphorylated in response to beta-adrenergic stimulation.
CC -1- SIMILARITY: Belongs to the phospholamban family.
CC
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CC
CC -----
CC EMBL; M59039; AAA62738.1; -
CC EMBL; M59037; -; NOT ANNOTATED_CDS.
CC EMBL; M59038; AAA63167.1; -
CC PIR; A39535; A39535.
CC HSSP; P26678; 1PLP.
CC InterPro; IPR005984; P.lamban.
CC TIGRfam; TIGR01294; P.lamban; 1.
CC Transmembrane, Phosphorylation; Acetylation.
KW DOMAIN 1 31 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 32 52 POTENTIAL.
FT MOD_RES 1 1 ACETYLATION (BY SIMILARITY).
FT MOD_RES 16 16 PHOSPHORYLATION (BY PKA) (BY SIMILARITY).
FT MOD_RES 17 17 PHOSPHORYLATION (BY CAMK) (BY SIMILARITY).
SQ SEQUENCE 52 AA; 6091 MW; F95F86C36A0C4D3B CRC64;
Query Match 88.2%; Score 67; DB 1; Length 52;
Best Local Similarity 86.7%; Pred. No. 7.1e-06;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEKVQYLTRSAIRRA 15
Db 1 MEKVQYLTRSAIRRA 15
RESULT 5
RL19-STRAW STANDARD; PRT; 116 AA.
AC Q82JW4;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE 50S ribosomal protein L19.
GN RPLS OR SAV2640.
OS Streptomyces avermitilis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=33903;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WA-4680 / ATCC 31267 / NCIM 12804 / NRRL 8165;
RX MEDLINE=21477403; PubMed=11572948;
RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
RA Shinose M., Takamashi Y., Horikawa H., Nakazawa H., Osonoe T.,
RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
RT "Genome sequence of an industrial microorganism Streptomyces
RT avermitilis: deducing the ability of producing secondary
RT metabolites."
RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220 (2001).
RN [2]

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SEQUENCE FROM N.A.
STRAIN-WA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE=2608306; PubMed=12692562;
Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
Sakaki Y., Hattori M., Omura S.;
"Complete genome sequence and comparative analysis of the industrial
microorganism Streptomyces avermitilis";
Nat. Biotechnol. 21:526-531(2003).
-!- FUNCTION: This protein is located at the 30S-50S ribosomal subunit
interface and may play a role in the structure and function of the
aminoacyl-tRNA binding site (By similarity).
-!- SIMILARITY: Belongs to the L19p family of ribosomal proteins.

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EMBL; AP005031; BAC70351.1; -
HAWAP; MF_00402; -; 1.
InterPro; IPR001857; Ribosomal_L19.
Pfam; PF01245; Ribosomal_L19; 1.
PRINTS; PR00061; RIBOSOMALL19.
ProDom; PD002979; Ribosomal_L19; 1.
TIGRfam; TIGR01024; rpls_bact; 1.
PROSITE; PS01015; RIBOSOMAL_L19; 1.
Ribosomal protein; Complete proteome.
Sequence 116 AA; 13186 MW; 47081773B07F6EB6 CRC64;

Query Match 55.3%; Score 42; DB 1; Length 116;
Best Local Similarity 43.8; Pred. No. 0.85; 3; Indels 0; Gaps 0;
Matches 7; Conservative 6; Mismatches 6;

Qy 1 MEKVQYIYTRSAIRAE 16
Db 81 VEKIELVTRGDEVRAK 96
::: :::
::: :::
::: :::
::: :::

RESULT 6
RL19_STRCO STANDARD; PRT; 116 AA.
ID RL19_STRCO STANDARD; PRT; 116 AA.
AC O69883;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 50S ribosomal protein L19.
GN RPLS OR SC05595 OR SC2E112.
OS Streptomyces coelicolor, and
OS Streptomyces lividans.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902, 1916,
RN [1]
RP SEQUENCE FROM N.A.
RP SPECIES=Streptomyces coelicolor; STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kisser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hirdlough J., Hornsby T., Howarth S.,
Huang C.-H., Kisser T., Larke L., Murphy L., Oliver K., O'Neill S.,
Rabbinowitz B., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Taylor K.,
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
coelicolor A3(2).";
RL Nature 417:141-147(2002).
RP SEQUENCE FROM N.A.

```

RC SPECIES=S.lividans; STRAIN=TK21;
RA Parro V., Mellado R.P.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: This protein is located at the 30S-50S ribosomal subunit
CC interface and may play a role in the structure and function of the
CC aminocyl-tRNA binding site (By similarity).
CC -!- SIMILARITY: Belongs to the L19p family of ribosomal proteins.
CC -----
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CC -----
CC EMBL; AL939124; CAA19387.1; -
CC EMBL; Z86111; CAB06800.1; -
CC PIR; T34780; T34780.
CC HAMAP; MF_00402; -; 1.
CC InterPro; IPR001857; Ribosomal_L19.
CC Pfam; PF01245; Ribosomal_L19; 1.
CC PRINTS; PR00061; RibosomalL19.
CC ProDom; PD002979; Ribosomal_L19; 1.
CC TIGRFAMs; TIGR01024; rpls_bact; 1.
CC PROSITE; PS01015; RIBOSOMAL_L19; 1.
CC KQ Ribosomal protein; Complete Proteome.
CC SQ SEQUENCE 116 AA; 13142 MW; 37D782C673D0A90 CRC64;

Query Match 55.3%; Score 42; DB 1; Length 116;
Best local Similarity 43.8%; Pred. No. 0.85;
Matches 7; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MEKVQVLTGSAIRAE 16
Db 81 VEKIELTRGVRRAK 96
::: :::
::: :::

RESULT 7
RL19 BORBU STANDARD; PRT; 121 AA.
AC OS1642;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 50S ribosomal protein L19.
GN RPLS OR BBO699.
OS Borrelia burgdorferi (Lyme disease spirochete).
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=139;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=ATCC 35210 / B31;
RC MEDLINE=98065943; PubMed=9403685;
RA Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
RA Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
RA Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
RA Peterson J., Kervilange A.R., Quackenbush J., Salzberg S., Hanson M.,
RA van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,
RA Utterback T., Watthey L., McDonald L., Artiach P., Bowman C.,
RA Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
RA Smith H.O., Venter J.C.;
RT "Genomic sequence of a Lyme disease spirochaete, Borrelia
RT burgdorferi";
RL Nature 390:580-586(1997).
CC -!- FUNCTION: This protein is located at the 30S-50S ribosomal subunit
CC interface and may play a role in the structure and function of the
CC aminocyl-tRNA binding site (By similarity).
CC -!- SIMILARITY: Belongs to the L19p family of ribosomal proteins.
CC -----
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CC -----
 CC EMBL; AE001170; AAC67044.1; -
 CC PIR; B70187; B70187.
 CC TIGR; B0699; -
 CC HAMAP; MF_00402; -
 CC InterPro; IPR001857; Ribosomal_L19.
 CC Pfam; PF01245; Ribosomal_L19; 1.
 CC PRINTS; PR00061; Ribosomal_L19.
 CC ProDom; PD002979; Ribosomal_L19; 1.
 CC TIGRfam; TIGR01024; rplS_bact; 1.
 CC PROSITE; PS01015; RIBOSOMAL_L19; 1.
 CC Ribosomal protein; Complete proteome.
 CC SEQUENCE 121 AA; 14011 MW; A33F7BLE4DF24070 CRC64;

Query Match 53.9%; Score 41; DB 1; Length 121;
 Best Local Similarity 50.0%; Pred. No. 1.4;
 Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 MEKVQYLRSAIRRAE 16
 DB 80 IEKVEVLGRGKVRRAK 95

RESULT 8

HEM2 CHLRE
 ID HEM2_CHLRE STANDARD; PRT; 390 AA.
 AC Q42682;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Delta-aminolevulinic acid dehydratase, chloroplast precursor
 DE (SC 4.2.1.24) (Porphobilinogen synthase) (ALADH).
 GN ALAD.
 OS Chlamydomonas reinhardtii.
 ON Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
 OC Chlamydomonadaceae; Chlamydomonas.
 OX NCBI_TaxID=3055;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NO-;
 RX MEDLINE=95201253; PubMed=7894023;
 RA Matters G.L., Beale S.I.;
 RT "Structure and expression of the Chlamydomonas reinhardtii alad gene
 RT encoding the chlorophyll biosynthetic enzyme, delta-aminolevulinic
 RT acid dehydratase (porphobilinogen synthase).";
 RL Plant Mol. Biol. 27:607-617(1995).
 CC -!- CATALYTIC ACTIVITY: 2 5-aminolevulinate = porphobilinogen + 2
 CC H(2)O.
 CC -!- COFACTOR: Magnesium.
 CC -!- PATHWAY: Porphyrin biosynthesis; second step.
 CC -!- SUBUNIT: Homodimer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Chloroplast.
 CC -!- SIMILARITY: Belongs to the ALADH family.

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CC EMBL; U19876; AAA79515.1; -
 CC PIR; S53487; S53487.
 CC HSSP; P05373; 1AWS.
 CC InterPro; IPR001731; Alad_dehydratase.
 CC Pfam; PF00490; ALAD; 1.
 CC PRINTS; PR00144; DALDHDRASE.
 CC ProDom; PD002304; Alad_dehydratase; 1.

DR PROSITE; PS00169; D-ALA DEHYDRATASE; 1.
 KW Porphyrin biosynthesis; Chlorophyll biosynthesis; Lyase; Magnesium;
 KW Chloroplast; Transit peptide.
 FT TRANSIT 1 24
 FT CHAIN 25 390
 FT DOMAIN 172 190
 FT ACT_SITE 312 312
 FT SEQUENCE 390 AA; 43045 MW; 6114C4E0325A4242 CRC64;

Query Match 52.6%; Score 40; DB 1; Length 390;
 Best Local Similarity 46.7%; Pred. No. 7.4;
 Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 EKVOYLRSAIRRAE 16
 DB 198 ETIEVLGRGKVRRAE 212

RESULT 9

RL19_THETN
 ID RL19_THETN STANDARD; PRT; 115 AA.
 AC Q8R9X4;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE 50S ribosomal protein L19.
 GN RPLS OR TTE1457.
 OS Thermoanaerobacter tengcongensis.
 OC Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
 OC Thermoanaerobacteriaceae; Thermoanaerobacter.
 OX NCBI_TaxID=119072;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MB4 / JCM 11007;
 RX MEDLINE=21992816; PubMed=11997336;
 RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
 RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
 RA Tan H., Chen R., Wang J., Yu J., Yang H.;
 RT "A complete sequence of T. tengcongensis genome.";
 RL Genome Res. 12:689-700(2002).
 CC -!- FUNCTION: This protein is located at the 30S-50S ribosomal subunit
 CC interface and may play a role in the structure and function of the
 CC aminoacyl-tRNA binding site (By similarity).
 CC -!- SIMILARITY: Belongs to the L19P family of ribosomal proteins.

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CC EMBL; AE013104; AAM24679.1; -
 CC HAMAP; MF_00402; -
 CC InterPro; IPR001857; Ribosomal_L19.
 CC Pfam; PF01245; Ribosomal_L19; 1.
 CC PRINTS; PR00061; Ribosomal_L19.
 CC ProDom; PD002979; Ribosomal_L19; 1.
 CC TIGRfam; TIGR01024; rplS_bact; 1.
 CC PROSITE; PS01015; RIBOSOMAL_L19; 1.
 CC Ribosomal protein; Complete proteome.
 CC SEQUENCE 115 AA; 13395 MW; 9EB39A1B89D3122B CRC64;

Query Match 51.3%; Score 39; DB 1; Length 115;
 Best Local Similarity 37.5%; Pred. No. 3.1;
 Matches 6; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 MEKVQYLRSAIRRAE 16
 DB 80 LEKIEVIRRGKVRRAK 95

RESULT 10
 AMIR_PSEAE
 ID AMIR_PSEAE STANDARD; PRT; 196 AA.
 AC P10932; 1989 (Rel. 11, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Aliphatic amidase regulator.
 GN AMIR OR PA3363.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PAC433;
 RX MEDLINE=89211409; PubMed=2495988;
 RA Lowe N., Rice P.M., Drew R.E.;
 RT "Nucleotide sequence of the aliphatic amidase regulator gene (amir)
 of Pseudomonas aeruginosa.";
 RL FEBS Lett. 246:39-43(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 15692 / PA01;
 RX MEDLINE=20437337; PubMed=10984043;
 RA Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warren P.,
 RA Hickey M.J., Brinkman F.S.L., Huftagle W.O., Kowalik D.J., Lagrou M.,
 RA Garber R.L., Goltry L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
 RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 RA Raizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
 RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
 opportunistic pathogen.";
 RL Nature 406:959-964(2000).
 RN [3]
 RP CHARACTERIZATION.
 RX MEDLINE=95286483; PubMed=7539417;
 RA Wilson S.A., Drew R.E.;
 RT "Transcriptional analysis of the amidase operon from Pseudomonas
 aeruginosa.";
 RL J. Bacteriol. 177:3052-3057(1995).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF COMPLEX WITH AMIC.
 RC STRAIN=PAC1;
 RX MEDLINE=99437995; PubMed=10508151;
 RA O'Hara B.P., Norman R.A., Wan P.T., Roe S.M., Barrett T.E., Drew R.E.,
 RA Pearl L.H.;
 RT "Crystal structure and induction mechanism of Amic-Amir: a
 ligand-regulated transcription antitermination complex.";
 RL EMBO J. 18:5175-5186(1999).
 CC -!- FUNCTION: Positive controlling element of amIE, the gene for
 CC aliphatic amidase. Acts as a transcriptional antitermination
 CC factor. It is thought to allow RNA polymerase read through a rho-
 CC independent transcription terminator between the amIE promoter and
 CC gene.
 CC -!- SUBUNIT: Forms a complex with amIC.
 CC
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 CC
 CC EMBL; X13776; CAA32023.1; -;
 CC DR EMBL; AE004758; AAC06751.1; -;
 CC DR PIR; B83226; B83226.
 CC DR PIR; S03884; S03884.
 CC DR PDB; 1Q00; 23-DEC-99.
 CC DR InterPro; IPR005561; ANTAR.
 CC DR InterPro; IPR008327; Res_reg_antiterm.
 CC DR Pfam; PF03861; ANTAR; 1.

DR PIRSF; PIRSF036382; Res_reg_antiterm; 1.
 KW Transcription regulation; Transcription antitermination; 3D-structure;
 KW Complete proteome.
 FT CONFLICT 48 S -> A (IN REF. 1).
 FT CONFLICT 64 E -> G (IN REF. 1).
 FT CONFLICT 141 E -> D (IN REF. 1).
 FT CONFLICT 154 A -> V (IN REF. 1).
 FT CONFLICT 170 Y -> H (IN REF. 1).
 FT HELIX 3 9
 FT HELIX 10 12
 FT STRAND 14 18
 FT HELIX 23 35
 FT TURN 36 36
 FT STRAND 38 42
 FT STRAND 55 59
 FT TURN 64 64
 FT HELIX 65 75
 FT TURN 78 79
 FT STRAND 81 86
 FT HELIX 91 100
 FT TURN 101 101
 FT STRAND 104 107
 FT HELIX 112 114
 FT TURN 115 160
 FT HELIX 161 161
 FT HELIX 164 176
 FT TURN 177 179
 FT HELIX 182 189
 SQ SEQUENCE 196 AA; 21903 MW; 306A4F30B8E4C6C0 CRC64;
 Query Match 51.3%; Score 39; DB 1; Length 196;
 Best Local Similarity 53.3%; Pred. No. 5.4;
 Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 QY 2 EKQVYLTRSAIRRAE 16
 DB 166 EAHQYLSREAMKERE 180
 RESULT 11
 SN29_HUMAN
 ID SN29_HUMAN STANDARD; PRT; 258 AA.
 AC O95721;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Synaptosomal-associated protein 29 (SNAP-29) (Vesicle-membrane fusion
 DE protein SNAP-29) (Soluble 29 kDa NSF attachment protein).
 GN SNAP29.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=99069409; PubMed=9852078;
 RA Steegmaier M., Yang B., Yoo J.-S., Huang B., Shen M., Yu S., Luo Y.,
 RA Scheller R.H.;
 RT "Three novel proteins of the syntaxin/SNAP-25 family.";
 RL J. Biol. Chem. 273:34171-34179(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Schardt A., Kraemer E.-M., Werner H., Nave K.-A.;
 RT "Genomic organization of the human SNAP29 gene.";
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pancreas;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raba S.S., Locuallano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huylk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahney J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 CC -!- FUNCTION: INVOLVED IN MULTIPLE MEMBRANE TRAFFICKING STEPS.
 CC -!- SUBUNIT: BINDS TIGHTLY TO MULTIPLE SYNTAXINS.
 CC -!- SUBCELLULAR LOCATION: APPEARS TO BE MOSTLY MEMBRANE-BOUND,
 CC PROBABLY VIA INTERACTION WITH SYNTAXINS, BUT A SIGNIFICANT PORTION
 IS CYTOPLASMIC.
 CC -!- TISSUE SPECIFICITY: FOUND IN BRAIN, HEART, KIDNEY, LIVER, LUNG,
 CC PLACENTA, SKELETAL MUSCLE, SPLEEN AND PANCREAS.
 CC -!- SIMILARITY: BELONGS TO THE SNAP-25 FAMILY.
 CC -!- SIMILARITY: CONTAINS 1 t-SNARE COILED-COIL HOMOLOGY DOMAIN.
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 or send an email to license@isb-sib.ch).
 CC EMBL: AF115436; AAD11436.1; -;
 CC EMBL: AF278704; RAF91421.1; -;
 CC EMBL: BC009715; RAH09715.1; -;
 CC Genbank: HGNC:111133; SNAP29.
 CC MIM: 604202; -;
 CC GO: GO:0005886; C:plasma membrane; TAS.
 CC GO: GO:0005484; F:SNAP receptor activity; TAS.
 CC GO: GO:0006887; P:exocytosis; TAS.
 CC GO: GO:0006944; P:membrane fusion; TAS.
 CC GO: GO:0006903; P:nonselective vesicle targeting; TAS.
 CC InterPro: IPR000928; SNAP-25.
 CC InterPro: IPR000727; t-SNARE.
 CC Pfam: PF00835; SNAP-25; 1.
 CC Pfam: PF05739; SNARE; 1.
 CC SMART: SM00397; t-SNARE; 2.
 CC PROSITE: PS0192; t-SNARE; 1.
 CC Protein transport; Synaptosome; Coiled coil; Membrane.
 FT DOMAIN 76 107 COILED COIL (POTENTIAL).
 FT DOMAIN 198 258 t-SNARE COILED-COIL HOMOLOGY.
 SQ SEQUENCE 258 AA; 28970 MW; 7E1CDBA22D6F5A3C CRC64;
 Query Match 51.3%; Score 39; DB 1; Length 258;
 Best Local Similarity 46.7%; Pred. No. 7.3;
 Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
 QY 2 EKQVYLRSATIRAE 16
 Db 40 DRQQYLRLQEVLRRAE 54
 RESULT 12
 ID SYA THEAC STANDARD; PRT; 871 AA.
 AC QSHJW4;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Alanyl-tRNA synthetase (EC 6.1.1.7) (Alanine--tRNA ligase) (AlaRS).

GN ALAS OR TA0849.
 OS Thermoplasma acidophilum.
 OC Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;
 OC Thermoplasmataceae; Thermoplasma.
 OX NCBI_TaxID=2303;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DSM 1728;
 RX MEDLINE=20479972; PubMed=11029001;
 RA Ruepp A., Grail W., Santos-Martinez M.-L., Koretke K.K., Volker C.,
 RA Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Haumeister W.,
 RT "The genome sequence of the thermoacidophilic scavenger Thermoplasma
 acidophilum".
 RL Nature 407:508-513 (2000).
 CC -!- CATALYTIC ACTIVITY: ATP + L-alanine + tRNA(Ala) = AMP +
 diphosphate + L-alanyl-tRNA(Ala).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.
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 CC EMBL: AL445065; CAC11978.1; -;
 CC HAMAP: MF_00036; -; 1.
 CC InterPro: IPR002318; tRNA-synt_2c.
 CC InterPro: IPR006193; tRNA-synt_Ala.
 CC Pfam: PF01411; tRNA-synt_2c; 1.
 CC PRINTS: PR00980; TRNASYNTHALA.
 CC TIGRFAMs: TIGR00344; alaS; 1.
 CC PROSITE: PS50860; AA tRNA LIGASE II ALA; 1.
 CC Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
 KW Complete proteome.
 SQ SEQUENCE 871 AA; 99907 MW; 6A6B955478463666D CRC64;
 Query Match 51.3%; Score 39; DB 1; Length 871;
 Best Local Similarity 69.2%; Pred. No. 27;
 Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 3 KVOYLRSATIRRA 15
 Db 353 KGVYLRWLIRRA 365
 RESULT 13
 ID NUSB SYNEL STANDARD; PRT; 212 AA.
 AC Q8DK50;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE N utilization substance protein B homolog (NusB protein).
 GN NUSB OR TLL0787.
 OS Synchococcus elongatus (Thermosynechococcus elongatus).
 OC Bacteria; Cyanobacteria; Chroococcales; Synchococcus.
 OX NCBI_TaxID=32046;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BP-1;
 RX MEDLINE=22225144; PubMed=12240834;
 RA Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S.,
 RA Watanabe A., Iriiguchi M., Kawashima K., Kimura T., Kishida Y.,
 RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Nakazaki N.,
 RA Shimpō S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.,
 RT "Complete genome structure of the thermophilic cyanobacterium
 Thermosynechococcus elongatus SP-1".
 RL DNA Res. 9:123-130 (2002).
 CC -!- FUNCTION: Involved in the transcription termination process (By
 similarity).


```

RC STRAIN=5288c / AB972;
RA Oliver K, Harris D, Barrell B G., Rajandream M.A.;
RL Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.
RN [4]
RP CHARACTERIZATION.
RX MEDLINE=91093340; PubMed=1996005;
RA Franzoso A., Redding K., Crosby J., Fuller R.S., Schekman R.;
RL "Localization of components involved in protein transport and
RT processing through the Yeast Golgi apparatus.";
RL J. Cell Biol. 112:27-37(1991).
CC -!- FUNCTION: May play a role in vesicular budding and traffic between
CC compartments of the Golgi apparatus.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic; associated with the peripheral
CC Golgi membrane.
CC -!- DOMAIN: The highly charged acidic domain may serve a structural
CC role to interact with lipids or proteins on the cytoplasmic
CC surface of the Golgi apparatus.
CC -!- PTM: Phosphorylated.
CC -!- SIMILARITY: Contains 1 SEC7 domain.
CC -!- SIMILARITY: TO YEAST YEL022W.
CC
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CC
CC ENBL; J03918; AAB04031.1; -
CC ENBL; Z46727; CAA86696.1; -
CC ENBL; Z47813; CAA87801.1; -
CC PIR; S49764; S49764.
CC HSP; Q99418; 1PBV.
CC GERMOnline; I40661; -.
CC SD; S0002577; SEC7.
CC GO; GO:0005829; C:cytosol; IDA.
CC GO; GO:0005798; C:Golgi vesicle; IDA.
CC GO; GO:0005770; C:late endosome; IDA.
CC GO; GO:0005086; F:ARF guanyl-nucleotide exchange factor activity; IDA.
CC GO; GO:0006888; P:ER to Golgi transport; IMP.
CC GO; GO:0006891; P:intra-Golgi transport; IMP.
CC InterPro; IPR008938; ARM.
CC InterPro; IPR00904; Sec7.
CC Pfam; PF01369; Sec7; 1.
CC SMART; SM00222; Sec7; 1.
CC PROSITE; PS50130; SEC7; 1.
CC TRANSFAM; TFG01024; TFGIS_bact; 1.
CC TRANSFAM; TFG002979; Ribosomal_L19; 1.
CC TRANSFAM; TFG01024; TFGIS_bact; 1.
CC PROSITE; PS01015; RIBOSOMAL_L19; 1.
CC RIBOSOMAL protein; Complete proteome.
CC SQ SEQUENCE 113 AA; 13008 MW; 9BD1C9D25ADA453A CRC64;

Query Match 48.7%; Score 37; DB 1; Length 113;
Best Local Similarity 37.5%; Pred. No. 7.2;
Matches 6; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 MEKVYLTSAIRRAE 16
Db 80 LEKIEVVRGVDVRAK 95

RESULT 17
RL19_COREF
ID RL19_COREF STANDARD; PRT; 113 AA.
AC Q8NNZ0;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 50S ribosomal protein L19.
GY RPLS OR CGL2037.
OS Corynebacterium glutamicum (Brevibacterium flavum).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=1718;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
RA Nakagawa S.;
RL "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.";
Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: This protein is located at the 30S-50S ribosomal subunit
CC interface and may play a role in the structure and function of the
CC aminocyl-tRNA binding site (By similarity).
CC -!- SIMILARITY: Belongs to the L19p family of ribosomal proteins.

Query Match 50.0%; Score 38; DB 1; Length 2009;
Best Local Similarity 61.5%; Pred. No. 1e+02;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 VOYLTSAIRRAE 16
Db 668 VDYLTLALTRVS 680

RESULT 16
RL19_COREF
ID RL19_COREF STANDARD; PRT; 113 AA.
AC Q8FP56;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)

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DE 50S ribosomal protein L19.
GN RPLS OR CGL1932.
OS Corynebacterium efficiens.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=152794;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
RX MEDLINE=22723752; PubMed=12840036;
RA Nishio Y., Nakamura Y., Kawarabayashi Y., Usuda Y., Kimura E.,
RA Sugimoto S., Matsui K., Yamagishi A., Kikuchi H., Ikeo K.,
RA Gojobori T.;
RT "Comparative complete genome sequence analysis of the amino acid
RT replacements responsible for the thermostability of Corynebacterium
RL Genome Res. 13:1572-1579(2003).
CC -!- FUNCTION: This protein is located at the 30S-50S ribosomal subunit
CC interface and may play a role in the structure and function of the
CC aminocyl-tRNA binding site (By similarity).
CC -!- SIMILARITY: Belongs to the L19p family of ribosomal proteins.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC ENBL; AP005220; SAC18742.1; ALT_INIT.
CC HAMAP; MF 00402; - 1.
CC DR InterPro; IPR001857; Ribosomal_L19.
CC Pfam; PF01245; Ribosomal_L19; 1.
CC PRINTS; PR00061; RIBOSOMAL_L19.
CC PRODOM; PD002979; Ribosomal_L19; 1.
CC TIGRFAMs; TIGR01024; TFGIS_bact; 1.
CC PROSITE; PS01015; RIBOSOMAL_L19; 1.
CC RIBOSOMAL protein; Complete proteome.
CC SQ SEQUENCE 113 AA; 13008 MW; 9BD1C9D25ADA453A CRC64;

Query Match 48.7%; Score 37; DB 1; Length 113;
Best Local Similarity 37.5%; Pred. No. 7.2;
Matches 6; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 MEKVYLTSAIRRAE 16
Db 80 LEKIEVVRGVDVRAK 95

RESULT 17
RL19_COREF
ID RL19_COREF STANDARD; PRT; 113 AA.
AC Q8NNZ0;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 50S ribosomal protein L19.
GY RPLS OR CGL2037.
OS Corynebacterium glutamicum (Brevibacterium flavum).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=1718;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
RA Nakagawa S.;
RL "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.";
Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: This protein is located at the 30S-50S ribosomal subunit
CC interface and may play a role in the structure and function of the
CC aminocyl-tRNA binding site (By similarity).
CC -!- SIMILARITY: Belongs to the L19p family of ribosomal proteins.

```

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 DR EMBL; AP005280; BAB99430.1; -;
 DR HAMAP; MF 00402; -; 1.
 DR InterPro; IPR001857; Ribosomal L19.
 DR Pfam; PF01245; Ribosomal L19; 1.
 DR PRINTS; PR00061; Ribosomal L19.
 DR ProDom; PD002979; Ribosomal L19; 1.
 DR TIGRFAMs; TIGR01024; rplS bact; 1.
 DR PROSITE; PS01015; RIBOSOMAL_L19; 1.
 KW Ribosomal protein; Complete proteome.
 SQ SEQUENCE 113 AA; 12875 MW; 2692B361BAFBA229 CRC64;

 Query Match 48.7%; Score 37; DB 1; Length 113;
 Best Local Similarity 37.5%; Pred. No. 7.2; Indels 4; Mismatches 6; Gaps 0;
 Matches 6; Conservative 6; Mismatches 6; Indels 4; Gaps 0;

 Qy 1 MEKVQLTRSAIRRAE 16
 Db 80 IEKIEVIRRGDVRRAK 95

 RESULT 18
 ID YN83_SULTO STANDARD; PRT; 182 AA.
 AC Q96XYS;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DE Hypothetical protein ST2383.
 GN ST2383.
 OS Sulfolobus tokodaii.
 OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
 OC Sulfolobus.
 CC -! SIMILARITY: Belongs to the UPF0189 family.
 CC NCBI_TaxID=111955;
 RN SEQUENCE FROM N.A.
 RP STRAIN=JCM 10545 / 7;
 RX MEDLINE=21456156; PubMed=11572479;
 RA Kawarabayashi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
 RA Sekine M., Baba S.-I., Ankaï A., Kosugi H., Hosoyama A., Fukui S.,
 RA Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
 RA Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
 RA Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
 RA Oshima T., Kikuchi H.;
 RT "Complete genome sequence of an aerobic thermophilic
 RT Crenarchaeon, Sulfolobus tokodaii strain 7."
 RL DNA Res. 8:123-140(2001).
 CC -! SIMILARITY: Belongs to the UPF0189 family.

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 DR EMBL; AF000989; BAB57492.1; -;
 DR HAMAP; MF 01205; -; 1.
 DR InterPro; IPR002589; Alpp.
 DR Pfam; PF01661; Alpp; 1.
 DR SMART; SM00506; Alpp; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 182 AA; 20183 MW; 1E0A072586AF8947 CRC64;

Query Match 48.7%; Score 37; DB 1; Length 182;
 Best Local Similarity 46.7%; Pred. No. 12;
 Matches 7; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

 Qy 2 EKQVLTSAIRRAE 16
 Db 90 EKLEAIRNALRAAE 104

 RESULT 19
 ID PSD_CHLCV STANDARD; PRT; 299 AA.
 AC Q82LL3;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DE Phosphatidylserine decarboxylase proenzyme (EC 4.1.1.65) [Contains:
 DE Phosphatidylserine decarboxylase alpha chain; Phosphatidylserine
 DE decarboxylase beta chain].
 GN PSD OR CCA00927.
 OS Chlamydomonas reinhardtii.
 OC Bacteria; Chlamydiales; Chlamydiales; Chlamydiales; Chlamydiales.
 CC NCBI_TaxID=83557;
 RN SEQUENCE FROM N.A.
 RP STRAIN=GPIC;
 RX MEDLINE=22569155; PubMed=12682364;
 RA Read T.D., Myers G.S.A., Brunham R.C., Nelson W.C., Paulsen I.T.,
 RA Heidelberg J., Holtzapple E., Khouri H., Federova N.B., Carthy H.A.,
 RA Unayam L.A., Haft D.H., Peterson J., Beanan M.J., White O.,
 RA Salzberg S.L., Hsia R.-C., McClarty G., Rank R.G., Bavoil P.M.,
 RA Fraser C.M.;
 RT "Genome sequence of Chlamydomonas reinhardtii (Chlamydia pflavica GPIC):
 RT examining the role of niche-specific genes in the evolution of the
 RT Chlamydiales."
 RL Nucleic Acids Res. 31:2134-2147(2003).
 CC -! CATALYTIC ACTIVITY: Phosphatidyl-L-serine =
 CC -! COFACTOR: Pyruvyl group (By similarity).
 CC -! SIMILARITY: Belongs to the phosphatidylserine decarboxylase
 CC family. Subfamily 2.

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 DR EMBL; AB016997; AAP05666.1; -;
 DR TIGR; CCA00927; -;
 DR HAMAP; MF 00663; -; 1.
 DR InterPro; IPR003817; PS_Dcarbxyase.
 DR Pfam; PF02666; PS_Dcarbxyase; 1.
 DR TIGRFAMs; TIGR00163; PS decarb; 1.
 KW Phospholipid biosynthesis; Lyase; Decarboxylase; Pyruvate; Zymogen;
 CC Complete proteome.
 CHAIN 1 257 PHOSPHATIDYL SERINE DECARBOXYLASE BETA
 CHAIN (BY SIMILARITY).
 FT CHAIN 258 299 PHOSPHATIDYL SERINE DECARBOXYLASE ALPHA
 FT SITE 257 258 CLEAVAGE (NONHYDROLYTIC) (BY SIMILARITY).
 FT MOD_RES 258 258 CONVERTED TO A PYRUVYL GROUP (BY
 FT SIMILARITY).
 SQ SEQUENCE 299 AA; 34223 MW; 6F8EB837D97EB4E0 CRC64;

 Query Match 48.7%; Score 37; DB 1; Length 299;
 Best Local Similarity 50.0%; Pred. No. 20;
 Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

 Qy 1 MEKVQLTRSAIRRAE 14

[illegible]

```

RN TISSUE=Liver;
RP MEDLINE=91378267; PubMed=1897938;
RC Schwab D.A., Wilson J.E.;
RX "Complete amino acid sequence of the type III isozyme of rat
RA hexokinase, deduced from the cloned cDNA.";
RT Arch. Biochem. Biophys. 285:365-370(1991).
RL [2]
RN TISSUE=Liver;
RP TISSUE=Liver;
RC White J.A.;
RX Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RA -1- CATALYTIC ACTIVITY: ATP + D-hexose = ADP + D-hexose 6-phosphate.
RT ENZYME REGULATION: Hexokinase is an allosteric enzyme inhibited by
RL its product Glc-6-P.
RN TISSUE=Liver;
RP TISSUE=Liver;
RC -1- PATHWAY: First step of
RX several metabolic pathways.
RA -1- SUBUNIT: Monomer.
RX EXTENSIVE SEQUENCE SIMILARITY TO EACH OTHER. THE CATALYTIC
RA ACTIVITY IS ASSOCIATED WITH THE C-TERMINUS WHILE REGULATORY
RT FUNCTION IS ASSOCIATED WITH THE N-TERMINUS.
RL -1- MISCELLANEOUS: In vertebrates there are four major glucose-
RN phosphorylating isoenzymes, designated hexokinase I, II, III and
RP IV (glucokinase).
RC -1- SIMILARITY: Belongs to the hexokinase family.
RX This SWISS-PROT entry is copyright. It is produced through a collaboration
RA between the Swiss Institute of Bioinformatics and the EMBL outstation -
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RC or send an email to license@isb-sib.ch).
RX EMBL: U73859; AAB18253.1; --
RP PIR: S13913; S13913.
RC HSP; P05708; IBG3.
RX InterPro: IPR001312; Hexokinase.
RA Pfam: PF03727; hexokinase2; 2.
RT Pfam: PF00349; hexokinase; 2.
RL PRINTS; PR00475; HEXOKINASE.
RN ProDom: PD001109; Hexokinase; 2.
RP PROSITE; PS00378; HEXOKINASES; 2.
RC Transferase; Kinase; Glycolysis; Allosteric enzyme; Repeat;
RX ATP-binding; Membrane.
RA DOMAIN 1 488 REGULATORY.
RP DOMAIN 489 924 CATALYTIC.
RC DOMAIN 162 188 GLUCOSE-BINDING (POTENTIAL).
RX DOMAIN 604 630 GLUCOSE-BINDING (POTENTIAL).
RA NP_BIND 95 100 ATP (POTENTIAL).
RP NP_BIND 542 547 ATP (POTENTIAL).
RC SEQUENCE 924 AA; 100253 MW; 0162C1591AF040AC CRC64;
RX Query Match 48.7%; Score 37; DB 1; Length 924;
RA Best Local Similarity 53.3%; Pred. No. 68;
RT Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
RN QY 2 EKVOYLTRSAIRRAE 16
RP Db 638 QDVVYLRLAIRRRQ 652

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RESULT 25
H4Y BLEJA STANDARD; PRT; 47 AA.
AC P80738;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Histone H4 (Fragment).
OS Blepharisma japonicum.
OC Eukaryota; Alveolata; Ciliophora; Heterotricha; Heterotrichida;
OC Blepharismidae; Blepharisma.
OX NCBI_TaxID=5961;

```

```

RN [1]
RP SEQUENCE.
RC STRAIN=A5-3;
RX MEDLINE=97257506; PubMed=9103980;
RA Salvini M., Bini E., Santucci A., Batistoni R.;
RT "H4 histone in the macronucleus of Blepharisma japonicum (Protozoa,
RL Ciliophora, Heterotrichida).";
RN FEMS Microbiol. Lett. 149:93-98(1997).
RP -1- FUNCTION: Histone H4, along with histone H3, plays a central role
RC in nucleosome formation.
RX -1- SUBUNIT: The nucleosome is an octamer containing two molecules
RA each of H2A, H2B, H3 and H4. The octamer wraps approximately 146
RT bp of DNA.
RL -1- SIMILARITY: Belongs to the histone H4 family.
RX InterPro: IPR001951; Histone_H4.
RA PRINTS; PR00623; HISTONEH4.
RN ProDom: PD001827; Histone H4; 1.
RP PROSITE; PS00047; HISTONE_H4; PARTIAL.
RC Chromosomal protein; Nucleosome core; Nuclear protein; DNA-binding.
RX NON_TER 47 47
RP SEQUENCE 47 AA; 4961 MW; D743BEA73B76BADA CRC64;
RC Query Match 47.4%; Score 36; DB 1; Length 47;
RX Best Local Similarity 53.8%; Pred. No. 4.3;
RA Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
RN QY 2 EKVOYLTRSAIRR 14
RP Db 27 ENIQGILKPAIRR 39

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Search completed: October 1, 2004, 12:15:17
Job time : 9.8 secs

90 36 47.4 331 16 Q8XV42 Q8XV42 raltostonia s
91 36 47.4 335 5 Q98847 Q98847 dictyostelli
92 36 47.4 335 5 Q23896 Q23896 dictyostelli
93 36 47.4 338 16 Q82BY5 Q82BY5 streptomyces
94 36 47.4 368 16 Q92P72 Q92P72 rhizobium m
95 36 47.4 372 10 Q8GX4 Q8GX4 arabidopsis
96 36 47.4 409 16 Q914C6 Q914C6 pseudomonas
97 36 47.4 432 16 Q8F7A1 Q8F7A1 leptosira
98 36 47.4 528 5 Q9GU06 Q9GU06 trichomonas
99 36 47.4 549 17 Q97ZB3 Q97ZB3 sulfobolus
100 36 47.4 588 17 Q9HLG9 Q9HLG9 thermoplasm

ALIGNMENTS

RESULT 1

Q82JW4 Q82JW4 PRELIMINARY; PRT; 116 AA.
AC Q82JW4
DT 01-JUN-2003 (TRENBLrel. 24, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Putative ribosomal protein L19.
GN RLS OR SAV2640.
OS Streptomyces avermitilis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomycetes.
OX NCBI_TaxID=33903;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=21477403; PubMed=11572948;
RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osomoe T.,
RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.,
RT "Genome sequence of an industrial microorganism Streptomyces
RT avermitilis: deducing the ability of producing secondary
RT metabolites".
RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=22608306; PubMed=1292562;
RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
RA Sakaki Y., Hattori M., Omura S.,
RT "Complete genome sequence and comparative analysis of the industrial
RT microorganism Streptomyces avermitilis".
RL Nat. Biotechnol. 21:526-531(2003).
DR EMBL; AP005011; BAC70351.1; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0005840; C:ribosome; IEA.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR InterPro; IPR001857; Ribosomal_L19.
DR PRINTS; PR00061; RIBOSOMAL_L19.
DR PRODOM; PD002979; Ribosomal_L19; 1.
DR TIGRFAMS; TIGR01024; rplS bact; 1.
DR PROSITE; PS01015; RIBOSOMAL_L19; 1.
KW Ribosomal protein; Complete proteome.
SQ SEQUENCE 116 AA; 13186 MW; 47081773B07F6EB6 CRC64;

Query Match 55.3%; Score 42; DB 16; Length 116;
Best Local Similarity 43.8%; Pred. No. 6.4;
Matches 7; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MEKVQYLTRSAIRAE 16

Db 81 VEKIELVTRGDVERAK 96

RESULT 2

Q8DBN7 Q8DBN7 PRELIMINARY; PRT; 527 AA.
AC Q8DBN7
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Methyl-accepting chemotaxis protein.
GN VV11774
OS Vibrio vulnificus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrrio.
OX NCBI_TaxID=672;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CMCP6;
RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,
RA Choy H.E.;
RT "Complete genome sequence of Vibrio vulnificus CMC6".
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB016802; AA010185.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0006935; P:chemotaxis; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR004089; Chmtaxis_trans.
DR InterPro; IPR003560; HAMP.
DR Pfam; PF00672; HAMP; 1.
DR Pfam; PF00015; MCPsignal; 1.
DR SMART; SM00304; HAMP; 2.
DR SMART; SM00283; MA; 1.
DR PROSITE; PS50111; CHEMOTAXIS_TRANSLOC_2; 1.
DR PROSITE; PS50885; HAMP; 1.
KW Complete proteome.
SQ SEQUENCE 527 AA; 56644 MW; B4104FFC0C968D99 CRC64;

Query Match 55.3%; Score 42; DB 16; Length 527;
Best Local Similarity 56.2%; Pred. No. 32;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MEKVQYLTRSAIRAE 16

Db 431 MEKQSQAQSSVARAE 446

RESULT 3

Q9REV7 Q9REV7 PRELIMINARY; PRT; 417 AA.
AC Q9REV7
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE HCNC (Hydrogen cyanide synthase HCNC).
GN HCNC OR PA2195.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RA Pessi G., Haas D.;
RT "Analysis of the Pseudomonas aeruginosa hydrogen cyanide synthase
RT (hcnABC) regulatory region".
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Coltray L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,


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Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
*Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen."
RL Nature 406:959-964 (2000).
DR EMBL; AF208523; AAF21030.1; -
DR EMBL; AB004646; AAG05583.1; -
DR PIR; H83370; H83370.
DR GO; GO:0009331; C:glycerol-3-phosphate dehydrogenase complex; IEA.
DR GO; GO:0004368; G:glycerol-3-phosphate dehydrogenase activity; IEA.
DR GO; GO:0016493; F:oxidoreductase activity; IEA.
DR GO; GO:0006072; P:electron transport; IEA.
DR GO; GO:0006076; FAD Gly3P dh.
DR InterPro; IPR000447; FAD Gly3P dh.
DR InterPro; IPR000205; NAD BS.
DR InterPro; IPR000437; ProK_lipprot_s.
DR Pfam; PF01266; DAD; 1.
DR PRINTS; PR01001; FADG3PDH.
DR PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
KW Complete proteome.
SQ SEQUENCE 417 AA; 45281 MW; 63F5DB8A3118F318 CRC64;

Query Match 53.9%; Score 41; DB 16; Length 417;
Best Local Similarity 53.3%; Pred. No. 38;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 EKVOYLTRSAIRAE 16
DB 154 EQRWLDREELRAE 168
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RESULT 4
Q8WM34 PRELIMINARY; PRT; 79 AA.
ID Q8WM34
AC Q8WM34;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE MHC class II DR alpha 1 domain (Fragment).
DR URMA-DRB.
OS Ursus maritimus (Polar bear) (Thalactos maritimus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.
OC NCBI_taxid=29073;
CX [1]
RN SEQUENCE FROM N.A.
RP Wei Z., Hupp G.;
RT "Extensive MHC class II DRB diversity in polar bears.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF458922; AAL67451.1; -
DR GO; GO:0014021; C:integral to membrane; IEA.
DR GO; GO:0045012; F:MHC class II receptor activity; IEA.
DR GO; GO:0019884; P:antigen presentation, exogenous antigen; IEA.
DR GO; GO:0019886; P:antigen processing, exogenous antigen via M...; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000353; MHC II beta.
DR Pfam; PF009369; MHC II beta.1.
DR ProDom; PD000328; MHC II beta.1.
DR Glycoprotein; MHC II-Transmembrane.
FT NON_TER 1
FT NON_TER 79
SQ SEQUENCE 79 AA; 9526 MW; 2BA8F98505542C3D CRC64;

Query Match 52.6%; Score 40; DB 7; Length 79;
Best Local Similarity 53.3%; Pred. No. 10;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 EKVOYLTRSAIRAE 16
DB 15 EQRWLDREELRAE 29
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RESULT 5

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[illegible]

RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.,
RA "Functional annotation of a full-length mouse cDNA collection."
RN Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung,
RA Strausberg R.,
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RN SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Hypothalamus;
RX MEDLINE=22354683; PubMed=12466851;
RA The PANTOM Consortium
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
DR EMBL; AY008722; AAC32076.1; -
DR EMBL; AK007065; BAB24850.1; -
DR EMBL; BC030066; AAH30066.1; -
DR EMBL; AX039203; BAC30277.1; -
DR MGD; MGI:1914724; Snp29.
DR InterPro; IPR000928; Snp29.
DR InterPro; IPR000727; T-SNARE.
DR Pfam; PFO0835; Snp29-25; 1.
DR Pfam; PFO5739; Snp29-25; 1.
DR PROSITE; PS0192; T-SNARE; 1.
SQ SEQUENCE 260 AA; 29572 MW; DD813A78C605576F CRC64;

Query Match 52.6%; Score 40; DB 11; Length 260;
Best Local Similarity 43.8%; Pred. No. 36;
Matches 7; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 MEKVQYLRSAIRAE 16
::: ||| : ||||
DB 39 IDRQYLRQEVLRRAE 54

RESULT 10
Q906Q3 PRELIMINARY; PRT; 527 AA.
AC Q906Q3;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE RNA-dependent RNA polymerase (Fragment).
GN POL.
OS Grapevine leafroll-associated virus 1.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Closteroviridae;
OC Ampelovirus.
OX NCBI_TaxID=47985;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20141373; PubMed=10675398;
RA Fazeli C.F., Rezaian M.A.;
RT "Nucleotide sequence and organization of ten open reading frames in
RT the genome of Grapevine leafroll-associated virus 1 and identification
RT of three subgenomic RNAs."
RL J. Gen. Virol. 81:605-615(2000).
DR EMBL; AF195822; AAR22738.1; -
DR GO; GO:0003723; RNA binding; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR GO; GO:0003688; P:transcription; IEA.
DR GO; GO:0019079; P:Viral genome replication; IEA.
DR InterPro; IPR001785; RNA_dep_RNApol12.
DR InterPro; IPR007095; RNA_pol_DS_Ps.
DR InterPro; IPR007094; RNA_pol_PsVir.
DR Pfam; PFO0978; RNA_dep_RNApol12; 1.
RNA-directed RNA polymerase.
FT NON_TER 1
SQ SEQUENCE 527 AA; 59276 MW; C445CE1169B46132 CRC64;

Query Match 52.6%; Score 40; DB 12; Length 527;
Best Local Similarity 80.0%; Pred. No. 76;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 QYLTRSAIRR 14
||: |||||
DB 95 QYVRSAIRR 104

RESULT 11
Q8CFM4 PRELIMINARY; PRT; 998 AA.
ID Q8CFM4;
AC Q8CFM4;
DT 01-MAR-2003 (T-EMBLrel. 23, Created)
DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Breast tumor;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013626; AAH13626.1; -
DR InterPro; IPR008160; Collagen.
DR Pfam; PFO1391; Collagen; 12.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 998 AA; 95451 MW; 2AB4BA953B7084A6 CRC64;

Query Match 52.6%; Score 40; DB 11; Length 998;
Best Local Similarity 42.9%; Pred. No. 1.5e+02;
Matches 6; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 1 MEKVQYLRSAIRR 14
||: |||||
DB 974 METIQWISRTLR 987

RESULT 12
Q87GQ3 PRELIMINARY; PRT; 1104 AA.
ID Q87GQ3;
AC Q87GQ3;
DT 01-JUN-2003 (T-EMBLrel. 24, Created)
DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN VPA1262.
OS Vibrio parahaemolyticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=670;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RIMD 2210633 / Serotype O3:K6;
RX MEDLINE=2620739;
RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
RA Iijima Y., Najiima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
RT "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
RT distinct from that of V. cholerae."
RL Lancet 361:743-749(2003).
DR EMBL; AP005088; BAC62605.1; -
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 1104 AA; 128574 MW; 61C89EE3AB30C5DD CRC64;

Query Match 52.6%; Score 40; DB 16; Length 1104;
Best Local Similarity 42.9%; Pred. No. 1.7e+02;
Matches 6; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

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QY      1 MEKVQYLTRSAIRRA 14
Db      853 LSKIEHITPSAVRR 866

RESULT 13
OS8310 ID OS8310 PRELIMINARY; PRT; 1108 AA.
AC OS8310;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-JAN-1999 (TREMBLrel. 09, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE 1108AA long hypothetical cell division control protein.
GN PH0606.
OS Pyrococcus horikoshii.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=53953;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OT3.
EX MEDLINE=98344137; PubMed=9679194;
RA Kawarabayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
RA Funahashi T., Tanaka T., Kudo H., Yamazaki J., Kushida N., Oguchi A.,
RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb P.T., Horikoshi K.,
RA Masuchi Y., Shizuya H., Kikuchi H.;
RT "Complete sequence and gene organization of the genome of a hyper-
RT thermophilic archaeobacterium, Pyrococcus horikoshii OT3."
RL DNA Res. 5:55-76(1998).
DR ENBL; AF000003; BAA29695.1; -.
DR PIR; E71104; E71104.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0008094; F:DNA dependent ATPase activity; IEA.
DR GO; GO:0009100; P:cytokinesis; IEA.
DR GO; GO:0008270; P:DNA replication initiation; IEA.
DR GO; GO:0016539; P:protein splicing; IEA.
DR InterPro; IPR003586; Hedgehog_hintC.
DR InterPro; IPR006142; INTEIN.
DR InterPro; IPR006141; Intein_S.
DR InterPro; IPR001208; MCM.
DR InterPro; IPR008045; MCM_2.
DR Pfam; PF00493; MCM; 1.
DR PRINTS; PR00379; INTEIN.
DR PRINTS; PR01657; MCMFAMILY.
DR PRINTS; PR01658; MCMPROTEIN2.
DR ProDom; PD001041; MCM; 2.
DR SMART; SM00305; HintC; 2.
DR SMART; SM00306; HintN; 2.
DR SMART; SM00350; MCM; 1.
DR TIGRFAMs; TIGR01443; intein_Cterm; 2.
DR TIGRFAMs; TIGR01445; intein_Nterm; 2.
DR PROSITE; PS00818; INTEIN_C_TER; 2.
DR PROSITE; PS00817; INTEIN_N_TER; 2.
DR PROSITE; PS00511; MCM_2; 3.
KW Cell division; Complete proteome.
SQ SEQUENCE 1108 AA; 125967 MW; 92D2578B31351F75 CRC64;

Query Match 52.6%; Score 40; DB 17; Length 1108;
Best Local Similarity 53.3%; Pred. NO. 1.7e+02;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY      1 MEKVQYLTRSAIRRA 15
Db      668 MEVKDYLTREVRKA 682

RESULT 14
Q9UFE6 ID Q9UFE6 PRELIMINARY; PRT; 452 AA.
AC Q9UFE6;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Hypothetical protein (Fragment).
GN DKFZF434N2421.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Blum H., Bauersachs S., Mewes H.W., Gassenhuber J., Wiemann S.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL122116; CAB59275.1; -.
DR PIR; T34542; T34542.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 452 AA; 51951 MW; 05CEA84AF4A118FD CRC64;

Query Match 52.0%; Score 39.5; DB 4; Length 452;
Best Local Similarity 66.7%; Pred. NO. 80;
Matches 10; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

QY      2 EKVOYLTRSAIRRAE 16
Db      329 EEVTHLTRS-LRRAE 342

RESULT 15
Q9NT17 ID Q9NT17 PRELIMINARY; PRT; 1027 AA.
AC Q9NT17;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Hypothetical protein (Fragment).
GN DKFZF434H1210.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Dusterhoef A., Lauber J., Mewes H.W., Gassenhuber J., Wiemann S.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL137585; CAB70827.1; -.
DR PIR; T46296; T46296.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 1027 AA; 116278 MW; 11ADC67903264B35 CRC64;

Query Match 52.0%; Score 39.5; DB 4; Length 1027;
Best Local Similarity 66.7%; Pred. NO. 1.9e+02;
Matches 10; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

QY      2 EKVOYLTRSAIRRAE 16
Db      904 EEVTHLTRS-LRRAE 917

RESULT 16
Q95213 ID Q95213 PRELIMINARY; PRT; 1120 AA.
AC Q95213;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Colled-coll related protein DEEPST (Mitotic spindle-associated
DE protein p126).

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OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
  Fuji F., Hirama C., Nakamura Y., Ogaewara N., Kuhara S.,
  Horikoshi K.
RA "Complete genome sequence of the alkaliphilic bacterium Bacillus
  halodurans and genomic sequence comparison with Bacillus subtilis."
RT Nucleic Acids Res. 28:4317-4331(2000).
CC -1- SIMILARITY: TO THE LYSR FAMILY OF TRANSCRIPTIONAL REGULATORS.
DR ENBL; AP001510; BAB04558.1; -.
DR PIR; G83754; G83754.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000847; HTH_LySR.
DR InterPro; IPR005119; LysR_subst.
DR Pfam; PF00126; HTH 1; 1.
DR Pfam; PF03466; LysR_substrate; 1.
DR PRINTS; PS00039; HTHLYSR.
DR PROSITE; PS00044; HTH_LYSR.
KW DNA-binding; Transcription regulation; Complete proteome.
SQ SEQUENCE 283 AA; 32220 MW; D13E4BA4AE6B66B CRC64;

Query Match 51.3%; Score 39; DB 16; Length 283;
Best Local Similarity 46.7%; Pred. No. 61;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 EKQVYLTRSAIRAE 16
  |||:::|::|
DB 250 EKRYNMTALLRKE 264

RESULT 21
Q9A0Y9 PRELIMINARY; PRT; 364 AA.
AC Q9A0Y9
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical protein SPY0549.
GN SPY0549.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SF370 / ATCC 700294 / Serotype M1;
RX MEDLINE=21192684; PubMed=11296296;
RA Ferreretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
  Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
  Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,
  Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes."
  Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
RL ENBL; AB006512; AAK3542.1; -.
RW Hypothetical protein; Complete proteome.
SQ SEQUENCE 364 AA; 41754 MW; 03BBD36F4234020 CRC64;

Query Match 51.3%; Score 39; DB 16; Length 364;
Best Local Similarity 53.8%; Pred. No. 79;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 EKQVYLTRSAIR 14
  |||:::|::|
DB 307 EKIQYQTRSMYK 319

RESULT 22

```

```

Q88LL1 PRELIMINARY; PRT; 406 AA.
AC Q88LL1
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN PP1920.
OS Pseudomonas putida (strain KT2440).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=160488;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22423060; PubMed=12534463;
RA Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
  Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
  Brinkac L., Beanan M., DeBoy R.T., Daugherty S., Kolonay J.,
  Madupu R., Nelson W., White O., Peterson J., Khouri H., Hance I.,
  Chris Lee P., Holtzapple E., Scanlan D., Tran K., Moazzez A.,
  Utterback T., Rizzo M., Lee K., Kosack D., Moestl D., Wedler H.,
  Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S.,
  Kiewitz C., Eisen J., Timmels K.N., Duesterhoft A., Tuemmler B.,
  Fraser C.M.;
RA "Complete genome sequence and comparative analysis of the
  metabolically versatile Pseudomonas putida KT2440."
RL Environ. Microbiol. 4:799-808(2002).
DR EMBL; AE016781; AAG7537.1; -.
DR TIGR; PP1920; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 406 AA; 47318 MW; 7CD8C30DF0D3C6E2 CRC64;

Query Match 51.3%; Score 39; DB 16; Length 406;
Best Local Similarity 75.0%; Pred. No. 89;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 KVQYLTRSAIR 14
  |||:::|::|
DB 273 KKQVLTREAIR 284

RESULT 23
Q9V1D2 PRELIMINARY; PRT; 481 AA.
AC Q9V1D2
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein PYRAB04950.
GN PYRAB04950 OR PAB0334.
OS Pyrococcus abyssi.
OC Archaea; Euryarchaeota; Thermococci; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=29292;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CE5 / Oreay;
RA Heilig R.;
RT "Pyrococcus abyssi genome sequence: insights into archaeal chromosome
  structure and evolution."
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ248284; CAB49417.1; -.
DR PIR; B75167; B75167.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005267; F:potassium channel activity; IEA.
DR GO; GO:0006813; P:potassium ion transport; IEA.
DR InterPro; IPR001622; K-channel_pore.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 481 AA; 55855 MW; 685FE30056A45259 CRC64;

Query Match 51.3%; Score 39; DB 17; Length 481;
Best Local Similarity 50.0%; Pred. No. 11e+02;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

```

QY 2 EKVOYLTRSAIRRA 15
 DB 38 EKIKYIKRAPERA 51

RESULT 24
 Q868U8
 ID Q868U8 PRELIMINARY; PRT; 644 AA.
 AC Q868U8
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Beta-(gamma)-placatin precursor.
 OS Euplotes aediculatus.
 OC Eukaryota; Alveolata; Ciliophora; Spirotrichea; Hypotrichia;
 OC Euplotida; Euplotidae; Euplotes.
 OX NCBI_TaxID=5940;
 RN [1]
 RN SEQUENCE FROM N.A.
 RX PubMed=12615971.
 RA Kloetzel J.A., Baroin-Tourancheau A., Miceli C., Barchetta S.,
 RA Farnar J., Banerjee D., Fleury-Aubusson A.;
 RT "Cytoskeletal proteins with N-terminal signal peptides: plateins in
 RT the ciliate Euplotes define a new family of artikulins.";
 RL J. Cell Sci. 116:1291-1303(2003).
 RN [2]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=22559397; PubMed=12674476;
 RA Kloetzel J.A., Baroin-Tourancheau A., Miceli C., Barchetta S.,
 RA Farnar J., Banerjee D., Fleury-Aubusson A.;
 RT "Plateins: a novel family of signal peptide-containing artikulins in
 RT euplotid ciliates.";
 RL J. Eukaryot. Microbiol. 50:19-33(2003).
 DR EMBL; AY124991; AAM94464.1; --
 KW Signal.
 FT SIGNAL
 SQ SEQUENCE 644 AA; 74972 MW; 729BE314EFB7417A CRC64;

Query Match 51.3%; Score 39; DB 5; Length 644;
 Best Local Similarity 54.5%; Pred. No. 1.5e+02;
 Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 3 KVOYLTRSAIR 13
 DB 395 EIQVTRAVR 405

RESULT 25
 Q7XTS9
 ID Q7XTS9 PRELIMINARY; PRT; 688 AA.
 AC Q7XTS9
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE OSJNB0008M17.1 protein.
 GN OSJNB0008M17.1.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzeae; Oryza.
 OX NCBI_TaxID=4530;
 RN [1]
 RN SEQUENCE FROM N.A.
 RA Han B., Feng Q., Huang Y.C., Li Y., Zhu J.J., Zhao Q., Hu X.,
 RA Liu Y.L., Mu J., Yu Z., Chen L., Fan D.L., Weng Q.J., Zhang L.,
 RA Lu Y.Q., Yu S.L., Liu X.H., Lu T.T., Zhang Y.J., Lu Y., Li C., Li T.,
 RA Zhang Y., Hu H., Jia P.X., Qian Y.M., Ying K., Zhou B., Chen Z.H.,
 RA Hao P., Zhang L., Wu M., Zhang R.Q., Guan J.P., Fu G., Wang S.Y.,
 RA Ren S.X., Lv G., Lin W., Gu W.Q., Zhu G.F., Tu Y.F., Jia J., Yin H.F.,
 RA Zhang Y., Cai Z., Chen J., Kang H., Chen X.Y., Shao C.Y., Sun Y.,
 RA Hu Q.P., Zhang X.L., Zhang W., Wang L.J., Ding C.W., Sheng H.H.,
 RA Gu J.L., Chen S.T., Ni L., Zhu F.H., Hong G.F.;

RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL662950; CAD41786.1; --
 SQ SEQUENCE 688 AA; 76908 MW; CD8298225DB66523 CRC64;

Query Match 51.3%; Score 39; DB 10; Length 688;
 Best Local Similarity 66.7%; Pred. No. 1.6e+02;
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 QYLTRSAIRRAE 16
 DB 562 QWVTRSAIRRE 573

Search completed: October 1, 2004, 12:17:35
 Job time : 53.8 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 1, 2004, 11:56:15 ; Search time 63.2 Seconds
(without alignments)
71.531 Million cell updates/sec

Title: US-09-830-779-19_COPY_1_16
Perfect score: 75
Sequence: 1 MEKVQLTRSAIRRAS 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : A_Geneseq_20Jan04.*

1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	75	100.0	16	AAV71009	Human Pho
2	75	100.0	35	AAV71012	Penetrati
3	75	100.0	36	AAV71011	Penetrati
4	75	100.0	36	AAE45175	Human SER
5	75	100.0	52	AAV71003	Human mut
6	75	100.0	52	AAV71002	Human Pho
7	75	100.0	52	ABP06592	Human ORF
8	75	100.0	52	ABP06592	Human ORF
9	75	100.0	52	ABP06592	Human ORF
10	75	100.0	52	ABP06592	Human ORF
11	75	100.0	52	ABP06592	Human ORF
12	75	100.0	52	ABP06592	Human ORF
13	75	100.0	79	AAV71019	Human SER
14	72	96.0	52	AAV71006	Human mut
15	72	96.0	52	AAV71018	Human mut
16	72	96.0	52	AAV71018	Human mut
17	71	94.7	35	AAV71014	Human mut
18	71	94.7	36	AAV71013	Human mut
19	71	94.7	52	ABB79404	Human pho
20	71	94.7	52	ABP06592	Human ORF
21	71	94.7	79	AAV71018	Human mut
22	70	93.3	52	AAV71005	Human mut
23	69	92.0	52	AAV71004	Human mut
24	66	88.0	52	AAV71007	Human mut
25	41	54.7	116	ADC87928	Ribosomal

26	41	54.7	451	4	AA96582	Putative
27	40	53.3	121	6	ABU19318	Protein e
28	39	52.0	364	5	ABP29187	Streptoco
29	38	50.7	113	6	ABU26060	Protein e
30	38	50.7	389	2	AA929657	TGF-beta
31	38	50.7	390	2	AA929657	TGF-beta
32	38	50.7	408	5	ABP27526	Streptoco
33	37	49.3	339	4	ABP70120	Drosophil
34	37	49.3	376	5	ABP27525	Streptoco
35	37	49.3	359	4	ABG24741	Novel hum
36	36.5	48.7	331	2	AAW71592	Human mye
37	36	48.0	96	4	AAU47163	Proteinib
38	36	48.0	96	6	ABM43682	Proteinib
39	36	48.0	113	4	AA91979	C glutami
40	36	48.0	114	6	ABU24669	Protein e
41	36	48.0	155	5	ABP04260	Human ORF
42	36	48.0	207	6	ABU43491	Protein e
43	36	48.0	275	4	ABU52746	Human met
44	36	48.0	387	4	ABM5660	Drosophil
45	36	48.0	401	4	ABM5661	Drosophil
46	36	48.0	409	6	ABU38335	Protein e
47	36	48.0	434	4	AAE01344	Arabidops
48	36	48.0	434	6	AAE01348	Arabidops
49	36	48.0	434	6	AAE36344	Arabidops
50	36	48.0	465	6	ABU20943	Protein e
51	36	48.0	486	7	ADE58782	Human pro
52	36	48.0	511	4	AAU59773	Proteinib
53	36	48.0	511	6	ABM56292	Proteinib
54	36	48.0	596	6	ABM56049	Proteinib
55	36	48.0	720	5	AAE25100	Human kin
56	36	48.0	765	4	AAE85514	Human pro
57	36	48.0	924	2	AAW37430	Rat hexox
58	36	48.0	924	2	AAW37430	Rat hexox
59	36	48.0	924	2	AAW37430	Rat hexox
60	35.5	47.3	319	4	ABM70712	Phototrab
61	35	46.7	24	2	AAV36671	Drosophil
62	35	46.7	24	6	ADA11925	Human nov
63	35	46.7	61	4	AAW21036	Peptide #
64	35	46.7	61	4	ABBA3216	Peptide #
65	35	46.7	61	4	ABBA1248	Peptide #
66	35	46.7	61	4	AAW35032	Peptide #
67	35	46.7	61	4	AAW37056	Peptide #
68	35	46.7	61	4	ABP25244	Protein #
69	35	46.7	61	4	ABP26300	Protein #
70	35	46.7	61	4	AAW74917	Human bon
71	35	46.7	61	4	AAW74917	Human bon
72	35	46.7	61	4	AAW74917	Human bon
73	35	46.7	61	4	AAW62113	Human bra
74	35	46.7	61	4	AAW62113	Human bra
75	35	46.7	61	4	ABG58610	Human liv
76	35	46.7	62	4	AAW94354	Human pep
77	35	46.7	62	4	AAW94354	Human pep
78	35	46.7	69	4	AAU47311	Proteinib
79	35	46.7	69	6	ABM43830	Proteinib
80	35	46.7	76	5	ABP07326	Human ORF
81	35	46.7	96	5	ABP07326	Human ORF
82	35	46.7	131	6	ABU33987	Protein e
83	35	46.7	131	6	AAV36660	Fragment
84	35	46.7	131	6	ADA11914	Human nov
85	35	46.7	137	3	AAW08367	Arabidops
86	35	46.7	137	3	AAW08367	Arabidops
87	35	46.7	137	3	AAW08367	Arabidops
88	35	46.7	144	4	ABM58535	Drosophil
89	35	46.7	147	4	AAU46685	Proteinib
90	35	46.7	147	6	ABM43204	Proteinib
91	35	46.7	156	4	AAU23445	Novel hum
92	35	46.7	190	4	ABM52490	Human pro
93	35	46.7	207	6	ABU43247	Protein e
94	35	46.7	209	4	ABG02969	Protein e
95	35	46.7	211	5	ABP40291	Staphyloc
96	35	46.7	220	3	AAW48818	Arabidops
97	35	46.7	220	3	AAW48818	Arabidops
98	35	46.7	220	3	AAW48818	Arabidops

99 35 46.7 220 3 AG08266 Arabidops
100 35 46.7 234 6 AB029277 Protein e

ALIGNMENTS

RESULT 1

AA71009
ID AAY71009 standard; peptide; 16 AA.

XX AC AAY71009;
XX KW Phospholamban; PLB; human; sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a;
XX DT 29-AUG-2000 (first entry)
XX DE Human Phospholamban (PLB) cargo peptide.
XX KW Phospholamban; PLB; human; sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a;
XX KW cardiant; cardiomyocyte; transport peptide; penetratin; cargo peptide;
XX KW contractilin; cardiac contractility; inhibitor; cardiac disease;
XX KW treatment; heart failure; myocardial dysfunction.

XX OS Homo sapiens.
XX PN WO200025804-A2.

XX PD 11-MAY-2000.

XX PF 02-NOV-1999; 99WO-US025692.

XX PR 02-NOV-1998; 98US-0106718P.

XX PR 27-JUL-1999; 99US-0145883P.

XX PA (REGC) UNIV CALIFORNIA.

XX PI Chien K, Dillman W, Minamisawa S, He H, Hoshijima M, Meyer M;
XX PI Scott C, Wang Y, Silverman GJ;

XX DR WPI; 2000-365393/31.

XX PT Treating cardiac diseases, e.g. heart failure or myocardial dysfunction
XX PT comprises enhancing cardiac contractility by inhibiting interaction
XX PT between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine
XX PT triphosphatase.

XX PS Example 4; Page 50; 56pp; English.

XX CC The patent discloses a method for the treatment of heart failure, using
XX CC small peptide complexes and recombinant proteins, that induces
XX CC phospholamban (PLB) deficiency and inhibits the interaction between PLB
XX CC and sarcoplasmic reticulum Ca 2+ ATPase (SERCA2a) within cardiomyocytes.
XX CC The peptide complex comprises of transport peptide like penetratin and
XX CC cargo peptide selected from mutant PLB, native PLB or antibody against
XX CC PLB protein (contractilin). Penetratin-PLB peptide functions as a
XX CC dominant negative inhibitor of PLB-SERCA2a interaction, enhances cardiac
XX CC contractility and reduces blood pressure. This method is useful for the
XX CC treatment of cardiac disease e.g. heart failure and myocardial
XX CC dysfunction. The present amino acid sequence is the cargo peptide from
XX CC human PLB amino terminal residues 1-16. It could be derived from any
XX CC segment of wild type or mutant PLB protein. The cargo peptide is linked
XX CC to the transport peptide by a covalent linkage

XX SQ Sequence 16 AA;

Query Match 100.0%; Score 75; DB 3; Length 16;

Best Local Similarity 100.0%; Pred. No. 1e-05;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRAS 16
|||||

Db 1 MEKVQYLTRSAIRRAS 16

RESULT 2

AA71012

ID AAY71012 standard; peptide; 35 AA.

XX AC AAY71012;

XX DT 29-AUG-2000 (first entry)

XX DE Penetratin-based recombinant phospholamban peptide, TAT-PLB.

XX KW Phospholamban; PLB; human; sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a;
XX KW cardiant; cardiomyocyte; transport peptide; penetratin; cargo peptide;
XX KW contractilin; cardiac contractility; inhibitor; cardiac disease;
XX KW treatment; heart failure; myocardial dysfunction; recombinant peptide;
XX KW HIV; TAT protein.

XX OS Homo sapiens.

XX OS Human immunodeficiency virus.

XX PH Key Location/Qualifiers

XX FT Region 5..15

XX FT /note= "Corresponds to denatured human immunodeficiency
XX FT virus (HIV) TAT protein"

XX FT Region 16..35

XX FT /note= "Corresponds to human phospholamban (PLB) amino
XX FT terminal peptide"

XX PN WO200025804-A2.

XX PD 11-MAY-2000.

XX PF 02-NOV-1999; 99WO-US025692.

XX PR 02-NOV-1998; 98US-0106718P.

XX PR 27-JUL-1999; 99US-0145883P.

XX PA (REGC) UNIV CALIFORNIA.

XX PI Chien K, Dillman W, Minamisawa S, He H, Hoshijima M, Meyer M;
XX PI Scott C, Wang Y, Silverman GJ;

XX DR WPI; 2000-365393/31.

XX PT Treating cardiac diseases, e.g. heart failure or myocardial dysfunction
XX PT comprises enhancing cardiac contractility by inhibiting interaction
XX PT between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine
XX PT triphosphatase.

XX PS Example 5; Page 52; 56pp; English.

XX CC The patent discloses a method for the treatment of heart failure, using
XX CC small peptide complexes and recombinant proteins, that induces
XX CC phospholamban (PLB) deficiency and inhibits the interaction between PLB
XX CC and sarcoplasmic reticulum Ca 2+ ATPase (SERCA2a) within cardiomyocytes.
XX CC The peptide complex comprises of transport peptide like penetratin and
XX CC cargo peptide selected from mutant PLB, native PLB or antibody against
XX CC PLB protein (contractilin). Penetratin-PLB peptide functions as a
XX CC dominant negative inhibitor of PLB-SERCA2a interaction, enhances cardiac
XX CC contractility and reduces blood pressure. This method is useful for the
XX CC treatment of cardiac disease e.g. heart failure and myocardial
XX CC dysfunction. The present sequence is the penetratin-based recombinant
XX CC peptide TAT-PLB, comprising the amino terminal end of human PLB native
XX CC protein, attached to the 3' end of denatured human immunodeficiency virus
XX CC (HIV). TAT protein. Penetratin is a class of peptides, with translocating
XX CC properties having the ability to carry hydrophilic compounds across the
XX CC plasma membrane

XX SQ Sequence 35 AA;

Query Match 100.0%; Score 75; DB 3; Length 35;

Best Local Similarity 100.0%; Pred. No. 2.4e-06;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRAS 16
 DB 16 MEKVQYLTRSAIRAS 31
 RESULT 3
 AAY71011
 ID RAY71011 standard; peptide; 36 AA.
 XX AAY71011;
 AC
 XX 29-AUG-2000 (first entry)
 DT
 XX
 DE Penetratin-based recombinant phospholamban peptide, PLB-ANT.
 XX
 KW Phospholamban; PLB; human; sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a;
 KW cardiant; cardiomyocyte; transport peptide; penetratin; cargo peptide;
 KW contractilin; cardiac contractility; inhibitor; cardiac disease;
 KW treatment; heart failure; myocardial dysfunction; recombinant peptide;
 KW fruit fly; antennapedia; ANT.
 XX
 OS Homo sapiens.
 OS Drosophila sp.
 XX
 XX
 EH Key Location/Qualifiers
 FT 1..20
 FT /note= "Corresponds to human phospholamban (PLB) amino
 FT terminal peptide"
 FT 21..36
 FT /note= "Corresponds to Drosophila antennapedia (ANT)
 FT transport peptide"
 XX
 PN WO200025804-A2.
 XX
 PD 11-MAY-2000.
 XX
 XX 02-NOV-1999; 99WO-US025692.
 PF
 PR 02-NOV-1998; 98US-0106718P.
 PR 27-JUL-1999; 99US-0145883P.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 XX Chien K, Dillman W, Minamisawa S, He H, Hoshijima M, Meyer M;
 PI Scott C, Wang Y, Silverman GT;
 PI
 DR WPI; 2000-365393/31.
 XX
 PT Treating cardiac diseases, e.g. heart failure or myocardial dysfunction
 PT comprises enhancing cardiac contractility by inhibiting interaction
 PT between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine
 PT triphosphatase.
 XX
 PS Example 5; Page 52; 56pp; English.
 XX
 CC The patent discloses a method for the treatment of heart failure, using
 CC small peptide complexes and recombinant proteins, that induces
 CC phospholamban (PLB) deficiency and inhibits the interaction between PLB
 CC and sarcoplasmic reticulum Ca 2+ ATPase (SERCA2a) within cardiomyocytes.
 CC The peptide complex comprises of transport peptide like penetratin and
 CC cargo peptide selected from mutant PLB, native PLB or antibody against
 CC PLB protein (contractilin). Penetratin-PLB peptide functions as a
 CC dominant negative inhibitor of PLB-SERCA2a peptide functions as a
 CC contractility and reduces blood pressure. This method is useful for the
 CC treatment of cardiac disease e.g. heart failure and myocardial
 CC dysfunction. The present sequence is the penetratin-based recombinant
 CC peptide PLB-ANT, comprising the amino terminal end of human PLB native
 CC protein, attached to the 5' end of the Drosophila antennapedia (ANT)
 CC transport peptide. Penetratin is a class of peptides, with translocating
 CC properties having the ability to carry hydrophilic compounds across the
 CC plasma membrane
 XX
 SQ Sequence 36 AA;

Query Match 100.0%; Score 75; DB 3; Length 36;
 Best Local Similarity 100.0%; Pred. No. 2.5e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MEKVQYLTRSAIRAS 16
 DB 1 MEKVQYLTRSAIRAS 16
 RESULT 4
 ADE45175
 ID ADE45175 standard; peptide; 36 AA.
 XX
 AC ADE45175;
 XX
 DT 29-JAN-2004 (first entry)
 DE Human SERCA_2 inhibitor phospholamban, cytosolic domain.
 XX
 KW Human; SERCA_2; phospholamban; PLB;
 KW Ca2+ ATPase of the sarco/endoplasmic reticulum; protein co-ordinate data;
 KW cardiant.
 XX
 OS Homo sapiens.
 OS
 XX US6538022-B1.
 PN
 XX 25-MAR-2003.
 PD
 XX 18-FEB-1999; 99US-00252063.
 PF
 XX 24-SEP-1997; 97US-00937117.
 PR
 XX (ORIN) ORION CORP.
 PA
 XX Pollesello P, Ovaska M, Tenhunen J, Vidgren J;
 PI Yliperttula-Ikonen M, Tilgmann C, Lotta T, Kaivola J;
 PI
 DR WPI; 2004-019625/02.
 XX
 XX New compound, useful for relieving inhibitory effects of phospholamban on
 PT cardiac SR Ca2+-ATPase by deactivating phospholamban and stimulating Ca2+
 PT -ATPase.
 XX
 PS Disclosure; SEQ ID NO 9; 65pp; English.
 XX
 CC The invention relates to a compound which deactivates, and exhibits
 CC affinity for, a phospholamban (PLB) protein (an inhibitor of SERCA_2,
 CC Ca2+ ATPase of the sarco/endoplasmic reticulum) appearing as ADE45167-
 CC ADE45173. The compound has a structure containing three of the four
 CC moieties: an electronegative moiety associating with an S1 binding site
 CC of the phospholamban cytosolic domain when the compound is bound to it,
 CC the binding site comprises Tyr-6, Arg-9 and/or Arg-13; an electronegative
 CC moiety associating with an S2 binding site of the phospholamban cytosolic
 CC domain when the compound is bound to it, the S2 binding site comprises
 CC Arg-14; a hydrophobic moiety associating with an S3 binding site of the
 CC phospholamban cytosolic domain when the compound is bound, the binding
 CC site comprises Met-26, Lys-27 and/or Leu-28; and a hydrophobic moiety
 CC associating with an S4 binding site of the phospholamban cytosolic domain
 CC when the compound is bound, the binding site comprises Phe-32 and/or Phe-
 CC 35. The compound is not 3-benzyl-5,7-bis ((1H-tetrazol-5-yl)-methoxy)-4-
 CC methyl-2H-methyl-2H-1-benzopyran-2-one. Also included are deactivating
 CC phospholamban, comprising administering the novel compound to stimulate
 CC the Ca 2+ -ATPase. The compound is useful for relieving the inhibitory
 CC effects of phospholamban on cardiac SERCA_2. The present sequence is the
 CC cytosolic domain of human phospholamban.
 XX
 SQ Sequence 36 AA;

Query Match 100.0%; Score 75; DB 8; Length 36;
 Best Local Similarity 100.0%; Pred. No. 2.5e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVOYLTRSAIRRAS 16
Db 1 MEKVOYLTRSAIRRAS 16

RESULT 5
AA71003
ID AAY71003 standard; protein; 52 AA.
XX
AC AAY71003;

XX 29-AUG-2000 (first entry)
XX Human mutant phospholamban (PLB) V49A protein.
XX Phospholamban; PLB; human; sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a;
KW cardiant; cardiomyocyte; transport peptide; penetratin; cargo peptide;
KW contractilin; cardiac contractility; inhibitor; cardiac disease;
KW treatment; heart failure; myocardial dysfunction; mutant.

XX Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Key
FT Misc-difference 49 /note= "Wild type Val replaced with Ala"
FT

XX WO200025804-A2.

XX 11-MAY-2000.
XX 02-NOV-1999; 99WO-US025692.
XX 02-NOV-1998; 98US-0106718P.
XX 27-JUL-1999; 99US-0145883P.

XX (REGC) UNIV CALIFORNIA.

XX Chien K, Dillman W, Minamisawa S, He H, Hoshijima M, Meyer M;
PI Scott C, Wang Y, Silverman GJ;
XX WPI; 2000-365393/31.

XX Treating cardiac diseases, e.g. heart failure or myocardial dysfunction
PT comprises enhancing cardiac contractility by inhibiting interaction
PT between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine
PT triphosphatase.

XX Disclosure; Page 48; 56pp; English.

XX The patent discloses a method for the treatment of heart failure, using
CC small peptide complexes and recombinant proteins, that induces
CC phospholamban (PLB) deficiency and inhibits the interaction between PLB
CC and sarcoplasmic reticulum Ca 2+ ATPase (SERCA2a) within cardiomyocytes.
CC The peptide complex comprises of transport peptide like penetratin and
CC cargo peptide selected from mutant PLB, native PLB or antibody against
CC PLB protein (contractilin). Penetratin-PLB peptide functions as a
CC dominant negative inhibitor of PLB-SERCA2a interaction, enhances cardiac
CC contractility and reduces blood pressure. This method is useful for the
CC treatment of cardiac disease e.g. heart failure and myocardial
CC dysfunction. The present amino acid sequence is the human mutant PLB
CC protein, comprising a sense mutation Val49Ala. This mutant sequence when
CC overexpressed in the transformed cardiomyocytes, shows increased
CC contractility than the wild type PLB sequence

XX Sequence 52 AA;

Query Match 100.0%; Score 75; DB 3; Length 52;
Best Local Similarity 100.0%; Pred. No. 3.7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVOYLTRSAIRRAS 16

Db 1 MEKVOYLTRSAIRRAS 16

RESULT 6
AA71002
ID AAY71002 standard; protein; 52 AA.
XX
AC AAY71002;

XX 29-AUG-2000 (first entry)
XX Human Phospholamban (PLB) wild type protein.

XX Phospholamban; PLB; human; sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a;
KW cardiant; cardiomyocyte; transport peptide; penetratin; cargo peptide;
KW contractilin; cardiac contractility; inhibitor; cardiac disease;
KW treatment; heart failure; myocardial dysfunction.

XX Homo sapiens.

XX Key Location/Qualifiers
FH Key
FT Domain
FT /label= Domain Ia
FT /note= "Rich in alpha-helical confirmation with a net
FT positive charge"
FT 21..30
FT /label= Domain Ib
FT /note= "Cytoplasmic sector of the monomer"
FT 31..52
FT /label= Domain II
FT /note= "Transmembrane sector made of uncharged residues
FT responsible for stabilising the pentamer formation"

XX WO200025804-A2.

XX 11-MAY-2000.

XX 02-NOV-1999; 99WO-US025692.
XX 02-NOV-1998; 98US-0106718P.
XX 27-JUL-1999; 99US-0145883P.

XX (REGC) UNIV CALIFORNIA.

XX Chien K, Dillman W, Minamisawa S, He H, Hoshijima M, Meyer M;
PI Scott C, Wang Y, Silverman GJ;
XX WPI; 2000-365393/31.

XX Treating cardiac diseases, e.g. heart failure or myocardial dysfunction
PT comprises enhancing cardiac contractility by inhibiting interaction
PT between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine
PT triphosphatase.

XX Disclosure; Page 47; 56pp; English.

XX The patent discloses a method for the treatment of heart failure, using
CC small peptide complexes and recombinant proteins, that induces
CC phospholamban (PLB) deficiency and inhibits the interaction between PLB
CC and sarcoplasmic reticulum Ca 2+ ATPase (SERCA2a) within cardiomyocytes.
CC The peptide complex comprises of transport peptide like penetratin and
CC cargo peptide selected from mutant PLB, native PLB or antibody against
CC PLB protein (contractilin). Penetratin-PLB peptide functions as a
CC dominant negative inhibitor of PLB-SERCA2a interaction, enhances cardiac
CC contractility and reduces blood pressure. This method is useful for the
CC treatment of cardiac disease e.g. heart failure and myocardial
CC dysfunction. The present amino acid sequence is the human PLB wild type
CC protein, a potent inhibitor of SERCA2a activity. It primarily exists in a
CC pentameric form. It is a mediator in the regulation of myocardial
CC function by catecholamines through the cAMP cascade

XX Sequence 52 AA;

Query Match 100.0%; Score 75; DB 3; Length 52;
 Best Local Similarity 100.0%; Pred. No. 3.7e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRAS 16
 |||||
 DB 1 MEKVQYLTRSAIRRAS 16

RESULT 7
 ID ABP06592
 AC ABP06592 standard; protein; 52 AA.
 XX
 XX
 DT 25-JUN-2002 (first entry)
 DE Human ORFX protein sequence SEQ ID NO:13166.
 KW Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;
 KW hyperproliferative disorder; psoriasis; benign tumour; haemorrhage;
 KW degenerative disorder; osteoarthritis; neurodegenerative disorder;
 KW cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;
 KW hypertension; hypothyroidism; cholesterol ester storage disease;
 KW immune deficiency; immune disorder; infectious disease;
 KW autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
 KW myasthenia gravis.
 KW Homo sapiens.
 OS
 XX
 XX WO200192523-A2.
 XX
 XX 06-DEC-2001.
 XX
 XX 29-MAY-2001; 2001WO-US010836.
 XX
 XX 30-MAY-2000; 2000US-0206132P.
 PR 29-AUG-2000; 2000US-0228716P.
 XX
 XX (CURA-) CURAGEN CORP.
 PA
 XX
 XX Shinkets RA, Leach MD;
 PI
 XX WPI; 2002-106308/14.
 DR N-PSDB; ABN22344.
 DR
 XX
 XX Novel human polypeptides and polynucleotides useful for diagnosing,
 PT preventing and treating cardiovascular disease, neurodegenerative,
 PT hyperproliferative disorders and autoimmune disorders.
 XX
 XX Disclosure; SEQ ID NO 13166; 1037pp; English.

The present invention describes substantially purified human proteins (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1 in the specification). ABN15762 to ABN27252 encode the human ORFX proteins given in ABP00010 to ABP11500. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated syndrome in humans, and in the manufacture of a medicament for treating a syndrome associated with ORFX-associated disorder. ORFX polynucleotide sequences can be used in gene therapy. ORFX sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosis of liver, psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage, osteoarthritis, neurodegenerative disorders, disorders related to organ transplantation, cardiovascular diseases, diabetes mellitus, systemic lupus erythematosus, hypertension, hypothyroidism, cholesterol ester storage disease, various immune deficiencies and disorders, infectious diseases, autoimmune disorders such as multiple sclerosis, rheumatoid arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. ORFX proteins are also useful for treating burns, incisions, ulcers, for treating osteoporosis, bone degenerative disorders, or periodontal disease, and for gut protection or regeneration and treatment of lung or liver fibrosis,

CC reperfusion injury in various tissues and conditions resulting from
 CC systemic cytokine damage. N.B. The sequence data for this patent did not
 CC form part of the printed specification, but was obtained in electronic
 CC format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX
 SQ Sequence 52 AA;
 Query Match 100.0%; Score 75; DB 5; Length 52;
 Best Local Similarity 100.0%; Pred. No. 3.7e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRAS 16
 |||||
 DB 1 MEKVQYLTRSAIRRAS 16

RESULT 8
 ADE45172
 ID ADE45172 standard; protein; 52 AA.
 XX
 AC ADE45172;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Mouse SERCA_2 inhibitor phospholamban.
 XX
 KW Mouse; SERCA_2; phospholamban; PLB;
 KW Ca2+ ATPase of the sarco/endoplasmic reticulum; protein co-ordinate data;
 KW cardiant.
 XX
 XX Mus sp.
 OS
 XX US6538022-B1.
 FN
 XX 25-MAR-2003.
 PD
 XX 18-FEB-1999; 99US-00252063.
 PF
 XX 24-SEP-1997; 97US-00937117.
 PR
 XX (ORIN) ORION CORP.
 PA
 XX
 XX Pollesello P, Ovaeka M, Tenhunen J, Vidgren J;
 PI Yliperttula-Ikonen M, Tilgmann C, Lotta T, Kaivola J;
 XX
 XX WPI; 2004-019625/02.
 DR
 XX New compound, useful for relieving inhibitory effects of phospholamban on
 PT cardiac SR Ca2+-ATPase by deactivating phospholamban and stimulating Ca2+
 PT -ATPase.
 XX
 XX Claim 1; SEQ ID NO 6; 65pp; English.

The invention relates to a compound which deactivates, and exhibits affinity for, a phospholamban (PLB) protein (an inhibitor of SERCA_2, Ca2+ ATPase of the sarco/endoplasmic reticulum) appearing as ADE45167-ADE45173. The compound has a structure containing three of the four moieties: an electronegative moiety associating with an S1 binding site of the phospholamban cytosolic domain when the compound is bound to it, the binding site comprises Tyr-6, Arg-9 and/or Arg-13; an electronegative moiety associating with an S2 binding site of the phospholamban cytosolic domain when the compound is bound to it, the S2 binding site comprises Arg-14; a hydrophobic moiety associating with an S3 binding site of the phospholamban cytosolic domain when the compound is bound, the binding site comprises Met-20, Lys-27 and/or Leu-28; and a hydrophobic moiety associating with an S4 binding site of the phospholamban cytosolic domain when the compound is bound, the binding site comprises Phe-32 and/or Phe-35. The compound is not 3-benzyl-5,7-bis ((1H-tetrazol-5-yl)-methoxy)-4-methyl-2H-methyl-2H-1-benzopyran-2-one. Also included are deactivating phospholamban, comprising administering the novel compound to stimulate the Ca 2+ -ATPase. The compound is useful for relieving the inhibitory effects of phospholamban on cardiac SERCA_2. The present sequence is a phospholamban.

XX SQ Sequence 52 AA; Query Match 100.0%; Score 75; DB 8; Length 52;
 Best Local Similarity 100.0%; Pred. No. 3.7e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRAS 16
 DB 1 MEKVQYLTRSAIRRAS 16
 |||||
 |||||

RESULT 9
 ADE45170
 ID ADE45170 standard; protein; 52 AA.
 XX AC ADE45170;
 XX DT 29-JAN-2004 (first entry)
 XX DE Rabbit SERCA_2 inhibitor phospholamban.
 XX KW Rabbit; SERCA_2; phospholamban; PLB;
 KW Ca2+ ATPase of the sarco/endoplasmic reticulum; protein co-ordinate data;
 KW cardiant.
 XX OS Oryctolagus cuniculus.
 XX PN US6538022-B1.
 XX PD 25-MAR-2003.
 XX PF 18-FEB-1999; 99US-00252063.
 XX PR 24-SEP-1997; 97US-00937117.
 XX PA (ORIN) ORION CORP.
 XX PI Pollesello P, Ovaska M, Tenhunen J, Vidgren J;
 PI Yliperttula-Ikonen M, Tilgmann C, Lotta T, Kaivola J;
 DR WPI; 2004-019625/02.
 XX New compound, useful for relieving inhibitory effects of phospholamban on
 PT cardiac SR Ca2+-ATPase by deactivating phospholamban and stimulating Ca2+
 PT -ATPase.
 XX Claim 1; SEQ ID NO 4; 65pp; English.
 XX The invention relates to a compound which deactivates, and exhibits
 CC affinity for, a phospholamban (PLB) protein (an inhibitor of SERCA_2,
 CC Ca2+ ATPase of the sarco/endoplasmic reticulum) appearing as ADE45167-
 CC ADE45173. The compound has a structure containing three of the four
 CC moieties: an electronegative moiety associating with an S1 binding site
 CC of the phospholamban cytosolic domain when the compound is bound to it,
 CC the binding site comprises Tyr-6, Arg-9 and/or Arg-13; an electronegative
 CC moiety associating with an S2 binding site of the phospholamban cytosolic
 CC domain when the compound is bound to it, the S2 binding site comprises
 CC Arg-14; a hydrophobic moiety associating with an S3 binding site of the
 CC domain when the compound is bound to it, the S3 binding site comprises
 CC Arg-14; a hydrophobic moiety associating with an S4 binding site of the
 CC phospholamban cytosolic domain when the compound is bound, the binding
 CC site comprises Met-20, Lys-27 and/or Leu-28; and a hydrophobic moiety
 CC associating with an S4 binding site of the phospholamban cytosolic domain
 CC when the compound is bound, the binding site comprises Phe-32 and/or Phe-
 CC 35. The compound is not 3-benzyl-5,7-bis ((1H-tetrazol-5-yl)-methoxy)-4-
 CC -methyl-2H-methyl-2H-1-benzopyran-2-one. Also included are deactivating
 CC phospholamban, comprising administering the novel compound to stimulate
 CC the Ca 2 + -ATPase. The compound is useful for relieving the inhibitory
 CC effects of phospholamban on cardiac SERCA_2. The present sequence is a
 CC phospholamban.
 XX Sequence 52 AA;
 SQ Query Match 100.0%; Score 75; DB 8; Length 52;
 Best Local Similarity 100.0%; Pred. No. 3.7e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ Sequence 52 AA; Query Match 100.0%; Score 75; DB 8; Length 52;
 Best Local Similarity 100.0%; Pred. No. 3.7e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRAS 16
 DB 1 MEKVQYLTRSAIRRAS 16
 |||||
 |||||

RESULT 10
 ADE45171
 ID ADE45171 standard; protein; 52 AA.
 XX AC ADE45171;
 XX DT 29-JAN-2004 (first entry)
 XX DE Rat SERCA_2 inhibitor phospholamban.
 XX KW Rat; SERCA_2; phospholamban; PLB;
 KW Ca2+ ATPase of the sarco/endoplasmic reticulum; protein co-ordinate data;
 KW cardiant.
 XX OS Rattus sp.
 XX PN US6538022-B1.
 XX PD 25-MAR-2003.
 XX PF 18-FEB-1999; 99US-00252063.
 XX PR 24-SEP-1997; 97US-00937117.
 XX PA (ORIN) ORION CORP.
 XX PI Pollesello P, Ovaska M, Tenhunen J, Vidgren J;
 PI Yliperttula-Ikonen M, Tilgmann C, Lotta T, Kaivola J;
 DR WPI; 2004-019625/02.
 XX New compound, useful for relieving inhibitory effects of phospholamban on
 PT cardiac SR Ca2+-ATPase by deactivating phospholamban and stimulating Ca2+
 PT -ATPase.
 XX Claim 1; SEQ ID NO 5; 65pp; English.
 XX The invention relates to a compound which deactivates, and exhibits
 CC affinity for, a phospholamban (PLB) protein (an inhibitor of SERCA_2,
 CC Ca2+ ATPase of the sarco/endoplasmic reticulum) appearing as ADE45167-
 CC ADE45173. The compound has a structure containing three of the four
 CC moieties: an electronegative moiety associating with an S1 binding site
 CC of the phospholamban cytosolic domain when the compound is bound to it,
 CC the binding site comprises Tyr-6, Arg-9 and/or Arg-13; an electronegative
 CC moiety associating with an S2 binding site of the phospholamban cytosolic
 CC domain when the compound is bound to it, the S2 binding site comprises
 CC Arg-14; a hydrophobic moiety associating with an S3 binding site of the
 CC phospholamban cytosolic domain when the compound is bound, the binding
 CC site comprises Met-20, Lys-27 and/or Leu-28; and a hydrophobic moiety
 CC associating with an S4 binding site of the phospholamban cytosolic domain
 CC when the compound is bound, the binding site comprises Phe-32 and/or Phe-
 CC 35. The compound is not 3-benzyl-5,7-bis ((1H-tetrazol-5-yl)-methoxy)-4-
 CC -methyl-2H-methyl-2H-1-benzopyran-2-one. Also included are deactivating
 CC phospholamban, comprising administering the novel compound to stimulate
 CC the Ca 2 + -ATPase. The compound is useful for relieving the inhibitory
 CC effects of phospholamban on cardiac SERCA_2. The present sequence is a
 CC phospholamban.
 XX Sequence 52 AA;
 SQ Query Match 100.0%; Score 75; DB 8; Length 52;
 Best Local Similarity 100.0%; Pred. No. 3.7e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC	associating with an S4 binding site of the phospholamban cytosolic domain
CC	when the compound is bound, the binding site comprises Phe-32 and/or Phe-
CC	35. The compound is not 3-benzyl-5,7-bis ((IH-tetrazol-5-yl)-methoxy)-4
CC	-methyl-2H-methyl-2H-1-benzopyran-2-one. Also included are deactivating
CC	phospholamban, comprising administering the novel compound to stimulate
CC	the Ca ²⁺ + -ATPase. The compound is useful for relieving the inhibitory
CC	effects of phospholamban on cardiac SERCA_2. The present sequence is
CC	human phospholamban.
XX	
SQ	Sequence 52 AA;
Query Match	100.0%; Score 75; DB 8; Length 52;
Best Local Similarity	100.0%; Pred. No. 3.7e-06;
Matches	16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy	1 MEKVQLTRSAIRRAS 16
Db	1 MEKVQLTRSAIRRAS 16
RESULT 12	
AAV71019	
ID	AAV71019 standard; protein; 79 AA.
AC	AAV71019;
Dt	29-AUG-2000 (first entry)
XX	
H6	tagged penetratin-based recombinant protein, H6-(V49A)mutant-PLB-ANT.
Phospholamban	; PLB; human; sarcoplasmic reticulum Ca ²⁺ ATPase; SERCA2a;
cadiant	; cardiomyocyte; transport peptide; penetratin; cargo peptide;
contractilin	; cardiac contractility; inhibitor; cardiac disease; mutant;
treatment	; heart failure; myocardial dysfunction; recombinant protein;
fruit fly	; ANT; antennapedia; H6 tag; hexahistidine.
Homo sapiens.	
Drosophila sp.	
Synthetic.	
Key	Location/Qualifiers
Region	1..52
/note=	"Corresponds to mutant human phospholamban (PLB)
protein"	
Misc-difference	49
/note=	"Wild type Val replaced with Ala"
Region	53..58
/note=	"Corresponds to hexahistidine tag (H6)"
Region	63..78
/note=	"Corresponds to Drosophila antennapedia (ANT)
transport peptide"	
WO200025804-A2.	
11-MAY-2000.	
02-NOV-1999;	99WO-US025692.
02-NOV-1998;	98US-0106718P.
27-JUL-1999;	93US-0145893P.
(REGC) UNIV CALIFORNIA.	
Chien K, Dillman W, Minamisawa S, He H, Hoshijima M, Meyer M;	
Scott C, Wang Y, Silverman GJ;	
WPI; 2000-365393/31.	
Treating cardiac diseases, e.g. heart failure or myocardial dysfunction	
comprises enhancing cardiac contractility by inhibiting interaction	
between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine	
triphosphatase.	

PS Example 6; Page 56; 56pp; English.

XX The patent discloses a method for the treatment of heart failure, using

CC small peptide complexes and recombinant proteins, that induces

CC phospholamban (PLB) deficiency and inhibits the interaction between PLB

CC and sarcoplasmic reticulum Ca 2+ ATPase (SERCA2a) within cardiomyocytes.

CC The peptide complex comprises of transport peptide like penetratin and

CC cargo peptide selected from mutant PLB, native PLB or antibody against

CC PLB protein (contractilin). Penetratin-PLB peptide functions as a

CC dominant negative inhibitor of PLB-SERCA2a interaction, enhances cardiac

CC contractility and reduces blood pressure. This method is useful for the

CC treatment of cardiac disease e.g. heart failure and myocardial

CC dysfunction. The present sequence is the hexahistidine (H6) tagged

CC penetratin-based recombinant protein H6-mutantPLB-ANT, comprising the

CC human mutant (Val49Ala) PLB protein and Drosophila antennapedia (ANT)

CC transport peptide attached by a hexahistidine tag. This sequence is

CC expressed in Escherichia coli cells

XX Sequence 79 AA;

SQ

Query Match 100.0%; Score 75; DB 3; Length 79;

Best Local Similarity 100.0%; Pred. No. 5.8e-06;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRAS 16

DB 1 MEKVQYLTRSAIRRAS 16

RESULT 13

AAAY71017

ID AAY71017 standard; protein; 79 AA.

AC AAY71017;

XX 29-AUG-2000 (first entry)

DT

XX Hexahistidine tagged penetratin-based recombinant protein, H6-wtPLB-ANT.

DE

XX Phospholamban; PLB; human; sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a;

KW cardiant; cardiomyocyte; transport peptide; penetratin; cargo peptide;

KW contractilin; cardiac contractility; inhibitor; cardiac disease;

KW treatment; heart failure; myocardial dysfunction; recombinant protein;

KW fruit fly; ANT; antennapedia; H6 tag; hexahistidine.

XX

OS Homo sapiens.

OS Drosophila sp.

OS Synthetic.

PH Key Location/Qualifiers

FT Region 1..52 /note= "Corresponds to Human phospholamban (PLB) protein"

FT Region 53..58 /note= "Corresponds to hexahistidine tag (H6)"

FT Region 63..78 /note= "Corresponds to Drosophila antennapedia (ANT)

FT transport peptide"

XX WO200025804-A2.

XX 11-MAY-2000.

XX 02-NOV-1999; 99WO-US025692.

XX 02-NOV-1998; 98US-0106718P.

XX 27-JUL-1999; 99US-0145883P.

XX (REGC) UNIV CALIFORNIA.

XX Chien K, Dillman W, Minamisawa S, He H, Hoshijima M, Meyer M;

PI Scott C, Wang Y, Silverman GJ;

XX WPI; 2000-365393/31.

DR

XX Treating cardiac diseases, e.g. heart failure or myocardial dysfunction

PT comprises enhancing cardiac contractility by inhibiting interaction

PT between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine

PT triphosphatase.

XX Example 6; Page 54-55; 56pp; English.

XX The patent discloses a method for the treatment of heart failure, using

CC small peptide complexes and recombinant proteins, that induces

CC phospholamban (PLB) deficiency and inhibits the interaction between PLB

CC and sarcoplasmic reticulum Ca 2+ ATPase (SERCA2a) within cardiomyocytes.

CC The peptide complex comprises of transport peptide like penetratin and

CC cargo peptide selected from mutant PLB, native PLB or antibody against

CC PLB protein (contractilin). Penetratin-PLB peptide functions as a

CC dominant negative inhibitor of PLB-SERCA2a interaction, enhances cardiac

CC contractility and reduces blood pressure. This method is useful for the

CC treatment of cardiac disease e.g. heart failure and myocardial

CC dysfunction. The present sequence is the hexahistidine (H6) tagged

CC penetratin-based recombinant protein H6-wtPLB-ANT, comprising the wild

CC type human PLB protein and Drosophila antennapedia (ANT) transport

CC peptide attached by a hexahistidine tag. This sequence is expressed in

CC Escherichia coli cells

XX Sequence 79 AA;

SQ

Query Match 100.0%; Score 75; DB 3; Length 79;

Best Local Similarity 100.0%; Pred. No. 5.8e-06;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRAS 16

DB 1 MEKVQYLTRSAIRRAS 16

RESULT 14

AAAY71006

ID AAY71006 standard; protein; 52 AA.

AC AAY71006;

XX 29-AUG-2000 (first entry)

DT

XX Human mutant phospholamban (PLB) S16N protein.

DE

XX Phospholamban; PLB; human; sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a;

KW cardiant; cardiomyocyte; transport peptide; penetratin; cargo peptide;

KW contractilin; cardiac contractility; inhibitor; cardiac disease;

KW treatment; heart failure; myocardial dysfunction; mutant.

XX

OS Homo sapiens.

OS Synthetic.

PH Key Location/Qualifiers

FT Misc-difference 16 /note= "Wild type Ser replaced with Asn"

XX WO200025804-A2.

XX 11-MAY-2000.

XX 02-NOV-1999; 99WO-US025692.

XX 02-NOV-1998; 98US-0106718P.

XX 27-JUL-1999; 99US-0145883P.

XX (REGC) UNIV CALIFORNIA.

XX Chien K, Dillman W, Minamisawa S, He H, Hoshijima M, Meyer M;

PI Scott C, Wang Y, Silverman GJ;

XX WPI; 2000-365393/31.

DR

PT Treating cardiac diseases, e.g. heart failure or myocardial dysfunction
 PT comprises enhancing cardiac contractility by inhibiting interaction
 PT between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine
 triphosphatase.

XX Disclosure; Page 49; 56pp; English.

CC The patent discloses a method for the treatment of heart failure, using
 CC small peptide complexes and recombinant proteins, that induces
 CC phospholamban (PLB) deficiency and inhibits the interaction between PLB
 CC and sarcoplasmic reticulum Ca 2+ ATPase (SERCA2a) within cardiomyocytes.
 CC The peptide complex comprises of transport peptide like penetratin and
 CC cargo peptide selected from mutant PLB, native PLB or antibody against
 CC PLB protein (contractilin). Penetratin-PLB peptide functions as a
 CC dominant negative inhibitor of PLB-SERCA2a interaction, enhances cardiac
 CC contractility and reduces blood pressure. This method is useful for the
 CC treatment of cardiac disease e.g. heart failure and myocardial
 CC dysfunction. The present amino acid sequence is the human mutant PLB
 CC protein, comprising the mutation Ser16Asn. This mutant sequence when
 CC overexpressed in the transformed cardiomyocytes, shows increased
 CC contractility than the wild type PLB sequence

XX Sequence 52 AA;

Query Match 96.0%; Score 72; DB 3; Length 52;
 Best Local Similarity 93.8%; Pred. No. 1.3e-05;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEKVQLTRSAIRRAS 16
 |||||
 Db 1 MEKVQLTRSAIRRAAN 16

RESULT 15

ADE45168
 ID ADE45168 standard; protein; 52 AA.

XX ADE45168;
 AC ADE45168;

DT 29-JAN-2004 (first entry)

XX Pig SERCA_2 inhibitor phospholamban.

XX Pig; SERCA_2; phospholamban; PLB;
 KW Ca2+ ATPase of the sarco/endoplasmic reticulum; protein co-ordinate data;
 KW cardiant.

XX Sus sp.

XX US6538022-B1.

XX 25-MAR-2003.

XX 18-FEB-1999; 99US-00252063.

XX 24-SEP-1997; 97US-00937117.

XX (ORIN) ORION CORP.

XX Pollesello P, Ovaska M, Tenhunen J, Vidgren J;

XX Yliperttula-Ikonen M, Tilgmann C, Lotta T, Kaivola J;

XX WPI; 2004-019625/02.

XX New compound, useful for relieving inhibitory effects of phospholamban on
 PT cardiac SR Ca2+-ATPase by deactivating phospholamban and stimulating Ca2+
 PT -ATPase.

XX Claim 1; SEQ ID NO 2; 65pp; English.

XX The invention relates to a compound which deactivates, and exhibits
 CC affinity for, a phospholamban (PLB) protein (an inhibitor of SERCA_2,
 CC Ca2+ ATPase of the sarco/endoplasmic reticulum) appearing as ADE45167-
 CC Ca2+ ATPase of the sarco/endoplasmic reticulum) appearing as ADE45167-

CC ADE45173. The compound has a structure containing three of the four
 CC moieties: an electronegative moiety associating with an S1 binding site
 CC of the phospholamban cytosolic domain when the compound is bound to it,
 CC the binding site comprises Tyr-6, Arg-9 and/or Arg-13; an electronegative
 CC moiety associating with an S2 binding site of the phospholamban cytosolic
 CC domain when the compound is bound to it, the S2 binding site comprises
 CC Arg-14; a hydrophobic moiety associating with an S3 binding site of the
 CC phospholamban cytosolic domain when the compound is bound, the binding
 CC site comprises Met-20, Lys-27 and/or Leu-28; and a hydrophobic moiety
 CC associating with an S4 binding site of the phospholamban cytosolic domain
 CC when the compound is bound, the binding site comprises Phe-32 and/or Phe-
 CC 35. The compound is not 3-benzyl-5,7-bis ((1H-tetrazol-5-yl)-methoxy)-4-
 CC -methyl-2H-methyl-2H-1-benzopyran-2-one. Also included are deactivating
 CC phospholamban, comprising administering the novel compound to stimulate
 CC the Ca 2+ -ATPase. The compound is useful for relieving the inhibitory
 CC effects of phospholamban on cardiac SERCA_2. The present sequence is a
 CC phospholamban.

XX Sequence 52 AA;

Query Match 96.0%; Score 72; DB 8; Length 52;
 Best Local Similarity 93.8%; Pred. No. 1.3e-05;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEKVQLTRSAIRRAS 16

Db 1 MDXVQLTRSAIRRAS 16

RESULT 16

ADE45169
 ID ADE45169 standard; protein; 52 AA.

XX ADE45169;
 AC ADE45169;

DT 29-JAN-2004 (first entry)

XX Dog SERCA_2 inhibitor phospholamban.

XX Dog; SERCA_2; phospholamban; PLB;
 KW Ca2+ ATPase of the sarco/endoplasmic reticulum; protein co-ordinate data;
 KW cardiant.

XX Canis sp.

XX US6538022-B1.

XX 25-MAR-2003.

XX 18-FEB-1999; 99US-00252063.

XX 24-SEP-1997; 97US-00937117.

XX (ORIN) ORION CORP.

XX Pollesello P, Ovaska M, Tenhunen J, Vidgren J;

XX Yliperttula-Ikonen M, Tilgmann C, Lotta T, Kaivola J;

XX WPI; 2004-019625/02.

XX New compound, useful for relieving inhibitory effects of phospholamban on
 PT cardiac SR Ca2+-ATPase by deactivating phospholamban and stimulating Ca2+
 PT -ATPase.

XX Claim 1; SEQ ID NO 3; 65pp; English.

XX The invention relates to a compound which deactivates, and exhibits
 CC affinity for, a phospholamban (PLB) protein (an inhibitor of SERCA_2,
 CC Ca2+ ATPase of the sarco/endoplasmic reticulum) appearing as ADE45167-
 CC Ca2+ ATPase of the sarco/endoplasmic reticulum) appearing as ADE45167-
 CC ADE45173. The compound has a structure containing three of the four
 CC moieties: an electronegative moiety associating with an S1 binding site
 CC of the phospholamban cytosolic domain when the compound is bound to it,
 CC the binding site comprises Tyr-6, Arg-9 and/or Arg-13; an electronegative

CC moiety associating with an S2 binding site of the phospholamban cytosolic
 CC domain when the compound is bound to it, the S2 binding site comprises
 CC Arg-14; a hydrophobic moiety associating with an S3 binding site of the
 CC phospholamban cytosolic domain when the compound is bound, the binding
 CC site comprises Met-20, Lys-27 and/or Leu-28; and a hydrophobic moiety
 CC associating with an S4 binding site of the phospholamban cytosolic domain
 CC when the compound is bound, the binding site comprises Phe-32 and/or Phe-
 CC 33. The compound is not 3-benzyl-5,7-bis ((1H-tetrazol-5-yl)-methoxy)-4-
 CC -methyl-2H-1-benzopyran-2-one. Also included are deactivating
 CC phospholamban, comprising administering the novel compound to stimulate
 CC the Ca²⁺ + ATPase. The compound is useful for relieving the inhibitory
 CC effects of phospholamban on cardiac SERCA₂. The present sequence is a
 CC phospholamban.
 XX
 SQ Sequence 52 AA;

Query Match 96.0%; Score 72; DB 8; Length 52;
 Best Local Similarity 93.8%; Pred. No. 1.3e-05;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRAS 16
 Db 1 MDKVQYLTRSAIRRAS 16

RESULT 17
 AAY71014
 ID AAY71014 standard; peptide; 35 AA.

XX AAY71014;

XX 29-AUG-2000 (first entry)

DE Penetratin-based recombinant phospholamban peptide, TAT-mutant PLB.

XX Phospholamban; PLB; human; sarcoplasmic reticulum Ca²⁺ ATPase; SERCA2a;
 KW cardiant; cardiomyocyte; transport peptide; penetratin; cargo peptide;
 KW contractilin; cardiac contractility; inhibitor; cardiac disease; mutant;
 KW treatment; heart failure; myocardial dysfunction; recombinant protein;
 KW HIV; TAT protein.

XX Homo sapiens.
 OS Human immunodeficiency virus.

PH Key Location/Qualifiers

FT Region 5..15 "Corresponds to denatured human immunodeficiency
 virus (HIV) TAT protein"

FT Region 16..35

FT /note= "Corresponds to mutant human phospholamban (PLB)
 amino terminal peptide"

FT Misc-difference 31 /note= "Wild type Ser replaced with Glu"

XX WO200025804-A2.

XX 11-MAY-2000.

XX 02-NOV-1999; 99WO-US025692.

XX 02-NOV-1998; 98US-0106718P.

XX 27-JUL-1999; 99US-0145883P.

XX (REGC) UNIV CALIFORNIA.

XX Chien K, Dillman W, Minamisawa S, He H, Hoshijima M, Meyer M;
 PI Scott C, Wang Y, Silverman GU;

XX WPI; 2000-365393/31.

XX Treating cardiac diseases, e.g. heart failure or myocardial dysfunction
 PT comprises enhancing cardiac contractility by inhibiting interaction
 FT between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine

PT triphosphatase.
 XX
 PS Example 5; Page 53; 56pp; English.
 XX
 CC The patent discloses a method for the treatment of heart failure, using
 CC small peptide complexes and recombinant proteins, that induces
 CC phospholamban (PLB) deficiency and inhibits the interaction between PLB
 CC and sarcoplasmic reticulum Ca²⁺ ATPase (SERCA2a) within cardiomyocytes.
 CC The peptide complex comprises of transport peptide like penetratin and
 CC cargo peptide selected from mutant PLB, native PLB or antibody against
 CC PLB protein (contractilin). Penetratin-PLB peptide functions as a
 CC dominant negative inhibitor of PLB-SERCA2a interaction, enhances cardiac
 CC contractility and reduces blood pressure. This method is useful for the
 CC treatment of cardiac disease e.g. heart failure and myocardial
 CC dysfunction. The present sequence is the penetratin-based recombinant
 CC peptide TAT-mutant PLB, comprising the amino terminal end of human PLB
 CC mutant (Ser31Glu) protein, attached to the 3' end of denatured human
 CC immunodeficiency virus (HIV), TAT protein. Penetratin is a class of
 CC peptides, with translocating properties having the ability to carry
 CC hydrophilic compounds across the plasma membrane
 XX
 SQ Sequence 35 AA;

Query Match 94.7%; Score 71; DB 3; Length 35;
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRA 15
 Db 16 MEKVQYLTRSAIRRA 30

RESULT 18
 AAY71013

ID AAY71013 standard; peptide; 36 AA.

XX AAY71013;

XX 29-AUG-2000 (first entry)

DE Penetratin-based recombinant phospholamban peptide, mutant PLB-ANT.

XX Phospholamban; PLB; human; sarcoplasmic reticulum Ca²⁺ ATPase; SERCA2a;
 KW cardiant; cardiomyocyte; transport peptide; penetratin; cargo peptide;
 KW contractilin; cardiac contractility; inhibitor; cardiac disease; mutant;
 KW treatment; heart failure; myocardial dysfunction; recombinant protein;
 KW fruit fly; ANI; antennapedia.

XX Homo sapiens.

OS Drosophila sp.

PH Key Location/Qualifiers

FT Region 1..20 /note= "Corresponds to mutant human phospholamban (PLB)
 amino terminal peptide"

FT Misc-difference 16 /note= "Wild type Ser replaced with Glu"

FT Region 21..36

FT /note= "Corresponds to Drosophila antennapedia (ANT)
 transport peptide"

XX WO200025804-A2.

XX 11-MAY-2000.

XX 02-NOV-1999; 99WO-US025692.

XX 02-NOV-1998; 98US-0106718P.

XX 27-JUL-1999; 99US-0145883P.

XX (REGC) UNIV CALIFORNIA.

XX Chien K, Dillman W, Minamisawa S, He H, Hoshijima M, Meyer M;

PI Scott C, Wang Y, Silverman GJ;
 XX WPI; 2000-365393/31.
 XX
 XX Treating cardiac diseases, e.g. heart failure or myocardial dysfunction
 PT comprises enhancing cardiac contractility by inhibiting interaction
 PT between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine
 PT triphosphatase.
 XX
 XX Example 5; Page 53; 56pp; English.
 PS
 XX The patent discloses a method for the treatment of heart failure, using
 CC small peptide complexes and recombinant proteins, that induces
 CC phospholamban (PLB) deficiency and inhibits the interaction between PLB
 CC and sarcoplasmic reticulum Ca 2+ ATPase (SERCA2a) within cardiomyocytes.
 CC The peptide complex comprises of transport peptide like penetratin and
 CC cargo peptide selected from mutant PLB, native PLB or antibody against
 CC PLB protein (conectatilin). Penetratin-PLB peptide functions as a
 CC dominant negative inhibitor of PLB-SERCA2a interaction, enhances cardiac
 CC contractility and reduces blood pressure. This method is useful for the
 CC treatment of cardiac disease e.g. heart failure and myocardial
 CC dysfunction. The present sequence is the penetratin-based recombinant
 CC peptide, mutant PLB-ANT, comprising the amino terminal end of human PLB
 CC mutant (Ser16Glu) protein, attached to the 5' end of the Drosophila
 CC antennapedia (ANT) transport peptide. Penetratin is a class of peptides,
 CC with translocating properties having the ability to carry hydrophilic
 CC compounds across the plasma membrane
 XX
 XX Sequence 36 AA;
 SQ
 Query Match 94.7%; Score 71; DB 3; Length 36;
 Best Local Similarity 100.0%; Pred. No. 1.3e-05; Mismatches 0; Gaps 0;
 Matches 15; Conservative 0; Indels 0; Gaps 0;
 QY 1 MEKVQLTRSAIRRA 15
 DB 1 MEKVQLTRSAIRRA 15
 |||||
 RESULT 19
 ABB79404
 ID ABB79404 standard; peptide; 52 AA.
 AC ABB79404;
 XX
 XX 24-JUN-2002 (first entry)
 DT
 XX Human phospholamban pseudophosphorylation mutant S16E PLB.
 DE
 XX Human; phospholamban; PLB; cardiant; heart disease; gene therapy;
 KW cardiac function; mutant; mutein.
 XX
 XX Homo sapiens.
 OS
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 16
 FT /note= "Wildtype Ser substituted by Glu"
 XX
 XX US2002032167-A1.
 PN
 XX 14-MAR-2002.
 PD
 XX
 XX 11-SEP-2001; 2001US-00954571.
 PF
 XX
 XX 11-SEP-2000; 2000US-0231821P.
 PR
 XX
 XX (CHIE//) CHIEN K R.
 PA (HOSH//) HOSHJIMA M.
 PA (ROSS//) ROSS J.
 PA (IKED//) IKEDA Y.
 XX
 XX Chien KR, Hoshijima M, Ross J, Ikeda Y;
 XX

DR WPI; 2002-361185/39.
 XX
 XX Delivering a dose of a gene expression cassette in a fluid selectively to
 PT heart for sustained expression, useful for improving or enhancing cardiac
 PT function, by employing a viral vector together with a vascular
 PT permeabilizing agent.
 XX
 XX Example 6; Fig 1; 12pp; English.
 PS
 XX The invention relates to delivering a therapeutic dose of a gene
 CC expression cassette in a fluid selectively to heart for sustained
 CC expression, comprising employing a viral vector together with a vascular
 CC permeabilizing agent. The method is useful for gene therapy delivering
 CC genes for improving or enhancing cardiac function, particularly in
 CC hamster models of heart disease. The present sequence is that of a
 CC pseudophosphorylation mutant of phospholamban (S16EPLB). This point
 CC mutant is among a number of dominant negative mutants identified and
 CC characterised in WO00/25804 and used in the method of the present
 CC invention
 XX
 XX Sequence 52 AA;
 SQ
 Query Match 94.7%; Score 71; DB 5; Length 52;
 Best Local Similarity 100.0%; Pred. No. 2e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MEKVQLTRSAIRRA 15
 DB 1 MEKVQLTRSAIRRA 15
 |||||
 RESULT 20
 ADE45173
 ID ADE45173 standard; protein; 52 AA.
 AC ADE45173;
 XX
 XX 29-JAN-2004 (first entry)
 DT
 XX Chicken SERCA_2 inhibitor phospholamban.
 DE
 XX Chicken; SERCA_2; phospholamban; PLB;
 KW Ca2+ ATPase of the sarco/endoplasmic reticulum; protein co-ordinate data;
 KW cardiant.
 XX
 XX Gallus sp.
 OS
 XX US6538022-B1.
 PN
 XX 25-MAR-2003.
 PD
 XX 18-FEB-1999; 99US-00252063.
 PF
 XX 24-SEP-1997; 97US-00937117.
 PR
 XX (ORIN) ORION CORP.
 PA
 XX Pollesello P, Ovaska M, Tenhunen J, Vidgren J;
 PI Yliperttula-Ikonen M, Tilgmann C, Lotta T, Kaivola J;
 XX
 XX WPI; 2004-019625/02.
 DR
 XX New compound, useful for relieving inhibitory effects of phospholamban on
 PT cardiac SR Ca2+-ATPase by deactivating phospholamban and stimulating Ca2+
 FT -ATPase.
 PS
 XX Claim 1; SEQ ID NO 7; 65pp; English.
 XX
 XX The invention relates to a compound which deactivates, and exhibits
 CC affinity for, a phospholamban (PLB) protein (an inhibitor of SERCA_2,
 CC Ca2+ ATPase of the sarco/endoplasmic reticulum) appearing as ADE45167-
 CC ADE45173. The compound has a structure containing three of the four
 CC moieties: an electronegative moiety associating with an S1 binding site

CC of the phospholamban cytosolic domain when the compound is bound to it,
 CC the binding site comprises Tyr-6, Arg-9 and/or Arg-13; an electronegative
 CC moiety associating with an S2 binding site of the phospholamban cytosolic
 CC domain when the compound is bound to it, the S2 binding site comprises
 CC Arg-14; a hydrophobic moiety associating with an S3 binding site of the
 CC phospholamban cytosolic domain when the compound is bound, the binding
 CC site comprises Met-20, Lys-27 and/or Leu-28; and a hydrophobic moiety
 CC associating with an S4 binding site of the phospholamban cytosolic domain
 CC when the compound is bound, the binding site comprises Phe-32 and/or Phe-
 CC 35. The compound is not 3-benzyl-5,7-bis ((1H-tetrazol-5-yl)-methoxy)-4
 CC -methyl-2H-1-benzopyran-2-one. Also included are deactivating
 CC phospholamban, comprising administering the novel compound to stimulate
 CC the Ca²⁺-ATPase. The compound is useful for relieving the inhibitory
 CC effects of phospholamban on cardiac SERCA₂. The present sequence is a
 CC phospholamban.

XX SQ Sequence 52 AA;

Query Match 94.7%; Score 71; DB 8; Length 52;
 Best Local Similarity 87.5%; Pred. No. 2e-05;
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRAS 16
 DB 1 MEKVQYLTRSAIRRAS 16
 |||||:|||||
 |||||:|||||

RESULT 21

AAAY71018
 ID AAY71018 standard; protein; 79 AA.

XX AC AAY71018;

XX DT 29-AUG-2000 (first entry)

XX DE H6 tagged penetratin-based recombinant protein, H6-(S16E)mutant-PLB-ANT.
 XX KW Phospholamban; PLB; human; sarcoplasmic reticulum Ca²⁺ ATPase; SERCA2a;
 XX KW cardiant; cardiomyocyte; transport peptide; penetratin; cargo peptide;
 XX KW contractilin; cardiac contractility; inhibitor; cardiac disease; mutant;
 XX KW treatment; heart failure; myocardial dysfunction; recombinant protein;
 XX KW fruit fly; ANT; antennapedia; H6 tag; hexahistidine.

XX OS Homo sapiens.
 XX OS Drosophila sp.
 XX OS Synthetic.

XX FH Key Location/Qualifiers
 XX FT Region 1..52

XX FT /note= "Corresponds to mutant human phospholamban (PLB)
 XX FT protein"

XX FT Misc-difference 16

XX FT /note= "Wild type Ser replaced with Glu"

XX FT Region 53..58

XX FT /note= "Corresponds to hexahistidine tag (H6)"

XX FT Region 63..78

XX FT /notes "Corresponds to Drosophila antennapedia (ANT)
 XX FT transport peptide"

XX PN WO200025804-A2.

XX PD 11-MAY-2000.

XX PF 02-NOV-1999; 99WO-US025692.

XX PR 02-NOV-1998; 98US-0106718P.

XX PR 27-JUL-1999; 99US-0145883P.

XX PA (REGC) UNIV CALIFORNIA.

XX PI Chien K, Dillman W, Minamisawa S, He H, Hoshijima M, Meyer M;

XX PI Scott C, Wang Y, Silverman GJ;

XX XX

DR WPI; 2000-365393/31.

XX Treating cardiac diseases, e.g. heart failure or myocardial dysfunction
 PT comprises enhancing cardiac contractility by inhibiting interaction
 PT between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine
 PT triphosphatase.

XX Example 6; Page 55; 56pp; English.

XX The patent discloses a method for the treatment of heart failure, using
 CC small peptide complexes and recombinant proteins, that induces
 CC phospholamban (PLB) deficiency and inhibits the interaction between PLB
 CC and sarcoplasmic reticulum Ca²⁺ ATPase (SERCA2a) within cardiomyocytes.
 CC The peptide complex comprises of transport peptide like penetratin and
 CC cargo peptide selected from mutant PLB, native PLB or antibody against
 CC PLB protein (contractilin). Penetratin-PLB peptide functions as a
 CC dominant negative inhibitor of PLB-SERCA2a interaction. This method is useful for the
 CC treatment of cardiac disease e.g. heart failure and myocardial
 CC dysfunction. The present sequence is the hexahistidine (H6) tagged
 CC penetratin-based recombinant protein H6-mutant-PLB-ANT, comprising the
 CC human mutant (Ser16Glu) PLB protein and Drosophila antennapedia (ANT)
 CC transport peptide attached by a hexahistidine tag. This sequence is
 CC expressed in Escherichia coli cells

XX SQ Sequence 79 AA;

Query Match 94.7%; Score 71; DB 3; Length 79;

Best Local Similarity 100.0%; Pred. No. 3.1e-05;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRA 15

DB 1 MEKVQYLTRSAIRRA 15
 |||||:|||||
 |||||:|||||

RESULT 22

AAAY71005
 ID AAY71005 standard; protein; 52 AA.

XX AC AAY71005;

XX DT 29-AUG-2000 (first entry)

XX DE Human mutant phospholamban (PLB) R14E protein.

XX KW Phospholamban; PLB; human; sarcoplasmic reticulum Ca²⁺ ATPase; SERCA2a;
 XX KW cardiant; cardiomyocyte; transport peptide; penetratin; cargo peptide;
 XX KW contractilin; cardiac contractility; inhibitor; cardiac disease;
 XX KW treatment; heart failure; myocardial dysfunction; mutant.

XX OS Homo sapiens.

XX OS Synthetic.

XX FH Key Location/Qualifiers

XX FT Misc-difference 14

XX FT /note= "Wild type Arg replaced with Glu"

XX PN WO200025804-A2.

XX PD 11-MAY-2000.

XX PF 02-NOV-1999; 99WO-US025692.

XX PR 02-NOV-1998; 98US-0106718P.

XX PR 27-JUL-1999; 99US-0145883P.

XX PA (REGC) UNIV CALIFORNIA.

XX PI Chien K, Dillman W, Minamisawa S, He H, Hoshijima M, Meyer M;

XX PI Scott C, Wang Y, Silverman GJ;

XX XX WPI; 2000-365393/31.

comprises enhancing cardiac contractility by inhibiting interaction between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine triphosphatase.

XX Disclosure; Page 49; 56pp; English.

XX The patent discloses a method for the treatment of heart failure, using small peptide complexes and recombinant proteins, that induces phospholamban (PLB) deficiency and inhibits the interaction between PLB and sarcoplasmic reticulum Ca 2+ ATPase (SERCA2a) within cardiomyocytes.

XX The peptide complex comprises of transport peptide like penetratin and cargo peptide selected from mutant PLB, native PLB or antibody against PLB protein (contractilin). Penetratin-PLB peptide functions as a dominant negative inhibitor of PLB-SERCA2a interaction, enhances cardiac contractility and reduces blood pressure. This method is useful for the treatment of cardiac disease e.g. heart failure and myocardial dysfunction. The present amino acid sequence is the human mutant PLB protein, comprising the double mutation Lys3Glu and Arg15Glu. This mutant sequence, when overexpressed in the transformed cardiomyocytes, shows increased contractility than the wild type PLB sequence

XX Sequence 52 AA;

Query Match 88.0%; Score 66; DB 3; Length 52;
Best Local Similarity 87.5%; Pred. NO. 0.00016;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Caps 0;

OY 1 MEKVQYLTRSAIRAS 16
DB 1 MEEVQYLTRSAIRAS 16
:::|||||::|

RESULT 25
ADC87928
ID ADC87928 standard; protein; 116 AA.

XX
AC ADC87928;

XX 01-JAN-2004 (first entry)

XX Ribosomal protein similar to FCWP1 #144.

XX Antifungal protein; ribosomal protein; FCWP1; AlyAFP;
XX Plant fungal infection; Alternaria; Ascochyta; Botrytis; Cercospora;
XX Colletotrichum; Diplodia; Fusarium; Gaemanomyces; Helminthosporium;
XX Macrophomina; Mycosphaerella; Nectria; Peronospora; Phoma; Puthium;
XX Phymatotrichum; Phytophthora; Plasmodora; Podosphaera; Puccinia; Puthium;
XX Pyrenophora; Pyricularia; Pythium; Rhizoctonia; Sclerotium; Sclerotinia;
XX Septoria; Thielaviopsis; Venturia; Verticillium.

XX Unidentified.

XX US6573361-B1.

XX 03-JUN-2003.

XX 07-DEC-2000; 2000US-00732210.

XX 07-DEC-1999; 98US-0169340P.

XX 07-DEC-1999; 99US-0169513P.

XX (MONS) MONSANTO TECHNOLOGY LLC.

XX Bunkers GJ, Liang J, Mittanck CA, Seale JW, Wu YS;
XX WPI, 2003-754558/71.

XX Novel antifungal protein FCWP1, isolated from Fusarium culmorum, useful for controlling fungal infections in plants.

XX Example 21; SEQ ID NO 181; 27pp; English.

XX The invention relates to an isolated antifungal ribosomal protein from

XX fusarium culmorum, FCWP1. Also included is a fusion protein between the signal peptide of the antifungal protein AlyAFP from Alyssum and FCWP1, encoded by the nucleic acid appearing as ADC87758. The FCWP1 proteins are useful for controlling fungal infections in plants, such as those caused by Alternaria (e.g. Alternaria brassicola, Alternaria solani), Ascochyta (e.g. Ascochyta pisi); Botrytis (e.g. Botrytis cinerea), Cercospora (e.g. Cercospora kikuchii, Cercospora zea-maydis), Colletotrichum (e.g. Colletotrichum lindemuthianum), Diplodia (e.g. Diplodia maydis), Fusarium (e.g. Fusarium nivale, Fusarium oxysporum, Fusarium graminearum, Fusarium culmorum, Fusarium solani, Fusarium moniliforme, Fusarium roseum), Gaemanomyces (e.g. Gaemanomyces graminis f. sp. tritici), Helminthosporium (e.g. Helminthosporium turcicum, Helminthosporium carthorum, Helminthosporium maydis), Macrophomina (e.g. Macrophomina phaseolina, Magnaporthe grisea), Mycosphaerella (e.g. Mycosphaerella figiensis), Nectria (Nectria haematococca), Peronospora (e.g. Peronospora manshurica, Peronospora tabacina), Phoma (e.g. Phoma betae), Phymatotrichum (e.g. Phymatotrichum omnivorum), Phytophthora (e.g. Phytophthora cinnamomi, Phytophthora cactorum), Phytophthora phaseoli, Phytophthora parasitica, Phytophthora citrophthora, Phytophthora megasperma f. sp. sojae, Phytophthora infestans), Plasmodora (e.g. Plasmodora viticola), Podosphaera (e.g. Podosphaera leucotricha), Puccinia (e.g. Puccinia sorghi, Puccinia striiformis, Puccinia graminis f. sp. tritici, Puccinia asparagi, Puccinia recondita, Puccinia arachidis), Puthium (e.g. Puthium aphanidermatum), Pyrenophora (e.g. Pyrenophora tritici-repentens), Pyricularia (e.g. Pyricularia oryzae), Pythium (e.g. Pythium ultimum), Rhizoctonia (e.g. Rhizoctonia solani, Rhizoctonia cerealis), Sclerotium (e.g. Sclerotium rolfsii), Sclerotinia (e.g. Sclerotinia sclerotiorum), Septoria (e.g. Septoria lycopersici, Septoria glycines, Stagonospora nodorum / Phaeosphaeria nodorum, Septoria tritici), Thielaviopsis (e.g. Thielaviopsis basicola), Uncinula (e.g. Uncinula necator), Venturia (e.g. Venturia inaequalis) or Verticillium (e.g. Verticillium dahliae, Verticillium albo-atrum). Mutations in the proteolytic consensus sequences contained within FCWP1 provides improved stability of its antifungal activity. Also disclosed are ribosomal proteins with similar PI (>7) and molecular weight (<20kDa) to FCWP1, which may act as antifungal proteins. The present sequence represents one of the ribosomal proteins similar to FCWP1. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?docID=6573361B1.

XX SQ Sequence 116 AA;

Query Match 54.7%; Score 41; DB 7; Length 116;
Best Local Similarity 46.7%; Pred. NO. 14;
Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

OY 1 MEKVQYLTRSAIRRA 15
:::|::|::|::|
DB 81 VEKIELVTRGDVRRRA 95

Search completed: October 1, 2004, 12:13:19
Job time : 63.2 secs

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OM protein - protein search, using sw model

Run on: October 1, 2004, 12:07:51 ; Search time 17 Seconds

(without alignments)
48.589 Million cell updates/sec

Title: US-09-830-779-19_COPY_1_16

Perfect score: 75

Sequence: 1 MEKVQLTRSAIRAS 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Database :

Issued Patents AA:*
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6: /cgn2_6/prodata/2/iaa/5B_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	75	100.0	36	4	US-09-252-063-9
2	75	100.0	52	4	US-09-252-063-1
3	75	100.0	52	4	US-09-252-063-4
4	75	100.0	52	4	US-09-252-063-5
5	75	100.0	52	4	US-09-252-063-6
6	75	100.0	52	4	US-09-549-872B-15
7	72	96.0	52	4	US-09-252-063-2
8	72	96.0	52	4	US-09-252-063-3
9	72	96.0	52	4	US-09-549-872B-14
10	71	94.7	52	4	US-09-252-063-7
11	41	54.7	116	4	US-09-732-210-181
12	37	49.3	631	4	US-09-252-991A-18000
13	36	48.0	98	4	US-09-489-039A-7319
14	36	48.0	194	4	US-09-489-039A-11071
15	36	48.0	686	4	US-09-252-991A-19332
16	36	48.0	765	4	US-09-252-991A-24791
17	36	48.0	924	2	US-08-588-983-18
18	35	48.0	924	2	US-08-588-976-18
19	35	46.7	210	4	US-09-252-991A-28362
20	35	46.7	211	4	US-09-134-001C-5136
21	35	46.7	216	4	US-09-134-000C-6395
22	35	46.7	357	4	US-09-910-174B-14
23	35	46.7	357	4	US-09-620-461-14
24	35	46.7	497	4	US-09-277-263-4
25	35	46.7	516	4	US-09-277-263-2
26	34.5	46.0	835	2	US-08-968-751-4
27	34.5	46.0	864	4	US-09-323-872A-28

28	34.5	46.0	864	4	US-09-072-433-16
29	34	45.3	230	4	US-09-540-236-2466
30	34	45.3	238	4	US-09-107-532A-5165
31	34	45.3	310	4	US-09-107-532A-5580
32	34	45.3	331	4	US-09-328-352-5369
33	33.5	44.7	53	4	US-09-673-395A-511
34	33	44.0	24	4	US-09-561-490B-3
35	33	44.0	50	6	5169933-31
36	33	44.0	71	4	US-09-489-039A-9691
37	33	44.0	104	4	US-09-134-001C-4945
38	33	44.0	172	4	US-09-252-991A-24148
39	33	44.0	180	4	US-09-252-991A-18799
40	33	44.0	235	4	US-09-198-452A-752
41	33	44.0	276	2	US-08-712-072C-4
42	33	44.0	297	4	US-09-252-991A-16808
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44	33	44.0	320	4	US-09-543-681A-6145
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46	33	44.0	350	4	US-08-637-670-39
47	33	44.0	373	4	US-09-328-352-5753
48	33	44.0	374	4	US-09-679-279-6
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51	33	44.0	573	4	US-09-328-352-6420
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54	33	44.0	804	4	US-09-107-532A-6348
55	33	44.0	807	4	US-09-252-991A-18831
56	33	44.0	972	3	US-08-335-844A-24
57	33	44.0	972	4	US-09-129-366-24
58	33	44.0	1124	4	US-09-191-786-1
59	32	42.7	100	4	US-09-732-210-1175
60	32	42.7	113	4	US-09-732-210-681
61	32	42.7	139	4	US-08-065-844A-8
62	32	42.7	169	4	US-09-252-991A-32083
63	32	42.7	213	4	US-09-328-352-6122
64	32	42.7	390	1	US-07-669-171-2
65	32	42.7	390	1	US-08-132-405-1
66	32	42.7	390	1	US-08-395-939A-1
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68	32	42.7	390	6	5168051-2
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71	32	42.7	420	4	US-09-134-001C-3805
72	32	42.7	443	4	US-09-328-352-7207
73	32	42.7	457	3	US-09-416-213-2
74	32	42.7	457	4	US-09-416-214-2
75	32	42.7	457	4	US-09-035-676-2
76	32	42.7	483	4	US-09-252-991A-31365
77	32	42.7	571	4	US-09-489-039A-14334
78	32	42.7	589	4	US-09-328-352-7592
79	32	42.7	604	4	US-09-391-104-30
80	32	42.7	607	3	US-09-000-041A-2
81	32	42.7	607	3	US-09-211-704A-10
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87	32	42.7	667	2	US-08-455-355-6
88	32	42.7	667	4	US-09-367-512-5
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90	32	42.7	784	4	US-09-252-991A-20416
91	32	42.7	812	4	US-09-198-452A-978
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93	32	42.7	1044	4	US-09-252-991A-22493
94	32	42.7	1154	4	US-09-489-039A-7724
95	32	42.7	1799	4	US-09-134-000C-5178
96	32	42.7	2568	4	US-09-866-108A-3
97	31.5	42.0	343	4	US-09-489-039A-10330
98	31.5	42.0	1729	4	US-09-553-690-2
99	31	41.3	36	1	US-08-487-890A-29
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Sequence 5580, Ap
Sequence 5369, Ap
Sequence 511, Appl
Sequence 3, Appl
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Sequence 4945, Ap
Sequence 24148, A
Sequence 18799, A
Sequence 752, Appl
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Sequence 16808, A
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Patent No. 5171684
Sequence 39, Appl
Sequence 5753, Ap
Sequence 6, Appl
Sequence 104, Appl
Sequence 3679, Ap
Sequence 6420, Ap
Sequence 10702, A
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Sequence 20416, A
Sequence 978, Appl
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Sequence 29, Appl
Sequence 29, Appl

ALIGNMENTS

RESULT 1
 US-09-252-063-9
 ; Sequence 9, Application US/09252063
 ; Patent No. 6538022
 ; GENERAL INFORMATION:
 ; APPLICANT: Pollesello, Piero
 ; APPLICANT: Ovaska, Martti
 ; APPLICANT: Tenhunen, Jukka
 ; APPLICANT: Viigren, Jukka
 ; APPLICANT: Yliperttula-Ikonen, Marjo
 ; APPLICANT: Tilgmann, Carola
 ; APPLICANT: Lotka, Timo
 ; APPLICANT: Kaivola, Juha
 ; TITLE OF INVENTION: Compounds for Deactivating Phospholamban Function on
 ; TITLE OF INVENTION: Ca-ATPase (Phospholamban Inhibitors)
 ; FILE REFERENCE: 1102.0250001
 ; CURRENT APPLICATION NUMBER: US/09/252,063
 ; CURRENT FILING DATE: 1999-02-18
 ; EARLIER APPLICATION NUMBER: 08/937,117
 ; EARLIER FILING DATE: 1997-09-24
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 9
 ; LENGTH: 36
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: cystolic part
 ; OTHER INFORMATION: of phospholamban peptide
 US-09-252-063-9

Query Match 100.0%; Score 75; DB 4; Length 36;
 Best Local Similarity 100.0%; Pred. No. 2e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRAS 16
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 Db 1 MEKVQYLTRSAIRAS 16

RESULT 2
 US-09-252-063-1
 ; Sequence 1, Application US/09252063
 ; Patent No. 6538022
 ; GENERAL INFORMATION:
 ; APPLICANT: Pollesello, Piero
 ; APPLICANT: Ovaska, Martti
 ; APPLICANT: Tenhunen, Jukka
 ; APPLICANT: Viigren, Jukka
 ; APPLICANT: Yliperttula-Ikonen, Marjo
 ; APPLICANT: Tilgmann, Carola
 ; APPLICANT: Lotka, Timo
 ; APPLICANT: Kaivola, Juha
 ; TITLE OF INVENTION: Compounds for Deactivating Phospholamban Function on
 ; TITLE OF INVENTION: Ca-ATPase (Phospholamban Inhibitors)
 ; FILE REFERENCE: 1102.0250001
 ; CURRENT APPLICATION NUMBER: US/09/252,063
 ; CURRENT FILING DATE: 1999-02-18
 ; EARLIER APPLICATION NUMBER: 08/937,117
 ; EARLIER FILING DATE: 1997-09-24
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 1
 ; LENGTH: 52
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-252-063-1

Query Match 100.0%; Score 75; DB 4; Length 52;
 Best Local Similarity 100.0%; Pred. No. 3e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRAS 16
 |||||
 Db 1 MEKVQYLTRSAIRAS 16

RESULT 3
 US-09-252-063-4
 ; Sequence 4, Application US/09252063
 ; Patent No. 6538022
 ; GENERAL INFORMATION:
 ; APPLICANT: Pollesello, Piero
 ; APPLICANT: Ovaska, Martti
 ; APPLICANT: Tenhunen, Jukka
 ; APPLICANT: Viigren, Jukka
 ; APPLICANT: Yliperttula-Ikonen, Marjo
 ; APPLICANT: Tilgmann, Carola
 ; APPLICANT: Lotka, Timo
 ; APPLICANT: Kaivola, Juha
 ; TITLE OF INVENTION: Compounds for Deactivating Phospholamban Function on
 ; TITLE OF INVENTION: Ca-ATPase (Phospholamban Inhibitors)
 ; FILE REFERENCE: 1102.0250001
 ; CURRENT APPLICATION NUMBER: US/09/252,063
 ; CURRENT FILING DATE: 1999-02-18
 ; EARLIER APPLICATION NUMBER: 08/937,117
 ; EARLIER FILING DATE: 1997-09-24
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 4
 ; LENGTH: 52
 ; TYPE: PRT
 ; ORGANISM: Oryctolagus cuniculus
 US-09-252-063-4

Query Match 100.0%; Score 75; DB 4; Length 52;
 Best Local Similarity 100.0%; Pred. No. 3e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRAS 16
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RESULT 4
 US-09-252-063-5
 ; Sequence 5, Application US/09252063
 ; Patent No. 6538022
 ; GENERAL INFORMATION:
 ; APPLICANT: Pollesello, Piero
 ; APPLICANT: Ovaska, Martti
 ; APPLICANT: Tenhunen, Jukka
 ; APPLICANT: Viigren, Jukka
 ; APPLICANT: Yliperttula-Ikonen, Marjo
 ; APPLICANT: Tilgmann, Carola
 ; APPLICANT: Lotka, Timo
 ; APPLICANT: Kaivola, Juha
 ; TITLE OF INVENTION: Compounds for Deactivating Phospholamban Function on
 ; TITLE OF INVENTION: Ca-ATPase (Phospholamban Inhibitors)
 ; FILE REFERENCE: 1102.0250001
 ; CURRENT APPLICATION NUMBER: US/09/252,063
 ; CURRENT FILING DATE: 1999-02-18
 ; EARLIER APPLICATION NUMBER: 08/937,117
 ; EARLIER FILING DATE: 1997-09-24
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 5
 ; LENGTH: 52
 ; TYPE: PRT
 ; ORGANISM: Rattus sp.
 US-09-252-063-5

Query Match 100.0%; Score 75; DB 4; Length 52;
Best Local Similarity 100.0%; Pred. No. 3e-07; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEKVQYLTRSAIRRAS 16
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Db 1 MEKVQYLTRSAIRRAS 16

RESULT 5

US-09-252-063-6
; Sequence 6, Application US/09252063
; Patent No. 6538022
; GENERAL INFORMATION:
; APPLICANT: Pollesello, Piero
; APPLICANT: Ovaska, Martti
; APPLICANT: Tenhunen, Jukka
; APPLICANT: Viigren, Jukka
; APPLICANT: Yliperttula-Ikonen, Marjo
; APPLICANT: Tilgmann, Carola
; APPLICANT: Lotta, Timo
; APPLICANT: Kaivola, Juha
; TITLE OF INVENTION: Compounds for Deactivating Phospholamban Function on
; FILE REFERENCE: 1102.0250001
; CURRENT APPLICATION NUMBER: US/09/252.063
; CURRENT FILING DATE: 1999-02-18
; EARLIER APPLICATION NUMBER: 08/937,117
; EARLIER FILING DATE: 1997-09-24
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 6
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-252-063-6

Query Match 100.0%; Score 75; DB 4; Length 52;
Best Local Similarity 100.0%; Pred. No. 3e-07; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEKVQYLTRSAIRRAS 16
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Db 1 MEKVQYLTRSAIRRAS 16

RESULT 6

US-09-549-872B-15
; Sequence 15, Application US/09549872B
; Patent No. 6540996
; GENERAL INFORMATION:
; APPLICANT: Zwaal, Richard
; APPLICANT: Groenen, Jose
; APPLICANT: Bogaert, Thierry
; TITLE OF INVENTION: COMPOUND SCREENING METHODS
; FILE REFERENCE: D00590/70008 (JRV/RE)
; CURRENT APPLICATION NUMBER: US/09/549,872B
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: GB 9908670.4
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: US 60/129,596
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: GB 9912736.7
; PRIOR FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 15
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-549-872B-15

Query Match 100.0%; Score 75; DB 4; Length 52;
Best Local Similarity 100.0%; Pred. No. 3e-07; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEKVQYLTRSAIRRAS 16
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Db 1 MEKVQYLTRSAIRRAS 16

RESULT 7

US-09-252-063-2
; Sequence 2, Application US/09252063
; Patent No. 6538022
; GENERAL INFORMATION:
; APPLICANT: Pollesello, Piero
; APPLICANT: Ovaska, Martti
; APPLICANT: Tenhunen, Jukka
; APPLICANT: Viigren, Jukka
; APPLICANT: Yliperttula-Ikonen, Marjo
; APPLICANT: Tilgmann, Carola
; APPLICANT: Lotta, Timo
; APPLICANT: Kaivola, Juha
; TITLE OF INVENTION: Compounds for Deactivating Phospholamban Function on
; FILE REFERENCE: 1102.0250001
; CURRENT APPLICATION NUMBER: US/09/252.063
; CURRENT FILING DATE: 1999-02-18
; EARLIER APPLICATION NUMBER: 08/937,117
; EARLIER FILING DATE: 1997-09-24
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Sus sp.
US-09-252-063-2

Query Match 96.0%; Score 72; DB 4; Length 52;
Best Local Similarity 93.8%; Pred. No. 1.1e-06; Indels 0; Gaps 0;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEKVQYLTRSAIRRAS 16
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Db 1 MDKVQYLTRSAIRRAS 16

RESULT 8

US-09-252-063-3
; Sequence 3, Application US/09252063
; Patent No. 6538022
; GENERAL INFORMATION:
; APPLICANT: Pollesello, Piero
; APPLICANT: Ovaska, Martti
; APPLICANT: Tenhunen, Jukka
; APPLICANT: Viigren, Jukka
; APPLICANT: Yliperttula-Ikonen, Marjo
; APPLICANT: Tilgmann, Carola
; APPLICANT: Lotta, Timo
; APPLICANT: Kaivola, Juha
; TITLE OF INVENTION: Compounds for Deactivating Phospholamban Function on
; FILE REFERENCE: 1102.0250001
; CURRENT APPLICATION NUMBER: US/09/252.063
; CURRENT FILING DATE: 1999-02-18
; EARLIER APPLICATION NUMBER: 08/937,117
; EARLIER FILING DATE: 1997-09-24
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 3
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Canis sp.
US-09-252-063-3

Query Match 96.0%; Score 72; DB 4; Length 52;
Best Local Similarity 93.8%; Pred. No. 1.1e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRAS 16
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Db 1 MDKVQYLTRSAIRRAS 16

RESULT 9

US-09-549-872B-14
; Sequence 14, Application US/09549872B
; Patent No. 6540996
; GENERAL INFORMATION:
; APPLICANT: Zwaal, Richard
; APPLICANT: Groenen, Jose
; APPLICANT: Bogaert, Thierry
; TITLE OF INVENTION: COMPOUND SCREENING METHODS
; FILE REFERENCE: D0059077008 (GRV/RE)
; CURRENT APPLICATION NUMBER: US/09/549,872B
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: GB 9908670.4
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: US 60/129,596
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: GB 9912736.7
; PRIOR FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Sus sp.
US-09-549-872B-14

Query Match 96.0%; Score 72; DB 4; Length 52;
Best Local Similarity 93.8%; Pred. No. 1.1e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRAS 16
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Db 1 MDKVQYLTRSAIRRAS 16

RESULT 10

US-09-252-063-7
; Sequence 7, Application US/09252063
; Patent No. 6538022
; GENERAL INFORMATION:
; APPLICANT: Pollesello, Piero
; APPLICANT: Ovaska, Martti
; APPLICANT: Tenhunen, Jukka
; APPLICANT: Vidgren, Jukka
; APPLICANT: Yliperttula-Ikonen, Marjo
; APPLICANT: Tilgmann, Carola
; APPLICANT: Lotia, Timo
; APPLICANT: Kaivola, Jukka
; TITLE OF INVENTION: Compounds for Deactivating Phospholamban Function on
; TITLE OF INVENTION: Ca-ATPase (Phospholamban Inhibitors)
; FILE REFERENCE: 1102.025C001
; CURRENT APPLICATION NUMBER: US/09/252,063
; CURRENT FILING DATE: 1999-02-18
; EARLIER APPLICATION NUMBER: 08/937,117
; EARLIER FILING DATE: 1997-09-24
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Gallus sp.
US-09-252-063-7

Query Match 94.7%; Score 71; DB 4; Length 52;
Best Local Similarity 87.5%; Pred. No. 1.7e-06;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRAS 16
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Db 1 MEKVQYLTRSAIRRAS 16

RESULT 11

US-09-732-210-181
; Sequence 181, Application US/09732210
; Patent No. 6573361
; GENERAL INFORMATION:
; APPLICANT: Bunkers, Greg J.
; APPLICANT: Liang, Jihong
; APPLICANT: Mittanck, Cindy A.
; APPLICANT: Seale, Jeffrey W.
; APPLICANT: Wu, Yonnie S.
; TITLE OF INVENTION: Anti-fungal Proteins and Methods for Their Use
; FILE REFERENCE: 38-21(15036)B
; CURRENT APPLICATION NUMBER: US/09/732,210
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/169,513
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: US 60/169,340
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 1753
; SEQ ID NO 181
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Streptomyces coelicolor
US-09-732-210-181

Query Match 54.7%; Score 41; DB 4; Length 116;
Best Local Similarity 46.7%; Pred. NO. 2;
Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRA 15
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Db 81 VEKIELVTRGVDVRA 95

RESULT 12

US-09-252-991A-18000
; Sequence 18000, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 18000
; LENGTH: 631
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18000

Query Match 49.3%; Score 37; DB 4; Length 631;
Best Local Similarity 50.0%; Pred. No. 76;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRR 14
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Db 430 VELLQFLPRSRVRR 443

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RESULT 13
US-09-489-039A-7319
; Sequence 7319, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 7319
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-7319

Query Match      48.0%; Score 36; DB 4; Length 98;
Best Local Similarity 58.3%; Pred.No.15;
Matches       7; Conservative   3; Mismatches    2; Indels     0; Gaps     0;

Qy      3 KVQLTRSAIR 14
| | : |||| : |
Db      51 KPQHLTRSGMEK 62

RESULT 14
US-09-489-039A-11071
; Sequence 11071, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 11071
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11071

Query Match      48.0%; Score 36; DB 4; Length 194;
Best Local Similarity 58.3%; Pred.No.32;
Matches       7; Conservative   3; Mismatches    2; Indels     0; Gaps     0;

Qy      1 MEKVQLTRSAL 12
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Db     111 MERVEYLLOSOI 122

RESULT 15
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; Sequence 19332, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONA
S AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
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; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6395
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-6395

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Best Local Similarity 50.0%; Pred. No. 56;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      5 QYLTRSAIRRAS 16
DB      161 QYINRETLARVS 172
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RESULT 22
US-09-910-174B-14
; Sequence 14, Application US/09910174B
; Patent No. 6630575
; GENERAL INFORMATION:
; APPLICANT: Coyle, Anthony J.
; APPLICANT: Fraser, Christopher C.
; APPLICANT: Manning, Stephen
; TITLE OF INVENTION: B7-H2 Molecules, No. 6630575el Members of the B7
; TITLE OF INVENTION: Family and Uses Thereof
; FILE REFERENCE: 35800/236524
; CURRENT APPLICATION NUMBER: US/09/910,174B
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 09/620,461
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 357
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-910-174B-14

Query Match          46.7%; Score 35; DB 4; Length 357;
Best Local Similarity 75.0%; Pred. No. 97;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      2 EKVOYLTR 9
DB      313 KKIQYLTR 320
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RESULT 23
US-09-620-461-14
; Sequence 14, Application US/09620461
; Patent No. 6635750
; GENERAL INFORMATION:
; APPLICANT: Coyle, Anthony J.
; APPLICANT: Fraser, Christopher C.
; APPLICANT: Manning, Stephen
; TITLE OF INVENTION: B7-H2 Molecules, No. 6635750el Members of the B7
; TITLE OF INVENTION: Family and Uses Thereof
; FILE REFERENCE: 5800-149
; CURRENT APPLICATION NUMBER: US/09/620,461
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 357
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-620-461-14

Query Match          46.7%; Score 35; DB 4; Length 357;
Best Local Similarity 75.0%; Pred. No. 97;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      2 EKVOYLTR 9
DB      313 KKIQYLTR 320
      |||:|||||
      |||:|||||

RESULT 24
US-09-277-262-4
; Sequence 4, Application US/09277262
; Patent No. 6395482
; GENERAL INFORMATION:
; APPLICANT: Karayiorou, Maria
; APPLICANT: Gogos, Joseph A
; TITLE OF INVENTION: METHODS OF DETERMINING A SUSCEPTIBILITY TO OR PRESENCE
; TITLE OF INVENTION: OF SCHIZOPHRENIA, OR A DISEASE OR DISORDER RELATED
; TITLE OF INVENTION: THERETO
; FILE REFERENCE: 600-1-223 CIP
; CURRENT APPLICATION NUMBER: US/09/277,262
; CURRENT FILING DATE: 1999-03-26
; EARLIER APPLICATION NUMBER: 09/229,530
; EARLIER FILING DATE: 1999-01-13
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-277-262-4

Query Match          46.7%; Score 35; DB 4; Length 497;
Best Local Similarity 43.8%; Pred. No. 1.4e+02;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY      1 MEKVQYLTRSAIRRAS 16
DB      452 MEVLPYLSRRALENSS 467
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RESULT 25
US-09-277-262-2
; Sequence 2, Application US/09277262
; Patent No. 6395482
; GENERAL INFORMATION:
; APPLICANT: Karayiorou, Maria
; APPLICANT: Gogos, Joseph A
; TITLE OF INVENTION: METHODS OF DETERMINING A SUSCEPTIBILITY TO OR PRESENCE
; TITLE OF INVENTION: OF SCHIZOPHRENIA, OR A DISEASE OR DISORDER RELATED
; TITLE OF INVENTION: THERETO
; FILE REFERENCE: 600-1-223 CIP
; CURRENT APPLICATION NUMBER: US/09/277,262
; CURRENT FILING DATE: 1999-03-26
; EARLIER APPLICATION NUMBER: 09/229,530
; EARLIER FILING DATE: 1999-01-13
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 516
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-277-262-2

Query Match          46.7%; Score 35; DB 4; Length 516;
Best Local Similarity 43.8%; Pred. No. 1.5e+02;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY      1 MEKVQYLTRSAIRRAS 16
DB      471 MEVLPYLSRRALENSS 486
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us-09-830-779-19_copy_1_16.ra1

Page 8

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Job time : 18 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 1, 2004, 12:18:23 ; Search time 63.4 Seconds
(without alignments)
81.211 Million cell updates/sec

Title: US-09-830-779-19_COPY_1_16

Perfect score: 75

Sequence: 1 MEKVQLTRSAIRRAS 16

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Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	75	100.0	35	16	US-10-705-791-11
3	75	100.0	36	16	US-10-705-791-10
4	75	100.0	52	12	US-09-954-571-2
5	75	100.0	52	12	US-09-954-571-4
6	75	100.0	52	12	US-09-954-571-5
7	75	100.0	52	14	US-10-371-101-15
8	75	100.0	52	16	US-10-408-765A-478
9	75	100.0	52	16	US-10-705-791-1
10	75	100.0	52	16	US-10-705-791-2
11	75	100.0	79	16	US-10-705-791-17
12	75	100.0	79	16	US-10-705-791-19
13	72	96.0	52	12	US-09-954-571-3
14	72	96.0	52	14	US-10-371-101-14
15	72	96.0	52	16	US-10-705-791-5

16	71	94.7	35	16	US-10-705-791-13	Sequence 13, Appl
17	71	94.7	36	16	US-10-705-791-12	Sequence 12, Appl
18	71	94.7	52	12	US-09-954-571-1	Sequence 1, Appl
19	71	94.7	79	16	US-10-705-791-18	Sequence 18, Appl
20	70	93.3	52	16	US-10-705-791-4	Sequence 4, Appl
21	69	92.0	52	16	US-10-705-791-3	Sequence 3, Appl
22	66	88.0	52	16	US-10-705-791-6	Sequence 6, Appl
23	66	88.0	44	12	US-10-424-599-238702	Sequence 238702,
24	64	84.7	44	12	US-10-425-114-46161	Sequence 46161, A
25	41	54.7	68	12	US-10-156-761-10177	Sequence 10177, A
26	41	54.7	116	14	US-10-369-493-21530	Sequence 21530, A
27	40	53.3	121	12	US-10-282-122A-47242	Sequence 47242, A
28	40	53.3	1108	15	US-10-369-493-1247	Sequence 1247, Ap
29	40	53.3	1108	15	US-10-437-963-20314	Sequence 20314, A
30	39	52.0	452	16	US-10-437-963-203101	Sequence 203101,
31	38	50.7	113	12	US-10-282-122A-53984	Sequence 53984, A
32	38	50.7	790	16	US-10-437-963-13951	Sequence 13951,
33	38	50.7	931	16	US-10-437-963-188757	Sequence 188757,
34	37	49.3	112	12	US-10-424-599-175485	Sequence 175485,
35	36.5	48.7	331	14	US-10-197-844-2	Sequence 2, Appl
36	36	48.0	75	16	US-10-437-963-202409	Sequence 202409,
37	36	48.0	111	12	US-10-424-599-170920	Sequence 170920,
38	36	48.0	111	12	US-10-424-599-195661	Sequence 195661,
39	36	48.0	113	9	US-09-738-626-5733	Sequence 5733, Ap
40	36	48.0	114	12	US-10-282-122A-52593	Sequence 52593, A
41	36	48.0	119	16	US-10-767-701-55916	Sequence 55916, A
42	36	48.0	207	12	US-10-282-122A-71415	Sequence 71415, A
43	36	48.0	297	16	US-10-437-963-195227	Sequence 195227,
44	36	48.0	344	15	US-10-131-410-177	Sequence 177, App
45	36	48.0	401	14	US-10-156-761-7673	Sequence 7673, Ap
46	36	48.0	409	12	US-10-282-122A-66259	Sequence 66259, A
47	36	48.0	417	12	US-10-389-647-494	Sequence 494, App
48	36	48.0	434	14	US-10-171-404A-46	Sequence 46, Appl
49	36	48.0	465	12	US-10-282-122A-48867	Sequence 48867, A
50	36	48.0	556	15	US-10-369-493-4879	Sequence 4879, Ap
51	36	48.0	629	16	US-10-437-963-153082	Sequence 153082,
52	36	48.0	690	16	US-10-437-963-195233	Sequence 195233,
53	36	48.0	720	16	US-10-433-794-20	Sequence 20, Appl
54	36	48.0	765	12	US-10-182-243-56	Sequence 56, Appl
55	36	48.0	765	14	US-10-128-174-3	Sequence 3, Appl
56	36	48.0	765	14	US-10-128-174-34	Sequence 34, Appl
57	36	48.0	765	14	US-10-128-174-35	Sequence 35, Appl
58	36	48.0	765	14	US-10-128-174-36	Sequence 36, Appl
59	36	48.0	765	14	US-10-128-174-37	Sequence 37, Appl
60	36	48.0	765	14	US-10-128-174-38	Sequence 38, Appl
61	36	48.0	765	14	US-10-128-174-39	Sequence 39, Appl
62	36	48.0	765	14	US-10-128-174-40	Sequence 40, Appl
63	36	48.0	765	14	US-10-128-174-41	Sequence 41, Appl
64	36	48.0	765	14	US-10-128-174-44	Sequence 44, Appl
65	36	48.0	808	16	US-10-437-963-195225	Sequence 195225,
66	36	48.0	861	14	US-10-156-761-11000	Sequence 11000, A
67	36	48.0	871	15	US-10-369-493-10043	Sequence 10043, A
68	36	48.0	871	16	US-10-437-963-128344	Sequence 128344,
69	36	48.0	1485	16	US-10-437-963-128382	Sequence 128382,
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71	36	48.0	1572	16	US-10-437-963-128334	Sequence 128334,
72	36	48.0	1639	16	US-10-437-963-128536	Sequence 128536,
73	36	48.0	1806	16	US-10-437-963-128530	Sequence 128530,
74	36	48.0	1841	16	US-10-437-963-128482	Sequence 128482,
75	36	48.0	1859	16	US-10-437-963-128415	Sequence 128415,
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77	36	48.0	1908	16	US-10-437-963-128442	Sequence 128442,
78	36	48.0	1936	16	US-10-437-963-128450	Sequence 128450,
79	36	48.0	1966	16	US-10-437-963-128339	Sequence 128339,
80	36	48.0	1987	16	US-10-437-963-128617	Sequence 128617,
81	36	48.0	2093	16	US-10-437-963-128540	Sequence 128540,
82	35	46.7	24	12	US-10-372-876-453	Sequence 453, App
83	35	46.7	24	14	US-09-864-761-40542	Sequence 40542, A
84	35	46.7	61	9	US-09-864-761-41598	Sequence 41598, A
85	35	46.7	62	10	US-09-764-891-3012	Sequence 3012, Ap
86	35	46.7	62	10	US-10-437-963-144511	Sequence 144511,
87	35	46.7	90	16	US-10-437-963-144511	Sequence 144511,
88	35	46.7	96	11	US-09-864-408A-4858	Sequence 4858, Ap

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; TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
; TITLE OF INVENTION: OF CARDIAC DISEASE
; FILE REFERENCE: 6627-PA9025
; CURRENT APPLICATION NUMBER: US/10/705,791
; CURRENT FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: 60/106,718
; PRIOR FILING DATE: 1998-11-02
; PRIOR APPLICATION NUMBER: PCT/US99/25692
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 11
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-705-791-11

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Query Match 100.0%; Score 75; DB 16; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MEKVQYLTRSAIRRAS 16
DB 16 MEKVQYLTRSAIRRAS 31

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RESULT 3
US-10-705-791-10
; Sequence 10, Application US/10705791
; Publication No. US20040121942A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; APPLICANT: Chien, Kenneth
; APPLICANT: Dillmann, Wolfgang
; APPLICANT: Minamisawa, Susanne
; APPLICANT: He, Huaping
; APPLICANT: Hoshijima, Masahiko
; APPLICANT: Meyer, Markus
; APPLICANT: Scott, Christopher
; APPLICANT: Wang, Yibin
; APPLICANT: Silverman, Gregg J.
; TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
; TITLE OF INVENTION: OF CARDIAC DISEASE
; FILE REFERENCE: 6627-PA9025
; CURRENT APPLICATION NUMBER: US/10/705,791
; CURRENT FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: 60/106,718
; PRIOR FILING DATE: 1998-11-02
; PRIOR APPLICATION NUMBER: PCT/US99/25692
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 10
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-705-791-10

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Query Match 100.0%; Score 75; DB 16; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MEKVQYLTRSAIRRAS 16
DB 1 MEKVQYLTRSAIRRAS 15

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RESULT 4
US-09-954-571-2
; Sequence 2, Application US/09954571
; Publication No. US20020032167A1
; GENERAL INFORMATION:
; APPLICANT: Chien, Kenneth R

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Sequence 152503,
Sequence 147002,
Sequence 61911, A
Sequence 103091,
Sequence 442, App
Sequence 442, App
Sequence 464, App
Sequence 71171, A
Sequence 57201, A
Sequence 164, App
Sequence 2255, App
Sequence 52269, A

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ALIGNMENTS

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RESULT 1
US-10-705-791-8
; Sequence 8, Application US/10705791
; Publication No. US20040121942A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; APPLICANT: Chien, Kenneth
; APPLICANT: Dillmann, Wolfgang
; APPLICANT: Minamisawa, Susanne
; APPLICANT: He, Huaping
; APPLICANT: Hoshijima, Masahiko
; APPLICANT: Meyer, Markus
; APPLICANT: Scott, Christopher
; APPLICANT: Wang, Yibin
; APPLICANT: Silverman, Gregg J.
; TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
; TITLE OF INVENTION: OF CARDIAC DISEASE
; FILE REFERENCE: 6627-PA9025
; CURRENT APPLICATION NUMBER: US/10/705,791
; CURRENT FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: 60/106,718
; PRIOR FILING DATE: 1998-11-02
; PRIOR APPLICATION NUMBER: PCT/US99/25692
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 8
; LENGTH: 16
; TYPE: PRT
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; US-10-705-791-8

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Query Match 100.0%; Score 75; DB 16; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MEKVQYLTRSAIRRAS 16
DB 1 MEKVQYLTRSAIRRAS 16

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RESULT 2
US-10-705-791-11
; Sequence 11, Application US/10705791
; Publication No. US20040121942A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; APPLICANT: Chien, Kenneth
; APPLICANT: Dillmann, Wolfgang
; APPLICANT: Minamisawa, Susanne
; APPLICANT: He, Huaping
; APPLICANT: Hoshijima, Masahiko
; APPLICANT: Meyer, Markus
; APPLICANT: Scott, Christopher
; APPLICANT: Wang, Yibin
; APPLICANT: Silverman, Gregg J.

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```
; APPLICANT: Hoshijima, Masahiko
; APPLICANT: Ross, John
; APPLICANT: Ikeda, Yasuhiro
; TITLE OF INVENTION: HIGH EFFICIENCY CARDIAC GENE TRANSFER
; FILE REFERENCE: 6627-PA0123
; CURRENT APPLICATION NUMBER: US/09/954,571
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: 60/231,821
; PRIOR FILING DATE: 2000-11-09
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-954-571-2
```

```
Query Match 100.0%; Score 75; DB 12; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 1 MEKVQYLTRSAIRRAS 16
Db 1 MEKVQYLTRSAIRRAS 16
```

RESULT 5

```
US-09-954-571-4
; Sequence 4, Application US/09954571
; Publication No. US20020032167A1
; GENERAL INFORMATION:
; APPLICANT: Chien, Kenneth R
; APPLICANT: Hoshijima, Masahiko
; APPLICANT: Ross, John
; APPLICANT: Ikeda, Yasuhiro
; TITLE OF INVENTION: HIGH EFFICIENCY CARDIAC GENE TRANSFER
; FILE REFERENCE: 6627-PA0123
; CURRENT APPLICATION NUMBER: US/09/954,571
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: 60/231,821
; PRIOR FILING DATE: 2000-11-09
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-954-571-4
```

```
Query Match 100.0%; Score 75; DB 12; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 MEKVQYLTRSAIRRAS 16
Db 1 MEKVQYLTRSAIRRAS 16
```

RESULT 6

```
US-09-954-571-5
; Sequence 5, Application US/09954571
; Publication No. US20020032167A1
; GENERAL INFORMATION:
; APPLICANT: Chien, Kenneth R
; APPLICANT: Hoshijima, Masahiko
; APPLICANT: Ross, John
; APPLICANT: Ikeda, Yasuhiro
; TITLE OF INVENTION: HIGH EFFICIENCY CARDIAC GENE TRANSFER
; FILE REFERENCE: 6627-PA0123
; CURRENT APPLICATION NUMBER: US/09/954,571
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: 60/231,821
; PRIOR FILING DATE: 2000-11-09
```

```
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Oryctolagus cuniculus
US-09-954-571-5
```

```
Query Match 100.0%; Score 75; DB 12; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 MEKVQYLTRSAIRRAS 16
Db 1 MEKVQYLTRSAIRRAS 16
```

RESULT 7

```
US-10-371-101-15
; Sequence 15, Application US/10371101
; Publication No. US20030149995A1
; GENERAL INFORMATION:
; APPLICANT: Zwaal, Richard
; APPLICANT: Groenen, Jose
; APPLICANT: Bogaert, Thierry
; TITLE OF INVENTION: COMPOUND SCREENING METHODS
; FILE REFERENCE: D00590.70035.US
; CURRENT APPLICATION NUMBER: US/10/371,101
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: GB 9908670.4
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: US 60/129,596
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: GB 9912736.7
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: 09/549,872
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-371-101-15
```

```
Query Match 100.0%; Score 75; DB 14; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 MEKVQYLTRSAIRRAS 16
Db 1 MEKVQYLTRSAIRRAS 16
```

RESULT 8

```
US-10-408-765A-478
; Sequence 478, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
```

```

; SEQ ID NO 478
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-478

Query Match      100.0%; Score 75; DB 16; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MEKVQYLTRSAIRRAS 16
DB      1 MEKVQYLTRSAIRRAS 16

RESULT 9
US-10-705-791-1
; Sequence 1, Application US/10705791
; Publication No. US20040121942A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; APPLICANT: Chien, Kenneth
; APPLICANT: Dillmann, Wolfgang
; APPLICANT: Minamisawa, Susanne
; APPLICANT: He, Huaping
; APPLICANT: Hoshijima, Masahiko
; APPLICANT: Meyer, Markus
; APPLICANT: Scott, Christopher
; APPLICANT: Wang, Yibin
; APPLICANT: Silverman, Gregg J.
; TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
; TITLE OF INVENTION: OF CARDIAC DISEASE
; FILE REFERENCE: 6627-PA9025
; CURRENT APPLICATION NUMBER: US/10/705,791
; CURRENT FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: 60/106,718
; PRIOR FILING DATE: 1998-11-02
; PRIOR APPLICATION NUMBER: PCT/US99/25692
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-705-791-1

Query Match      100.0%; Score 75; DB 16; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MEKVQYLTRSAIRRAS 16
DB      1 MEKVQYLTRSAIRRAS 16

RESULT 10
US-10-705-791-2
; Sequence 2, Application US/10705791
; Publication No. US20040121942A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; APPLICANT: Chien, Kenneth
; APPLICANT: Dillmann, Wolfgang
; APPLICANT: Minamisawa, Susanne
; APPLICANT: He, Huaping
; APPLICANT: Hoshijima, Masahiko
; APPLICANT: Meyer, Markus
; APPLICANT: Scott, Christopher
; APPLICANT: Wang, Yibin
; APPLICANT: Silverman, Gregg J.
; TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
; TITLE OF INVENTION: OF CARDIAC DISEASE

```

```

; FILE REFERENCE: 6627-PA9025
; CURRENT APPLICATION NUMBER: US/10/705,791
; CURRENT FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: 60/106,718
; PRIOR FILING DATE: 1998-11-02
; PRIOR APPLICATION NUMBER: PCT/US99/25692
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-705-791-2

Query Match      100.0%; Score 75; DB 16; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MEKVQYLTRSAIRRAS 16
DB      1 MEKVQYLTRSAIRRAS 16

RESULT 11
US-10-705-791-17
; Sequence 17, Application US/10705791
; Publication No. US20040121942A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; APPLICANT: Chien, Kenneth
; APPLICANT: Dillmann, Wolfgang
; APPLICANT: Minamisawa, Susanne
; APPLICANT: He, Huaping
; APPLICANT: Hoshijima, Masahiko
; APPLICANT: Meyer, Markus
; APPLICANT: Scott, Christopher
; APPLICANT: Wang, Yibin
; APPLICANT: Silverman, Gregg J.
; TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
; TITLE OF INVENTION: OF CARDIAC DISEASE
; FILE REFERENCE: 6627-PA9025
; CURRENT APPLICATION NUMBER: US/10/705,791
; CURRENT FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: 60/106,718
; PRIOR FILING DATE: 1998-11-02
; PRIOR APPLICATION NUMBER: PCT/US99/25692
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 79
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-705-791-17

Query Match      100.0%; Score 75; DB 16; Length 79;
Best Local Similarity 100.0%; Pred. No. 3e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MEKVQYLTRSAIRRAS 16
DB      1 MEKVQYLTRSAIRRAS 16

RESULT 12
US-10-705-791-19
; Sequence 19, Application US/10705791
; Publication No. US20040121942A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; APPLICANT: Chien, Kenneth
; APPLICANT: Dillmann, Wolfgang

```

```
; APPLICANT: Minamisawa, Susanne
; APPLICANT: He, Huaping
; APPLICANT: Hoshijima, Masahiko
; APPLICANT: Meyer, Markus
; APPLICANT: Scott, Christopher
; APPLICANT: Wang, Yibin
; APPLICANT: Silverman, Gregg J.
; TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
; FILE REFERENCE: 6627-PA9025
; CURRENT APPLICATION NUMBER: US/10/705,791
; CURRENT FILING DATE: 2003-11-10
; PRIOR FILING DATE: 1998-11-02
; PRIOR APPLICATION NUMBER: PCT/US99/25692
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19
; LENGTH: 79
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-705-791-19

Query Match          100.0%; Score 75; DB 16; Length 79;
Best Local Similarity 100.0%; Pred. No. 3e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRAS 16
Db 1 MEKVQYLTRSAIRRAS 16

RESULT 13
US-09-954-571-3
; Sequence 3, Application US/09954571
; Publication No. US20020032167A1
; GENERAL INFORMATION:
; APPLICANT: Chien, Kenneth R
; APPLICANT: Hoshijima, Masahiko
; APPLICANT: Ross, John
; APPLICANT: Ikeda, Yasuhiro
; TITLE OF INVENTION: HIGH EFFICIENCY CARDIAC GENE TRANSFER
; FILE REFERENCE: 6627-PA0123
; CURRENT APPLICATION NUMBER: US/09/954,571
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: 60/231,821
; PRIOR FILING DATE: 2000-11-09
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-954-571-3

Query Match          96.0%; Score 72; DB 12; Length 52;
Best Local Similarity 93.8%; Pred. No. 6.9e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRAS 16
Db 1 MEKVQYLTRSAIRRAS 16

RESULT 14
US-10-371-101-14
; Sequence 14, Application US/10371101
; Publication No. US20030149995A1
; GENERAL INFORMATION:
; APPLICANT: Zwaal, Richard
; APPLICANT: Groenen, Jose
; APPLICANT: Bogaert, Thierry
```

```
; TITLE OF INVENTION: COMPOUND SCREENING METHODS
; FILE REFERENCE: D00590.70035.US
; CURRENT APPLICATION NUMBER: US/10/371,101
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: GB 9908670.4
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: US 60/129,596
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: GB 9912736.7
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: 09/549,872
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Sus sp.
US-10-371-101-14

Query Match          96.0%; Score 72; DB 14; Length 52;
Best Local Similarity 93.8%; Pred. No. 6.9e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRAS 16
Db 1 MDKVQYLTRSAIRRAS 16

RESULT 15
US-10-705-791-5
; Sequence 5, Application US/10705791
; Publication No. US20040121942A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; APPLICANT: Chien, Kenneth
; APPLICANT: Dillmann, Wolfgang
; APPLICANT: Minamisawa, Susanne
; APPLICANT: He, Huaping
; APPLICANT: Hoshijima, Masahiko
; APPLICANT: Meyer, Markus
; APPLICANT: Scott, Christopher
; APPLICANT: Wang, Yibin
; APPLICANT: Silverman, Gregg J.
; TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
; FILE REFERENCE: 6627-PA9025
; CURRENT APPLICATION NUMBER: US/10/705,791
; CURRENT FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: 60/106,718
; PRIOR FILING DATE: 1998-11-02
; PRIOR APPLICATION NUMBER: PCT/US99/25692
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-705-791-5

Query Match          96.0%; Score 72; DB 16; Length 52;
Best Local Similarity 93.8%; Pred. No. 6.9e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRAS 16
Db 1 MEKVQYLTRSAIRRAS 16

RESULT 16
US-10-705-791-13
; Sequence 13, Application US/10705791
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us-09-830-779-19_copy_1_16.rapb

Fri Oct 1 16:13:08 2004

```

; Publication No. US20040121942A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; APPLICANT: Chien, Kenneth
; APPLICANT: Dillmann, Wolfgang
; APPLICANT: Minamisawa, Susanne
; APPLICANT: He, Huaping
; APPLICANT: Hoshijima, Masahiko
; APPLICANT: Meyer, Markus
; APPLICANT: Scott, Christopher
; APPLICANT: Wang, Yibin
; APPLICANT: Silverman, Gregg J.
; TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
; TITLE OF INVENTION: OF CARDIAC DISEASE
; FILE REFERENCE: 6627-PA9025
; CURRENT APPLICATION NUMBER: US/10/705,791
; CURRENT FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: 60/106,718
; PRIOR FILING DATE: 1998-11-02
; PRIOR APPLICATION NUMBER: PCT/US99/25692
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 13
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: Mutant form of human protein sequence
US-10-705-791-13

Query Match          94.7%; Score 71; DB 16; Length 35;
Best Local Similarity 100.0%; Pred. No. 6.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRA 15
DB 16 MEKVQYLTRSAIRRA 30

RESULT 17
US-10-705-791-12
; Sequence 12, Application US/10705791
; Publication No. US20040121942A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; APPLICANT: Chien, Kenneth
; APPLICANT: Dillmann, Wolfgang
; APPLICANT: Minamisawa, Susanne
; APPLICANT: He, Huaping
; APPLICANT: Hoshijima, Masahiko
; APPLICANT: Meyer, Markus
; APPLICANT: Scott, Christopher
; APPLICANT: Wang, Yibin
; APPLICANT: Silverman, Gregg J.
; TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
; TITLE OF INVENTION: OF CARDIAC DISEASE
; FILE REFERENCE: 6627-PA9025
; CURRENT APPLICATION NUMBER: US/10/705,791
; CURRENT FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: 60/106,718
; PRIOR FILING DATE: 1998-11-02
; PRIOR APPLICATION NUMBER: PCT/US99/25692
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 12
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: Mutant form of human protein sequence
US-10-705-791-12

Query Match          94.7%; Score 71; DB 16; Length 36;
Best Local Similarity 100.0%; Pred. No. 7.2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MEKVQYLTRSAIRRA 15
DB 1 MEKVQYLTRSAIRRA 15

RESULT 18
US-09-954-571-1
; Sequence 1, Application US/09954571
; Publication No. US20020032167A1
; GENERAL INFORMATION:
; APPLICANT: Chien, Kenneth R
; APPLICANT: Hoshijima, Masahiko
; APPLICANT: Ikeda, Yasuhiro
; APPLICANT: Ross, John
; TITLE OF INVENTION: HIGH EFFICIENCY CARDIAC GENE TRANSFER
; FILE REFERENCE: 6627-PA0123
; CURRENT APPLICATION NUMBER: US/09/954,571
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: 60/231,821
; PRIOR FILING DATE: 2000-11-09
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 1
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Mutant form of human protein sequence
US-09-954-571-1

Query Match          94.7%; Score 71; DB 12; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRA 15
DB 1 MEKVQYLTRSAIRRA 15

RESULT 19
US-10-705-791-18
; Sequence 18, Application US/10705791
; Publication No. US20040121942A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; APPLICANT: Chien, Kenneth
; APPLICANT: Dillmann, Wolfgang
; APPLICANT: Minamisawa, Susanne
; APPLICANT: He, Huaping
; APPLICANT: Hoshijima, Masahiko
; APPLICANT: Meyer, Markus
; APPLICANT: Scott, Christopher
; APPLICANT: Wang, Yibin
; APPLICANT: Silverman, Gregg J.
; TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
; TITLE OF INVENTION: OF CARDIAC DISEASE
; FILE REFERENCE: 6627-PA9025
; CURRENT APPLICATION NUMBER: US/10/705,791
; CURRENT FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: 60/106,718
; PRIOR FILING DATE: 1998-11-02
; PRIOR APPLICATION NUMBER: PCT/US99/25692
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 18
; LENGTH: 79
; TYPE: PRT
; ORGANISM: Escherichia coli
; OTHER INFORMATION: Mutant form of human protein sequence
US-10-705-791-18

Query Match          94.7%; Score 71; DB 16; Length 79;

```

```
Best Local Similarity 100.0%; Pred. No. 1.7e-05; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0;

QY 1 MEKVQYLTRSAIRRA 15
Db 1 MEKVQYLTRSAIRRA 15

RESULT 20
US-10-705-791-4
; Sequence 4, Application US/10705791
; Publication No. US20040121942A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; APPLICANT: Chien, Kenneth
; APPLICANT: Dillmann, Wolfgang
; APPLICANT: Minamisawa, Susanne
; APPLICANT: He, Huaping
; APPLICANT: Hoshijima, Masahiko
; APPLICANT: Meyer, Markus
; APPLICANT: Scott, Christopher
; APPLICANT: Wang, Yibin
; APPLICANT: Silverman, Gregg J.
; TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
; FILE REFERENCE: 6627-PA9025
; CURRENT APPLICATION NUMBER: US/10/705,791
; CURRENT FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: 60/106,718
; PRIOR FILING DATE: 1998-11-02
; PRIOR APPLICATION NUMBER: PCT/US99/25692
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 4
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-705-791-4

Query Match 93.3%; Score 70; DB 16; Length 52;
Best Local Similarity 93.8%; Pred. No. 1.6e-05; Indels 1; Gaps 0;
Matches 15; Conservative 0; Mismatches 0;

QY 1 MEKVQYLTRSAIRRAS 16
Db 1 MEKVQYLTRSAIRRAS 16

RESULT 21
US-10-705-791-3
; Sequence 3, Application US/10705791
; Publication No. US20040121942A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; APPLICANT: Chien, Kenneth
; APPLICANT: Dillmann, Wolfgang
; APPLICANT: Minamisawa, Susanne
; APPLICANT: He, Huaping
; APPLICANT: Hoshijima, Masahiko
; APPLICANT: Meyer, Markus
; APPLICANT: Scott, Christopher
; APPLICANT: Wang, Yibin
; APPLICANT: Silverman, Gregg J.
; TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
; FILE REFERENCE: 6627-PA9025
; CURRENT APPLICATION NUMBER: US/10/705,791
; CURRENT FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: 60/106,718
; PRIOR FILING DATE: 1998-11-02
; PRIOR APPLICATION NUMBER: PCT/US99/25692
; PRIOR FILING DATE: 1999-11-02
```

```
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 3
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-705-791-3

Query Match 92.0%; Score 69; DB 16; Length 52;
Best Local Similarity 93.8%; Pred. No. 2.5e-05; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 1;

QY 1 MEKVQYLTRSAIRRAS 16
Db 1 MEKVQYLTRSAIRRAS 16

RESULT 22
US-10-705-791-6
; Sequence 6, Application US/10705791
; Publication No. US20040121942A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; APPLICANT: Chien, Kenneth
; APPLICANT: Dillmann, Wolfgang
; APPLICANT: Minamisawa, Susanne
; APPLICANT: He, Huaping
; APPLICANT: Hoshijima, Masahiko
; APPLICANT: Meyer, Markus
; APPLICANT: Scott, Christopher
; APPLICANT: Wang, Yibin
; APPLICANT: Silverman, Gregg J.
; TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
; FILE REFERENCE: 6627-PA9025
; CURRENT APPLICATION NUMBER: US/10/705,791
; CURRENT FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: 60/106,718
; PRIOR FILING DATE: 1998-11-02
; PRIOR APPLICATION NUMBER: PCT/US99/25692
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 6
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-705-791-6

Query Match 86.0%; Score 66; DB 16; Length 52;
Best Local Similarity 87.5%; Pred. No. 9.1e-05; Indels 1; Gaps 0;
Matches 14; Conservative 1; Mismatches 1;

QY 1 MEKVQYLTRSAIRRAS 16
Db 1 MEKVQYLTRSAIRRAS 16

RESULT 23
US-10-424-599-238702
; Sequence 238702, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(S3223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
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; SEQ ID NO 238702
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-10177
Query Match 54.7%; Score 41; DB 14; Length 116;
Best Local Similarity 46.7%; Pred. No. 10;
Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
QY 1 MEKVQYLTRSAIRRA 15
Db 81 VEKIELVTRGDVRRRA 95
Search completed: October 1, 2004, 12:48:44
Job time : 63.4 secs

; SEQ ID NO 238702
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Glycine max
US-10-424-599-238702
Query Match 54.7%; Score 41; DB 12; Length 44;
Best Local Similarity 46.2%; Pred. No. 3.5;
Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
QY 1 MEKVQYLTRSAIR 13
Db 25 LEKLEYITREIRK 37

RESULT 24
US-10-425-114-46161
; Sequence 46161, Application US/10425114
; Publication No. US20040034889A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425.114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 46161
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 701164165_FLI.pep
US-10-425-114-46161

Query Match 54.7%; Score 41; DB 12; Length 68;
Best Local Similarity 71.4%; Pred. No. 5.6;
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2 EKVOYLTRSAIRRA 15
Db 51 ETVAYLCRSAPRA 64

RESULT 25
US-10-156-761-10177
; Sequence 10177, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 10177

Query Match 54.7%; Score 41; DB 12; Length 68;
Best Local Similarity 71.4%; Pred. No. 5.6;
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2 EKVOYLTRSAIRRA 15
Db 51 ETVAYLCRSAPRA 64

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 1, 2004, 12:05:26 ; Search time 15.6 Seconds
(without alignments)
98.658 Million cell updates/sec

Title: US-09-830-779-19_COPY_1_16
Perfect score: 75
Sequence: 1 MEKVQLTRSAIRAS 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database: PIR 78:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	75	100.0	52	A40424	phospholamban - hu
2	75	100.0	52	S37638	phospholamban - ro
3	75	100.0	52	A49057	phospholamban - ra
4	75	100.0	52	B40424	phospholamban - ra
5	72	96.0	52	A29002	phospholamban - do
6	72	96.0	52	S05540	phospholamban - pi
7	71	94.7	52	A39535	phospholamban - ch
8	41	54.7	116	T34780	ribosomal protein
9	41	54.7	451	F75083	phospho-sugar muta
10	40	53.3	121	B70187	ribosomal protein
11	40	53.3	1108	E71104	probable cell divi
12	39	52.0	481	B75167	hypothetical prote
13	38	50.7	119	D69155	hypothetical prote
14	37	49.3	283	H68179	conserved hypotet
15	37	49.3	296	F70879	hypothetical prote
16	37	49.3	308	AC1867	hypothetical prote
17	37	49.3	2712	T05113	hypothetical prote
18	36	48.0	236	D69048	conserved hypotet
19	36	48.0	294	T0C104	probable dntp-4-de
20	36	48.0	335	A24785	hypothetical prote
21	36	48.0	409	F93493	probable MFS trans
22	36	48.0	410	T12833	hypothetical prote
23	36	48.0	417	H83370	hypothetical prote
24	36	48.0	434	T04263	hydrogen cyanide s
25	36	48.0	462	AH1033	phosphoprotein pho
26	36	48.0	486	I55449	probable exported
27	36	48.0	549	A90253	gene PPA protein
28	36	48.0	622	JC5425	hypothetical prote
29	36	48.0	736	I51691	transcription init
					disveilled homolo

30	36	48.0	924	S13913	hexokinase (EC 2.7
31	36	48.0	1148	D90815	transcription-tpa
32	36	48.0	1148	H85674	hypothetical prote
33	35	46.7	185	AG2026	hypothetical prote
34	35	46.7	196	B83226	aliphatic amidase
35	35	46.7	283	G83754	transcription regu
36	35	46.7	307	T21879	hypothetical prote
37	35	46.7	390	T09000	cysteine synthase
38	35	46.7	390	S53487	porphobilinogen sy
39	35	46.7	403	B69338	conserved hypotet
40	35	46.7	444	S68122	tubulin beta-4 cha
41	35	46.7	455	H71028	hypothetical prote
42	35	46.7	513	S02194	DNA-directed RNA p
43	35	46.7	535	T37189	hypothetical prote
44	35	46.7	561	G90303	hypothetical prote
45	35	46.7	626	S34120	DNA-directed DNA p
46	35	46.7	781	T50055	C2H2 zinc finger p
47	35	46.7	1013	T31211	trwC protein homol
48	35	46.7	1102	S65235	probable membrane
49	35	46.7	1710	T14005	phospholipase D (E
50	34.5	46.0	452	T34542	hypothetical prote
51	34.5	46.0	813	C97292	ATPases with chape
52	34.5	46.0	1027	T46296	hypothetical prote
53	34.5	46.0	1120	JC7765	mitotic spindle as
54	34	45.3	101	T39075	hypothetical prote
55	34	45.3	108	D85482	hypothetical prote
56	34	45.3	188	E90831	hypothetical prote
57	34	45.3	134	LNC116	16K galactose-bind
58	34	45.3	170	T36571	hypothetical prote
59	34	45.3	172	S62166	NADH2 dehydrogenas
60	34	45.3	172	S62167	NADH2 dehydrogenas
61	34	45.3	173	S44396	NADH2 dehydrogenas
62	34	45.3	173	S44397	NADH2 dehydrogenas
63	34	45.3	185	R52N6M	ribosomal protein
64	34	45.3	185	T03233	probable ribosomal
65	34	45.3	191	A65137	hypothetical 21.0
66	34	45.3	191	H91160	hypothetical prote
67	34	45.3	191	G86006	hypothetical prote
68	34	45.3	200	AE0788	cytochrome c-type
69	34	45.3	214	E81270	probable outer mem
70	34	45.3	239	T20603	hypothetical prote
71	34	45.3	292	G95926	probable saccharid
72	34	45.3	321	T44336	hypothetical prote
73	34	45.3	328	S70885	UDP-galactose 4-ep
74	34	45.3	367	AF2494	hypothetical prote
75	34	45.3	395	T00574	probable protein k
76	34	45.3	409	H85831	probable phospholip
77	34	45.3	431	H84392	O-acetyl homoserin
78	34	45.3	433	D75632	probable hemolysin
79	34	45.3	434	A69082	coenzyme F390 synt
80	34	45.3	525	AD2022	hypothetical prote
81	34	45.3	542	T46464	hypothetical prote
82	34	45.3	548	S56152	H+-transporting tw
83	34	45.3	576	AC3038	biotin carboxylase
84	34	45.3	576	H98247	pyruvate kinase (E
85	34	45.3	604	T45627	replication factor
86	34	45.3	604	T15091	hypothetical prote
87	34	45.3	662	T41512	u5 snrnp-like RNA
88	34	45.3	676	S74635	protoporphyrin IX
89	34	45.3	676	T46870	protoporphyrin IX
90	34	45.3	821	T19705	hypothetical prote
91	34	45.3	833	AB0448	probable insectici
92	34	45.3	838	A38172	adenylate cyclase
93	34	45.3	991	T25412	hypothetical prote
94	34	45.3	991	S01787	fatty-acid synthas
95	34	45.3	1857	S01787	related to TOM1 pr
96	34	45.3	3839	T45799	hypothetical prote
97	33	44.0	55	S3915	class II histocomp
98	33	44.0	62	S37135	histone H4 - bovin
99	33	44.0	102	H5B04	histone H4 - pig
100	33	44.0	102	H5B04	

ALIGNMENTS

RESULT 1

A40424
phospholamban - human
C:Species: Homo sapiens (man)
C>Date: 28-Feb-1992 #sequence_revision 27-Jun-1994 #text_change 18-Jun-1999
C:Accession: A40424
R:Fujii, J.; Zarin-Herzberg, A.; Willard, H.F.; Tada, M.; MacLennan, D.H.
J. Biol. Chem. 266, 11669-11675, 1991
A>Title: Structure of the rabbit phospholamban gene, cloning of the human cDNA, and assignment of the major phosphorylated protein in cardiac muscle sarcolemma
A:Reference number: A40424; MUID:91268032; PMID:1828805
A:Accession: A40424
A:Molecule type: mRNA
A:Residues: 1-52 <FW>
A:Cross-references: GB:M63603; NID:9189942; PIDN:AAA60083.1; PID:9189943
C:Comment: Phospholamban is expressed in cardiac muscle, slow twitch skeletal muscle, and after phosphorylation, the Ca++ pump is activated and the rate of muscle relaxation is increased. Helical transmembrane domains of five chains are thought to aggregate in the C-terminus.
A:Gene: GDB:PLN; PLB
A:Cross-references: GDB:128300; OMIM:172405
A:Map position: 6q22.1-6q22.1
C:Superfamily: phospholamban
C:Keywords: acetylated amino end; ATPase inhibitor; muscle; pentamer; phosphoprotein; transmembrane
F:31-52/Domain: transmembrane #status predicted <TM>
F:1/Modified site: acetylated amino end (Met) #status predicted
F:16/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predicted
F:17/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase) #status predicted

Query Match 100.0%; Score 75; DB 1; Length 52;
Best Local Similarity 100.0%; Pred. No. 5.4e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEKVQYLTRSAIRRAS 16
|||||
DB 1 MEKVQYLTRSAIRRAS 16
|||||

RESULT 2

S37638
phospholamban - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 05-Mar-1994 #sequence_revision 27-Jun-1994 #text_change 18-Jun-1999
C:Accession: S37638; I52270; I64795; I51840
R:Shanahan, C.M.; Weisberg, P.L.; Metcalfe, J.C.
Circ. Res. 73, 193-204, 1993
A>Title: Isolation of gene markers of differentiated and proliferating vascular smooth muscle cells
A:Reference number: S37637; MUID:93284726; PMID:8508530
A:Accession: S37638
A:Molecule type: mRNA
A:Residues: 1-52 <SHA>
A:Cross-references: EMBL:X71068; NID:9313809; PIDN:CAA50394.1; PID:9313810
R:Johns, D.C.; Feldman, A.M.
Biochem. Biophys. Res. Commun. 188, 927-933, 1992
A>Title: Identification of a highly conserved region at the 5' flank of the phospholamban gene
A:Reference number: I52270; MUID:93075183; PMID:1445334
A:Accession: I52270
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-52 <UOH>
A:Cross-references: GB:L03382; NID:9206134; PIDN:AAA41849.1; PID:9206136
R:Wang, X.S.; Nadal-Ginard, B.
Adv. Exp. Med. Biol. 304, 387-395, 1991
A>Title: Cloning phospholamban cDNA from rat aortic smooth muscle.
A:Reference number: I51840; MUID:92206263; PMID:1725098
A:Accession: I64795
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-52 <HWA>
A:Cross-references: GB:S95853; NID:9247932; PIDN:AAA21903.1; PID:9247933

A:Accession: I51840

A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-52 <HWA2>
A:Cross-references: GB:S95849; NID:9247934
C:Comment: Phospholamban is expressed in cardiac muscle, slow twitch skeletal muscle, and after phosphorylation, the calcium pump is activated and the rate of muscle relaxation is increased. Helical transmembrane domains of five chains are thought to aggregate in the C-terminus.
A:Key words: acetylated amino end; ATPase inhibitor; cardiac muscle; heart; pentamer; phospholamban
F:31-52/Domain: transmembrane #status predicted <TM>
F:1/Modified site: acetylated amino end (Met) #status predicted
F:16/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predicted
F:17/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase) #status predicted

Query Match 100.0%; Score 75; DB 1; Length 52;

Best Local Similarity 100.0%; Pred. No. 5.4e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRAS 16

|||||

DB 1 MEKVQYLTRSAIRRAS 16

|||||

RESULT 3

A49057
phospholamban - mouse
C:Species: Mus musculus (house mouse)
C>Date: 19-Dec-1993 #sequence_revision 27-Jun-1994 #text_change 18-Jun-1999
C:Accession: A49057
R:Ganim, J.R.; Luo, W.; Ponniah, S.; Grupp, I.; Kim, H.W.; Ferguson, D.G.; Kadambi, V.; N. C. Res. 71, 1021-1030, 1992
A>Title: Mouse phospholamban gene expression during development in vivo and in vitro.
A:Reference number: A49057; MUID:93088802; PMID:1394867
A:Accession: A49057
A:Molecule type: mRNA
A:Residues: 1-52 <GAS>
A:Cross-references: GB:946792; NID:9257745; PIDN:AAB23706.1; PID:9257746
A:Experimental source: cardiac muscle
A>Note: sequence extracted from NCBI backbone (NCBI:116999, NCBI:117001)
C:Comment: Phospholamban is expressed in cardiac muscle, slow twitch skeletal muscle, and after phosphorylation, the Ca++ pump is activated and the rate of muscle relaxation is increased. Helical transmembrane domains of five chains are thought to aggregate in the C-terminus.
A:Superfamily: phospholamban
C:Key words: acetylated amino end; ATPase inhibitor; muscle; pentamer; phosphoprotein; transmembrane
F:31-52/Domain: transmembrane #status predicted <TM>
F:1/Modified site: acetylated amino end (Met) #status predicted
F:16/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predicted
F:17/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase) #status predicted

Query Match 100.0%; Score 75; DB 1; Length 52;

Best Local Similarity 100.0%; Pred. No. 5.4e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRAS 16

|||||

DB 1 MEKVQYLTRSAIRRAS 16

|||||

RESULT 4

B40424
phospholamban - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 28-Feb-1992 #sequence_revision 27-Jun-1994 #text_change 18-Jun-1999
C:Accession: B40424; S02249
R:Fujii, J.; Zarin-Herzberg, A.; Willard, H.F.; Tada, M.; MacLennan, D.H.
J. Biol. Chem. 266, 11669-11675, 1991
A>Title: Structure of the rabbit phospholamban gene, cloning of the human cDNA, and assignment of the major phosphorylated protein in cardiac muscle sarcolemma
A:Reference number: A40424; MUID:91268032; PMID:1828805
A:Accession: B40424
A:Molecule type: DNA
A:Residues: 1-52 <FW>
A:Cross-references: GB:M63601; NID:9165636; PIDN:AAA31445.1; PID:9165639

R; Fujii, J.; Lytton, J.; Tada, M.; MacLennan, D.H.
 FEBS Lett. 227, 51-55, 1988
 A; Title: Rabbit cardiac and slow-twitch muscle express the same phospholamban gene.
 A; Reference number: S00249; MUID:88112222; PMID:2962883
 A; Accession: S00249
 A; Status: not compared with conceptual translation
 A; Molecule type: mRNA
 A; Residues: 1-52 <UY>
 A; Cross-references: GB:Y00761; NID:gl1661; PIDN:CAA68730.1; PID:g1662
 C; Comment: Phospholamban is expressed in cardiac muscle, slow twitch skeletal muscle, and after phosphorylation, the Ca++ pump is activated and the rate of muscle relaxation is increased.
 C; Genetics:
 A; Note: only one gene was detected
 C; Superfamily: Phospholamban
 C; Keywords: acetylated amino end; ATPase inhibitor; muscle; pentamer; phosphoprotein; transmembrane #status predicted <TM>
 F; 31-52/Domain: transmembrane #status predicted <TM>
 F; 1/Modified site: acetylated amino end (Met) #status predicted
 F; 16/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predicted
 F; 17/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase) #status predicted

Query Match 100.0%; Score 75; DB 1; Length 52;
 Best Local Similarity 100.0%; Pred. No. 5.4e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRAS 16
 DB 1 MEKVQYLTRSAIRRAS 16

RESULT 5
 phospholamban - dog
 C; Species: Canis lupus familiaris (dog)
 C; Date: 23-Aug-1987 #sequence revision 27-Jun-1994 #text_change 18-Jun-1999
 C; Accession: A29002; A26805; A2307; A24818; I46227
 R; Fujii, J.; Ueno, A.; Kitano, K.; Tanaka, S.; Kadoma, M.; Tada, M.
 J. Clin. Invest. 79, 301-304, 1987
 A; Title: The cDNA sequence of the major phospholamban mRNA in canine cardiac ventricular muscle.
 A; Reference number: A29002; MUID:87083954; PMID:3793929
 A; Accession: A29002
 A; Molecule type: mRNA
 A; Residues: 1-52 <YU>
 A; Cross-references: GB:M46012; NID:g164043; PIDN:AAA30884.1; PID:g164044
 R; Uyeda, A.; Kitano, K.; Fujii, J.; Kadoma, M.; Tada, M.; Tanaka, S.
 Nucleic Acids Res. 15, 6738, 1987
 A; Title: The cDNA sequence of the major phospholamban mRNA in canine cardiac ventricular muscle.
 A; Reference number: A26805; MUID:87316936; PMID:3628007
 A; Accession: A26805
 A; Molecule type: mRNA
 A; Residues: 1-52 <UY>
 A; Cross-references: GB:Y00399; NID:g911; PIDN:CAA68461.1; PID:g912
 R; Simmerman, H.K.B.; Collins, J.H.; Theibert, J.L.; Wegener, A.D.; Jones, L.R.
 J. Biol. Chem. 261, 13333-13341, 1986
 A; Title: Sequence analysis of phospholamban. Identification of phosphorylation sites and contents: partial sequence and phosphorylation sites
 A; Accession: A25307
 A; Molecule type: protein
 A; Residues: 10-45 <SIW>
 R; Fujii, J.; Kadoma, M.; Tada, M.; Toda, H.; Sakiyama, F.
 Biochem. Biophys. Res. Commun. 138, 1044-1050, 1986
 A; Title: Characterization of structural unit of phospholamban by amino acid sequencing
 A; Reference number: A24818; MUID:86323152; PMID:3753485
 A; Contents: partial sequence and acetylation site
 A; Accession: A24818
 A; Molecule type: protein
 A; Residues: 1-35, 'X', 37-40, 'X', 42-45 <FU2>
 R; Uyeda, A.; Kitano, K.; Fujii, J.; Kadoma, M.; Tada, M.; Tanaka, S.
 Nucleic Acids Symp. Ser. 17, 121-124, 1986
 A; Title: Characterization of recombinant cDNA clones for canine cardiac phospholamban.
 A; Reference number: 146227; MUID:87174860; PMID:3562256

A; Accession: I46227
 A; Status: translated from GB/EMBL/DBJ
 A; Molecule type: mRNA
 A; Residues: 1-52 <UY>
 A; Cross-references: GB:M35393; NID:g164045; PIDN:AA41618.1; PID:g164046
 C; Comment: Phospholamban is expressed in cardiac muscle, slow twitch skeletal muscle, and after phosphorylation, the Ca++ pump is activated and the rate of muscle relaxation is increased.
 C; Superfamily: phospholamban
 C; Keywords: acetylated amino end; ATPase inhibitor; muscle; pentamer; phosphoprotein; transmembrane #status predicted <TM>
 F; 31-52/Domain: transmembrane #status predicted <TM>
 F; 1/Modified site: acetylated amino end (Met) #status experimental
 F; 16/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status experimental
 F; 17/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase) #status experimental

Query Match 96.0%; Score 72; DB 1; Length 52;
 Best Local Similarity 93.8%; Pred. No. 2e-06;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRAS 16
 DB 1 MDKVQYLTRSAIRRAS 16

RESULT 6
 S05540
 phospholamban - pig
 C; Species: Sus scrofa domestica (domestic pig)
 C; Date: 21-Nov-1993 #sequence revision 27-Jun-1994 #text_change 18-Jun-1999
 C; Accession: S05540
 R; Verboomen, H.; Wuytack, F.; Eggermont, J.A.; de Jaegere, S.; Missaen, L.; Raeymaekers, Biochem. J. 262, 353-356, 1989
 A; Title: cDNA cloning and sequencing of phospholamban from pig stomach smooth muscle.
 A; Reference number: S05540; MUID:90056437; PMID:2530978
 A; Accession: S05540
 A; Molecule type: mRNA
 A; Residues: 1-52 <VER>
 A; Cross-references: EMBL:X15075; NID:g2055; PIDN:CAA33171.1; PID:g2056
 C; Comment: Phospholamban is expressed in cardiac muscle, slow twitch skeletal muscle, and after phosphorylation, the Ca++ pump is activated and the rate of muscle relaxation is increased.
 C; Superfamily: phospholamban
 C; Keywords: acetylated amino end; ATPase inhibitor; muscle; pentamer; phosphoprotein; transmembrane #status predicted <TM>
 F; 31-52/Domain: transmembrane #status predicted <TM>
 F; 1/Modified site: acetylated amino end (Met) #status predicted
 F; 16/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predicted
 F; 17/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase) #status predicted

Query Match 96.0%; Score 72; DB 1; Length 52;
 Best Local Similarity 93.8%; Pred. No. 2e-06;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRAS 16
 DB 1 MDKVQYLTRSAIRRAS 16

RESULT 7
 A39535
 phospholamban - chicken
 C; Species: Gallus gallus (chicken)
 C; Date: 06-Mar-1992 #sequence revision 27-Jun-1994 #text_change 18-Jun-1999
 C; Accession: A39535; B39535; A44531
 R; Toyofuku, T.; Zak, R.
 J. Biol. Chem. 266, 5375-5383, 1991
 A; Title: Characterization of cDNA and genomic sequences encoding a chicken phospholamban.
 A; Reference number: A39535; MUID:91170195; PMID:1825996
 A; Accession: A39535
 A; Molecule type: mRNA
 A; Residues: 1-17, 'L', 19-52 <TOY>
 A; Cross-references: GB:M59039; NID:g212575; PIDN:AAA62738.1; PID:g212576
 A; Note: the authors translated the codon CTT for residue 18 as Ile
 A; Accession: B39535

A;Molecule type: DNA
A;Residues: 1-52 <TO>
A;Cross-references: GB:M59038
A;Note: the sequence of residues 33-52 and the corresponding nucleotide sequence are not submitted to GenBank, April 1991
R;Toyofuku, T.; Zak, R.
A;Reference number: A44531
A;Accession: A44531
A;Molecule type: DNA
A;Residues: 1-52 <TO>
A;Cross-references: GB:M59038
C;Comment: Phospholamban is expressed in cardiac muscle, slow twitch skeletal muscle, and after phosphorylation, the Ca++ pump is activated and the rate of muscle relaxation is increased.
C;Genetics:
A;Note: only one gene was detected
A;Note: the single intron is upstream of the coding region
C;Superfamily: phospholamban
C;Keywords: acetylated amino end; ATPase inhibitor; muscle; pentamer; phosphoprotein; trypsin; 31-52/Domain; transmembrane #status predicted <TM>
F;1/Modified site: acetylated amino end (Met) #status predicted
F;16/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predicted
F;17/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase) #status predicted
Query Match 94.7%; Score 71; DB 1; Length 52;
Best Local Similarity 87.5%; Pred. No. 3e-06;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEKVQYLTRSAIRRA 16
DB 1 MEKVQYLTRSAIRRA 16
RESULT 8
T34780
Ribosomal protein L19 - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 21-Jan-2000
C;Accession: T34780
R;Murphy, L.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, June 1998
A;Reference number: Z21557
A;Accession: T34780
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-116 <MUR>
A;Cross-references: EMBL:AL023797; PIDN:CAA19387.1; GSPDB:GN00070; SCOPDB:SC2E1.12
A;Experimental source: strain A3(2)
C;Genetics:
C;Superfamily: Escherichia coli ribosomal protein L19
Query Match 54.7%; Score 41; DB 2; Length 116;
Best Local Similarity 46.7%; Pred. No. 2.8;
Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
QY 1 MEKVQYLTRSAIRRA 15
DB 81 VEKIELVTRGDVRR 95
RESULT 9
F75083
Phospho-sugar mutase PAB1666 - Pyrococcus abyssi (strain Orsay)
C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C;Accession: F75083
R;anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure
A;Reference number: A75001
A;Accession: F75083
A;Status: preliminary

A;Molecule type: DNA
A;Residues: 1-451 <KAW>
A;Cross-references: GB:AJ248286; GB:AL096836; NID:G5458366; PIDN:CAB49971.1; PID:G5458483
A;Experimental source: strain Orsay
C;Genetics:
A;Gene: PAB1666
C;Superfamily: phosphomannomutase
Query Match 54.7%; Score 41; DB 2; Length 451;
Best Local Similarity 50.0%; Pred. No. 12;
Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
QY 1 MEKVQYLTRSAIRRA 16
DB 435 MEKAEKLVKDAIKKAS 450
RESULT 10
B70187
ribosomal protein L19 (rplS) - Lyme disease spirochete
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 13-Aug-1999
C;Accession: B70187
R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White, S.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, J.; Bowman, C.; Gariand, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.; Nature 390, 580-586, 1997
A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochete, Borrelia burgdorferi.
A;Reference number: A70100; MUID:98065943; PMID:9403685
A;Accession: B70187
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-121 <MLB>
A;Cross-references: GB:AE001170; GB:AE000783; NID:G2688623; PIDN:AA67044.1; PID:G2688623
A;Experimental source: strain B31
C;Superfamily: Escherichia coli ribosomal protein L19
Query Match 53.3%; Score 40; DB 2; Length 121;
Best Local Similarity 53.3%; Pred. No. 4.5;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 MEKVQYLTRSAIRRA 15
DB 80 IEKVEVLRKGKVRRA 94
RESULT 11
E71104
probable cell division control protein - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 05-Nov-1999
C;Accession: E71104
R;Kawarabayashi, Y.; Swada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekine, M.; Ohnuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi, DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic archaeon, Pyrococcus horikoshii.
A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Accession: E71104
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-1108 <KAW>
A;Cross-references: GB:AP000003; NID:G3236130; PIDN:BA29695.1; PID:dl030638; PID:G325701
A;Experimental source: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank
C;Genetics:
A;Gene: PH0606
Query Match 53.3%; Score 40; DB 2; Length 1108;
Best Local Similarity 53.3%; Pred. No. 47;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
QY 1 MEKVQYLTRSAIRRA 15

Db 668 MEVKDYLTREVERKA 682
 || ||||| :|||
 RESULT 12
 B75167
 hypothetical protein PAB0334 - Pyrococcus abyssi (strain Orsay)
 C:Species: Pyrococcus abyssi
 C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
 C:Accession: B75167
 R:anonymous, Genoscope
 submitted to the EMBL Data Library, July 1999
 A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure
 A:Reference number: A75001
 A:Accession: B75167
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-481 <KAW>
 A:Cross-references: GB:AJ248284; GB:AL096836; NID:G5457730; PIDN:CAB49417.1; PID:G545792
 A:Experimental source: strain Orsay
 C:Genetics:
 A:Gene: PAB0334

Query Match 52.0%; Score 39; DB 2; Length 481;
 Best Local Similarity 50.0%; Pred. No. 30;
 Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 EKQVYLTSAIRRA 15
 ||:|:|:|:|
 Db 38 EKIKYIKRAFFRA 51
 ||:|:|:|:|

RESULT 13
 D59155
 hypothetical protein MTH425 - Methanobacterium thermoautotrophicum (strain Delta H)
 C:Species: Methanobacterium thermoautotrophicum
 C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 24-Nov-1999
 C:Accession: D69155
 R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
 Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.;
 K. S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
 J. Bacteriol. 179, 7135-7155, 1997
 A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
 A:Reference number: A69000; MUID:98037514; PMID:9371463
 A:Accession: D69155
 A>Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-119 <MTH>
 A:Cross-references: GB:AE000827; GB:AE000666; NID:G2621489; PIDN:AAB84931.1; PID:G262149
 A:Experimental source: strain Delta H
 C:Genetics:
 A:Gene: MTH425
 A:Start codon: TTG
 C:Superfamily: Methanobacterium thermoautotrophicum hypothetical protein MTH425

Query Match 50.7%; Score 38; DB 2; Length 119;
 Best Local Similarity 37.5%; Pred. No. 11;
 Matches 6; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 MEKVQYLTSAIRRAS 16
 |:|:|:|:|:|:|
 Db 35 MDNIMYLTQSTYQSS 50
 |:|:|:|:|:|:|

RESULT 14
 H69179
 conserved hypothetical protein MTH601 - Methanobacterium thermoautotrophicum (strain Del
 C:Species: Methanobacterium thermoautotrophicum
 C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 17-Mar-2000
 C:Accession: H69179
 R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
 Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.;
 K. S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.

J. Bacteriol. 179, 7135-7155, 1997
 A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
 A:Reference number: A69000; MUID:98037514; PMID:9371463
 A:Accession: H69179
 A>Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-283 <MTH>
 A:Cross-references: GB:AE000842; GB:AE000666; NID:G2621676; PIDN:AAB85107.1; PID:G262168
 A:Experimental source: strain Delta H
 C:Genetics:
 A:Gene: MTH601
 C:Superfamily: hypothetical protein AFI307

Query Match 49.3%; Score 37; DB 2; Length 283;
 Best Local Similarity 63.6%; Pred. No. 40;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 YLTSAIRRAS 16
 ||||| :|||
 Db 209 YLTREAFKRAA 219
 ||||| :|||

RESULT 15
 F70879
 hypothetical protein RV2751 - Mycobacterium tuberculosis (strain H37RV)
 C:Species: Mycobacterium tuberculosis
 C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
 C:Accession: F70879
 R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.;
 Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.;
 Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.;
 Nature 393, 537-544, 1998
 A:Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
 A:Reference number: A70500; MUID:98295987; PMID:9634230
 A:Accession: F70879
 A>Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-296 <COL>
 A:Cross-references: GB:AL008967; GB:AL123456; NID:G3261491; PIDN:CAA15547.1; PID:e117388
 A:Experimental source: strain H37RV
 C:Genetics:
 A:Gene: RV2751

Query Match 49.3%; Score 37; DB 2; Length 296;
 Best Local Similarity 70.0%; Pred. No. 42;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 QYLTRSAIRR 14
 ||||| :|||
 Db 180 QYLTERAVRR 189
 ||||| :|||

RESULT 16
 AC1867
 hypothetical protein alr0484 [imported] - Nostoc sp. (strain PCC 7120)
 C:Species: Nostoc sp. PCC 7120
 A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
 C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
 C:Accession: AC1867
 R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
 Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
 DNA Res. 8, 205-213, 2001
 A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena
 A:Reference number: AB1807; MUID:21595285; PMID:11759840
 A:Accession: AC1867
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-308 <KUR>
 A:Cross-references: GB:BA000019; PIDN:BA072442.1; PID:G17129829; GSPDB:GN00179
 A:Experimental source: strain PCC 7120
 C:Genetics:
 A:Gene: alr0484

A:Gene: STY4756

Query Match 48.0%; Score 36; DB 2; Length 462;
Best Local Similarity 53.8%; Pred. No. 1e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 EKQYLTRSAIRR 14
:|:|:|:|:|:|
Db 294 DKVTWMTREASRR 306

Search completed: October 1, 2004, 12:19:44
Job time : 16.6 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 1, 2004, 12:04:01 ; Search time 8.8 Seconds
 (without alignments)
 94.673 Million cell updates/sec

Title: US-09-830-779-19_COPY_1_16
 Perfect score: 75
 Sequence: 1 MEKVQYLRESAIRRAS 16

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 100 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	75	100.0	52	1 PPLA_HUMAN	P26678 homo sapien
2	75	100.0	52	1 PPLA_MOUSE	P20006 mus musculu
3	72	96.0	52	1 PPLA_PIG	P07473 sus scrofa
4	71	94.7	52	1 PPLA_CHICK	P26677 gallus gall
5	41	54.7	116	1 RL19_STRAW	O821w4 streptomyc
6	41	54.7	116	1 RL19_STROCO	O69883 streptomyc
7	40	53.3	121	1 RL19_BORBU	O51642 borrelia bu
8	39	52.0	871	1 SYA_THEAC	Q9h1w4 thermoplasm
9	38	50.7	115	1 RL19_THETN	Q8r5x4 thermoanaer
10	38	50.7	299	1 PSD_CHLCV	Q821l3 chlamydophi
11	37	49.3	275	1 APAH_ACTAC	O52655 actinobacil
12	37	49.3	625	1 RPSD_XANAC	Q8PG33 xanthomonas
13	36	48.0	47	1 H4Y_BLEJA	P80738 blepharisma
14	36	48.0	97	1 H41_BLEJA	P80737 blepharisma
15	36	48.0	113	1 RL19_CORFP	Q8fp56 corynebacte
16	36	48.0	113	1 RL19_CORGL	Q8nnz0 corynebacte
17	36	48.0	434	1 P2C1_ARATH	Q49597 arabidopsis
18	36	48.0	486	1 2A5A_HUMAN	Q15172 h seline/th
19	36	48.0	624	1 RPSD_XANCP	Q8p4h2 xanthomonas
20	36	48.0	677	1 CHLD_XENP7	O07345 synechococc
21	36	48.0	736	1 CHLD_XENLA	P51142 xenopus lae
22	36	48.0	924	1 HXK3_PAT	P27926 rattus norv
23	36	48.0	1080	1 RPOB_MESVI	Q9mms5 mesostigma
24	35	46.7	144	1 RL28_DROME	Q9vzes5 desosiphila
25	35	46.7	196	1 AMIR_PSEAE	P10932 pseudomonas
26	35	46.7	390	1 HEM2_CHLRE	Q42682 chlamydomon
27	35	46.7	423	1 ERG_ANTWA	O82626 antirrhinum
28	35	46.7	497	1 PROD_MOUSE	Q8wu79 mus musculu
29	35	46.7	506	1 YC46_GUITH	O78439 guillardia
30	35	46.7	515	1 RPB2_METTW	P09844 methanobact
31	35	46.7	516	1 PROD_HUMAN	Q43272 homo sapien
32	35	46.7	626	1 DPO2_SULSO	Q07635 sulfolobus
33	35	46.7	876	1 SYA_THEVO	Q97ah7 thermoplasm

RESULT 1

34	45.3	101	1 YDHD_SCHPO	Q23358 schizosacch
35	45.3	134	1 LEG6_CHICK	P21668 gallus gall
36	45.3	172	1 NU6M_URIAL	P43207 uria aalge
37	45.3	172	1 NU6M_URILO	P43208 uria lomvia
38	45.3	173	1 NU6M_ALCTO	P43193 alica torda
39	45.3	173	1 NU6M_ALLAL	P43192 alle alle
40	45.3	185	1 RM16_MAZE	P27927 zea mays
41	45.3	185	1 RM16_ORISA	P46801 oriza sativ
42	45.3	191	1 YHGI_ECOLI	P46847 escherichia
43	45.3	258	1 SN29_HUMAN	Q95721 homo sapien
44	45.3	328	1 GALE_VIBCH	Q56623 vibrio chol
45	45.3	548	1 ATPA_KILUA	P49375 kluyveromyc
46	45.3	586	1 APYK_BACPY	P51182 bacillus ps
47	45.3	675	1 HPPA_XANCP	Q8p5a6 xanthomonas
48	45.3	676	1 CHLD_SYNY3	P72772 synechocyst
49	45.3	838	1 CYAA_PASMU	Q05766 pasteurella
50	45.3	852	1 RBMA_RAT	P70501 rattus norv
51	45.3	929	1 RBMA_HUMAN	P98175 homo sapien
52	45.3	1857	1 PAS2_PENPA	P15388 p fatty aci
53	44.0	55	1 YCXJ_CUSRE	P23035 cuscuta ref
54	44.0	102	1 H41_EMENI	P23750 emericeila
55	44.0	102	1 H42_ACRFO	P35059 acropora fo
56	44.0	102	1 H4_ACRFO	P59259 arabidopsis
57	44.0	102	1 H4_ARATH	Q27443 ascaris suu
58	44.0	102	1 H4_ASCSU	P02306 caenorhabdl
59	44.0	102	1 H4_CAEEL	P50566 chlamydomon
60	44.0	102	1 H4_CHLRE	P02307 drosophila
61	44.0	102	1 H4_DROME	P02304 homo sapien
62	44.0	102	1 H4_LYCES	P35057 lycopersico
63	44.0	102	1 H4_LYCES	P04914 neurospora
64	44.0	102	1 H4_NEUCR	P82888 olisthodisc
65	44.0	102	1 H4_OLILU	P35058 phanerocha
66	44.0	102	1 H4_PHACH	P04915 phaearum po
67	44.0	102	1 H4_PHYPO	P09322 schizosacch
68	44.0	102	1 H4_SCHPO	P27996 solaster st
69	44.0	102	1 H4_SOLST	P08436 volvox cart
70	44.0	102	1 H4_WOLCA	P59258 triticum ae
71	44.0	102	1 H4_WHEAT	P02309 saccharomyc
72	44.0	102	1 H4_YEAST	Q9ur70 mastigamoeb
73	44.0	107	1 H4_WASBA	Q81w36 bacillus an
74	44.0	114	1 RL19_BACAA	Q81w36 bacillus ce
75	44.0	114	1 RL19_BACCR	Q9xiq7 thermotoga
76	44.0	115	1 RL19_THEME	Q83104 tropheryma
77	44.0	115	1 RL19_TROWB	Q83866 tropheryma
78	44.0	115	1 RL19_TROWT	Q99um9 staphylococ
79	44.0	116	1 RL19_STAAM	Q8nx05 staphylococ
80	44.0	116	1 RL19_STAAM	Q8csu9 staphylococ
81	44.0	116	1 RL19_STAAP	Q78409 guillardia
82	44.0	118	1 RL19_STAAP	Q26347 methanobact
83	44.0	138	1 HIS3_METTH	Q9v560 aeropyrum p
84	44.0	150	1 RS13_AERPE	Q8p810 xanthomonas
85	44.0	212	1 NUSE_SYNEL	Q45798 rhodothermu
86	44.0	215	1 YGK1_YEAST	Q00460 pseudomonas
87	44.0	282	1 COBS_CLOTE	P39859 staphylococ
88	44.0	282	1 Y123_PYRAB	Q8p1j8 xanthomonas
89	44.0	257	1 Y123_PYRAB	Q8p9r7 xanthomonas
90	44.0	263	1 YP80_AERPE	Q89z26 bacteroides
91	44.0	271	1 EUTC_XANAC	Q10811 mycobacteri
92	44.0	272	1 EUTC_XANCP	Q8k4k2 chlorobium
93	44.0	286	1 GUB_RHOMR	Q8k4k2 chlorobium
94	44.0	326	1 TMOE_PSEME	Q8k4k2 chlorobium
95	44.0	351	1 CAPU_STAAM	Q8k4k2 chlorobium
96	44.0	421	1 ISPG_XANAC	Q8k4k2 chlorobium
97	44.0	465	1 ISPG_XANCP	Q8k4k2 chlorobium
98	44.0	465	1 TRME_BACTN	Q8k4k2 chlorobium
99	44.0	473	1 AMI3_MYCTU	Q8k4k2 chlorobium
100	44.0	487	1 SYC_CHLFE	Q8k4k2 chlorobium
100	44.0	490	1 GLFX_PYRFU	Q8k4k2 chlorobium

ALIGNMENTS

PPLA HUMAN
ID PPLA_HUMAN STANDARD; PRT; 52 AA.
AC P26678;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cardiac phospholamban (PLB)
GN PLN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=91268032; PubMed=1928805;
RA Fujii J., Zaitain-Herzberg A., Willard H.F., Tada M., MacLennan D.H.;
RT "Structure of the rabbit phospholamban gene, cloning of the human
PT cDNA, and assignment of the gene to human chromosome 6";
RL J. Biol. Chem. 266:11669-11675(1991).
RN [2]
RP SEQUENCE FROM N.A.
RA Salvatore C.A., Jacobson M.A.;
RL Submitted (XX-1992) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=9222499; PubMed=10198197;
RA McIernan C.F., Frye C.S., Lemster B.H., Kinder E.A.,
RA Ogletree-Hughes M.L., Moravec C.S., Feldman A.M.;
RT "The human phospholamban gene: structure and expression.";
RL J. Mol. Cell. Cardiol. 31:679-692(1999).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver.
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heisler F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalley D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP STRUCTURE BY NMR OF 1-25.
RX MEDLINE=95298769; PubMed=7779806;
RA Mortishire-Smith R.J., Pittenberger S.M., Burke C.J., Middaugh C.R.,
RA Gareky V.M., Johnson R.G.;
RT "Solution structure of the cytoplasmic domain of phospholamban:
phosphorylation leads to a local perturbation in secondary
structure";
RL Biochemistry 34:7603-7613(1995).
RN [6]
RP 3D-STRUCTURE MODELING.
RX MEDLINE=95269058; PubMed=7749920;
RA Adams P.D., Arkin I.T., Engelman D.M., Bruenger A.T.;
RT "Computational searching and mutagenesis suggest a structure for the
pentameric transmembrane domain of phospholamban";
RL Nat. Struct. Biol. 2:154-162(1995).
RN [7]
RP 3D-STRUCTURE MODELING.
RX MEDLINE=98170970; PubMed=9512019;

RA Herzyk P., Hubbard R.E.;
RT "Using experimental information to produce a model of the
transmembrane domain of the ion channel phospholamban.";
RL Biophys. J. 74:1203-1214(1998).
CC -!- FUNCTION: Phospholamban has been postulated to regulate the
activity of the calcium pump of cardiac sarcoplasmic reticulum.
CC -!- SUBUNIT: Homopentamer.
CC -!- SUBCELLULAR LOCATION: Membrane.
CC -!- TISSUE SPECIFICITY: Heart.
CC -!- PTM: Phosphorylated in response to beta-adrenergic stimulation.
CC -!- SIMILARITY: Belongs to the phospholamban family.
CC
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entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC
CC EMBL; M63603; AAA60083.1; -;
CC EMBL; M60411; AAA60109.1; -;
CC EMBL; AF177764; AAD55950.1; -;
CC EMBL; BC005269; AA050269.1; -;
CC PIR; A40424; A40424.
CC PDB; 1K9N; 14-NOV-01.
CC PDB; 1KCH; 28-NOV-01.
CC PDB; 1PLN; 29-DEC-99.
CC PDB; 1PLP; 31-JUL-95.
CC PDB; 1PSL; 03-JUN-95.
CC Genew; HGNC:9080; PLN.
CC MIM; 172405; -;
CC InterPro; IPR005984; P_lamban.
CC Pfam; PF04272; Phospholamban; 1.
CC TIGFams; TIGR01294; P_lamban; 1.
KW Transmembrane; Phosphorylation; Acetylation; 3D-structure.
FT DOMAIN 1 31
FT TRANSMEM 32 52
FT MOD_RES 1 1
FT MOD_RES 16 16
FT MOD_RES 17 17
FT TURN 2 3
FT HELIX 4 14
FT TURN 15 15
FT TURN 15 15
SQ SEQUENCE 52 AA; 6108 MW; 0766304A76A854D3 CRC64;
Query Match 100.0%; Score 75; DB 1; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEKVQYLTRSAIRAS 16
Db 1 MEKVQYLTRSAIRAS 16
RESULT 2
PPLA_MOUSE
ID PPLA_MOUSE STANDARD; PRT; 52 AA.
AC P20006;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cardiac phospholamban (PLB).
GN PLN.
OS Mus musculus (Mouse),
OS Rattus norvegicus (Rat), and
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090, 10116, 9986;
RN [1]
RP SEQUENCE FROM N.A.


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DR HSP; P26678; 1PLP.
DR MGD; MGI:97622; Pln.
DR InterPro; IPR005984; P lamban.
DR Pfam; PF04272; Phospholamban; 1.
DR TIGRFAMs; TIGR01294; P lamban; 1.
DR KW Transmembrane; Phosphorylation; Acetylation.
FT DOMAIN 1 31 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 32 52 POTENTIAL.
FT MOD_RES 1 1 ACETYLATION (BY SIMILARITY).
FT MOD_RES 16 16 PHOSPHORYLATION (BY PKA) (BY SIMILARITY).
FT MOD_RES 17 17 PHOSPHORYLATION (BY CAMK) (BY
FT SIMILARITY).
SQ SEQUENCE 52 AA; 6094 MW; 0763601F76A854D3 CRC64;

Query Match 100.0%; Score 75; DB 1; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps

Qy 1 MEKQVYLTRSARRAS 16
|||||
Db 1 MEKQVYLTRSARRAS 16

RESULT 3
ID PPLA_PIG STANDARD; PRT; 52 AA.
AC P07473;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cardiac phospholamban (PLB).
GN PLN.
OS Sus scrofa (Pig), and
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823, 9615;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=C.familiaris;
RA MEDLINE=87083954; PubMed=3793929;
RX Fujii J., Ueno A., Kitano K., Tanaka S., Kadoma M., Tada M.;
RT "Complete complementary DNA-derived amino acid sequence of canine
cardiac phospholamban."
RL J. Clin. Invest. 79:301-304(1987).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=C.familiaris; TISSUE=Heart ventricle;
RX MEDLINE=87316936; PubMed=3628007;
RA Uyeda A., Kitano K., Fujii J., Kadoma M., Tada M., Tanaka S.;
RT "The cDNA sequence of the major phospholamban mRNA in canine cardiac
ventricular muscle."
RL Nucleic Acids Res. 15:6738-6738(1987).
RN [3]
RP SEQUENCE OF 1-45
RC SPECIES=C.familiaris;
RX MEDLINE=86323152; PubMed=3753485;
RA Fujii J., Kadoma M., Tada M., Toda H., Sakiyama F.;
RT "Characterization of structural unit of phospholamban by amino acid
sequencing and electrophoretic analysis."
RL Biochem. Biophys. Res. Commun. 138:1044-1050(1986).
RN [4]
RP SEQUENCE OF 10-45.
RC SPECIES=C.familiaris;
RX MEDLINE=87008549; PubMed=3759968;
RA Simmerman H.K.B., Collins J.H., Theibert J.L., Wegener A.D.,
RA Jones L.R.;
RT "Sequence analysis of phospholamban. Identification of
phosphorylation sites and two major structural domains."
RL J. Biol. Chem. 261:13333-13341(1986).
RN [5]
RP PHOSPHORYLATION.
RC SPECIES=C.familiaris;

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RP SEQUENCE FROM N.A.
RC STRAIN=WA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=22608306; PubMed=12692562;
RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
RA Sakaki Y., Hattori M., Omura S.;
RT "Complete genome sequence and comparative analysis of the industrial
RT microorganism Streptomyces avermitilis.";
RL Nat. Biotechnol. 21:526-531(2003).
CC
CC -!- FUNCTION: This protein is located at the 30S-50S ribosomal subunit
CC interface and may play a role in the structure and function of the
CC aminoacyl-tRNA binding site (By similarity).
CC
CC -!- SIMILARITY: Belongs to the L19P family of ribosomal proteins.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AP005031; BAC70351.1; -
CC HAMAP; MF 00402; -; 1.
CC InterPro; IPR001857; Ribosomal_L19.
CC Pfam; PF01245; Ribosomal_L19; 1.
CC PRINTS; PR00061; RIBOSOMAL_L19.
CC PRODOM; PD002979; Ribosomal_L19; 1.
CC TIGRFAMS; TIGR01024; rplS_bact; 1.
CC DR PROSITE; PS01015; RIBOSOMAL_L19; 1.
CC DR PROSITE; PS01015; RIBOSOMAL_L19; 1.
CC KW Ribosomal protein; Complete proteome.
CC SEQUENCE 116 AA; 13186 MW; 4708173B07F6EB6 CRC64;
CC
CC Query Match 54.7%; Score 41; DB 1; Length 116;
CC Best Local Similarity 46.7%; Pred. No. 1;
CC Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
CC
CC QY 1 MEKVQLTRSAIRRA 15
CC :|:::|:|:|:|
CC DB 81 VEKIELVTRGDVRR 95
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CC RESULT 6
CC RL19_STRCO
CC ID RL19_STRCO STANDARD; PRT; 116 AA.
CC AC O69883;
CC DT 30-MAY-2000 (Rel. 39, Created)
CC DT 30-MAY-2000 (Rel. 39, Last sequence update)
CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
CC DE 50S ribosomal protein L19.
CC GN RPLS OR SC05595 OR SC2E1.12.
CC OS Streptomyces coelicolor, and
CC OS Streptomyces lividans.
CC OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
CC OC Streptomyces; Streptomyces; Streptomyces.
CC OX NCBI_TaxID=1902, 1916;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RC SPECIES=S.coelicolor; STRAIN=A3(2) / M145;
CC RX MEDLINE=21996410; PubMed=12009553;
CC RA Bentley S.D., Chater K.F., Harris D.E., Quail M.A., Kieser H.,
CC RA Thomson N.R., James K.D., Harris S., Chandra G., Chen C.W., Collins M.,
CC RA Harper D., Bateman A., Brown S., Chandra G., Hornsby T., Howarth S.,
CC RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
CC RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
CC RA Rabinowitz E., Rajandream M.A., Rutherford K., Rutter S.,
CC RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
CC RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
CC RA Hopwood D.A.;
CC RT "Complete genome sequence of the model actinomycete Streptomyces
CC coelicolor A3(2)";
CC RL Nature 417:141-147(2002).
CC RN [2]
CC RP SEQUENCE FROM N.A.

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RC SPECIES=S.lividans; STRAIN=TK11;
RA Parro V., Mellado R.P.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC
CC -!- FUNCTION: This protein is located at the 30S-50S ribosomal subunit
CC interface and may play a role in the structure and function of the
CC aminoacyl-tRNA binding site (By similarity).
CC
CC -!- SIMILARITY: Belongs to the L19P family of ribosomal proteins.
CC
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CC
CC EMBL; AL393124; CAAL19387.1; -
CC EMBL; Z86111; CAB06800.1; -
CC PIR; T34780; T34780.
CC HAMAP; MF 00402; -; 1.
CC InterPro; IPR001857; Ribosomal_L19.
CC Pfam; PF01245; Ribosomal_L19; 1.
CC PRINTS; PR00061; RIBOSOMAL_L19.
CC PRODOM; PD002979; Ribosomal_L19; 1.
CC TIGRFAMS; TIGR01024; rplS_bact; 1.
CC DR PROSITE; PS01015; RIBOSOMAL_L19; 1.
CC DR PROSITE; PS01015; RIBOSOMAL_L19; 1.
CC KW Ribosomal protein; Complete proteome.
CC SEQUENCE 116 AA; 13142 MW; 37D782C6763D0A90 CRC64;
CC
CC Query Match 54.7%; Score 41; DB 1; Length 116;
CC Best Local Similarity 46.7%; Pred. No. 1;
CC Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
CC
CC QY 1 MEKVQLTRSAIRRA 15
CC :|:::|:|:|:|
CC DB 81 VEKIELVTRGDVRR 95
CC
CC RESULT 7
CC RL19_BORBU
CC ID RL19_BORBU STANDARD; PRT; 121 AA.
CC AC O51642;
CC DT 15-DEC-1998 (Rel. 37, Created)
CC DT 15-DEC-1998 (Rel. 37, Last sequence update)
CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
CC DE 50S ribosomal protein L19.
CC GN RPLS OR BB0699.
CC OS Borrelia burgdorferi (Lyme disease spirochete).
CC OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
CC OX NCBI_TaxID=139;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RC STRAIN=ATCC 35210 / B31;
CC RX MEDLINE=98065943; PubMed=9403685;
CC RA Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
CC RA Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
CC RA Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
CC RA Peterson J., Kleravage A.R., Quackenbush J., Salzberg S., Hanson M.,
CC RA van Vugt J., Palmer N., Adams M.D., Gocayne J.D., Weidman C.,
CC RA Uitterback T., Watthey L., McDonald L., Artiach P., Bowman C.,
CC RA Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
CC Smith H.O., Venter J.C.;
CC RT "Genomic sequence of a Lyme disease spirochaete, Borrelia
CC burgdorferi.";
CC RL Nature 390:580-585(1997).
CC
CC -!- FUNCTION: This protein is located at the 30S-50S ribosomal subunit
CC interface and may play a role in the structure and function of the
CC aminoacyl-tRNA binding site (By similarity).
CC
CC -!- SIMILARITY: Belongs to the L19P family of ribosomal proteins.
CC
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EMBL; AE001170; AAC67044.1; -
TIGR; B0187; B70187.
HAMAP; MF 00402; -; 1.
InterPro; IPR001857; Ribosomal_L19.
Pfam; PF01245; Ribosomal_L19; 1.
PRINTS; PR00061; Ribosomal_L19.
ProDom; PD002979; Ribosomal_L19; 1.
TIGRFAMs; TIGR01024; rplS_bact; 1.
PROSITE; PS01015; RIBOSOMAL_L19; 1.
Ribosomal protein; Complete proteome.
SEQUENCE 121 AA; 14011 MW; A33F7B1E4DF24070 CRC64;

Query Match 53.3%; Score 40; DB 1; Length 121;
Best Local Similarity 53.3%; Pred. No. 1.7;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MEKVQLTRSAIRRA 15
:|||||:|:|
DB 80 IEKVEVLRRGKVRRA 94

RESULT 8
SYA_THEAC
ID SYA_THEAC STANDARD; PRT; 871 AA.
AC Q9JHW4;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alanyl-tRNA synthetase (EC 6.1.1.7) (Alanine--tRNA ligase) (AlaRS).
GN ALAS OR TA0849.
OS Thermoplasma acidophilum.
OC Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;
OC Thermoplasmataceae; Thermoplasma.
OX NCBI_TaxID=2303;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 1728;
EX MEDLINE=20479972; PubMed=11029001;
RA Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C.,
RA Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.,
RT "The genome sequence of the thermoacidophilic scavenger Thermoplasma
acidophilum.";
RL Nature 407:508-513(2000).
CC -!- CATALYTIC ACTIVITY: ATP + L-alanine + tRNA(Ala) = AMP +
diphosphate + L-alanyl-tRNA(Ala).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.

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EMBL; AL445065; CAC11978.1; -
HAMAP; MF 00036; -; 1.
InterPro; IPR002318; tRNA-synt_2c.
InterPro; IPR006193; tRNA_synt_Ala.
Pfam; PF01411; tRNA-synt_2c; 1.
PRINTS; PR00980; TRNASYNTHALA.
TIGRFAMs; TIGR00344; alas; 1.
PROSITE; PS0860; AA tRNA LIGASE II ALA; 1.
KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
Complete proteome.
SEQUENCE 871 AA; 99907 MW; 6AGB55478463666D CRC64;

Query Match 52.0%; Score 39; DB 1; Length 871;
Best Local Similarity 69.2%; Pred. No. 22;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 KQVQLTRSAIRRA 15
:|||||:|:|
DB 353 KGYLRLRLIRRA 365

RESULT 9
RL19_THETN
ID RL19_THETN STANDARD; PRT; 115 AA.
AC Q8R9X4;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 50S ribosomal protein L19.
GN RPLS OR TTE1457.
OS Thermoplasma tengcongensis.
OC Bacteria; Firmicutes; Clostridia; Thermoplasmales;
OC Thermoplasmales; Thermoplasmales; Thermoplasmales;
OX NCBI_TaxID=119072;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MB4 / JCM 11007;
RX MEDLINE=21992816; PubMed=11997336;
RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
RA Tan H., Chen R., Wang J., Yu J., Yang H.;
RT "A complete sequence of T. tengcongensis genome.";
RL Genome Res. 12:689-700(2002).
CC -!- FUNCTION: This protein is located at the 30S-50S ribosomal subunit
interface and may play a role in the structure and function of the
aminoacyl-tRNA binding site (by similarity).
CC -!- SIMILARITY: Belongs to the L19P family of ribosomal proteins.

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EMBL; AE013104; AAM24679.1; -
HAMAP; MF 00402; -; 1.
InterPro; IPR001857; Ribosomal_L19.
Pfam; PF01245; Ribosomal_L19; 1.
PRINTS; PR00061; RIBOSOMAL_L19.
ProDom; PD002979; Ribosomal_L19; 1.
TIGRFAMs; TIGR01024; rplS_bact; 1.
PROSITE; PS01015; RIBOSOMAL_L19; 1.
Ribosomal protein; Complete proteome.
SEQUENCE 115 AA; 13395 MW; 9EBE9A1B89D3122B CRC64;

Query Match 50.7%; Score 38; DB 1; Length 115;
Best Local Similarity 40.0%; Pred. No. 3.8;
Matches 6; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 MEKVQLTRSAIRRA 15
:|||||:|:|
DB 80 LEKIEVIRRGKVRRA 94

RESULT 10
PSD_CHLCV
ID PSD_CHLCV STANDARD; PRT; 299 AA.
AC Q82L13;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Phosphatidylserine decarboxylase proenzyme (EC 4.1.1.65) (Contains:

DE Phosphatidylserine decarboxylase alpha chain; Phosphatidylserine
DE decarboxylase beta chain).
GN PSD OR CCA00927.
OS Chlamydomophila caviae.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydomophila.
OX NCBI_TaxID=83557;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GPIC;
RX MEDLINE=22569155; PubMed=12682364;
RA Read T.D., Myers G.S.A., Brunhan R.C., Nelson W.C., Paulsen I.T.,
RA Heidelberg J., Holtzapffe E., Khouri H., Federova N.B., Carty H.A.,
RA Umayang L.A., Haft D.H., Peterson J., Beanan M.J., White O.,
RA Salzberg S.L., Hsia R.-C., McClarty G., Rank R.G., Bavol P.M.,
RA Fraser C.M.;
RT "Genome sequence of Chlamydomophila caviae (Chlamydia pitraci GPIC):
RT examining the role of niche-specific genes in the evolution of the
RT Chlamydiaceae";
RL Nucleic Acids Res. 31:2134-2147(2003).
CC -!- CATALYTIC ACTIVITY: Phosphatidyl-L-serine =
CC phosphatidylethanolamine + CO(2).
CC -!- COFACTOR: Pyruvoyl group (By similarity).
CC -!- SIMILARITY: Belongs to the phosphatidylserine decarboxylase
CC family. Subfamily 2.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AB016977; AAP05666.1; -.
CC TIGR; CCA00927; -.
DR HAMAP; MF 00663; -; 1.
DR InterPro; IPR003817; PS_Dcarbxyase.
DR InterPro; IPR005321; PS_decarb.
DR Pfam; PF02666; PS_Dcarbxyase; 1.
DR TIGRFAMs; TIGR00163; PS_decarb; 1.
DR Phospholipid biosynthesis; Lyase; Decarboxylase; Pyruvate; Zymogen;
KW Complete proteome.
FT CHAIN 1 257 PHOSPHATIDYL SERINE DECARBOXYLASE BETA
FT CHAIN (BY SIMILARITY).
FT CHAIN 258 299 PHOSPHATIDYL SERINE DECARBOXYLASE ALPHA
FT CHAIN (BY SIMILARITY).
FT SITE 257 258 CLEAVAGE (NONHYDROLYTIC) (BY SIMILARITY).
FT MOD_RES 258 258 CONVERTED TO A PYRUVOYL GROUP (BY
FT SIMILARITY).
SQ SEQUENCE 299 AA; 34223 MW; 6F8EB837D97E24E0 CRC64;
Query Match 50.7%; Score 38; DB 1; Length 299;
Best Local Similarity 43.8%; Pred. No. 11;
Matches 7; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
OY 1 MEKVOYLTRSAIRRAS 16
DB 1 MKKLQYIDRSTNQRT 16
RESULT 11
ID APAH ACTAC STANDARD; PRT; 275 AA.
AC OS2655;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Bis(5'-nucleosyl)-tetraphosphatase, symmetrical
DE (Diadenosine tetraphosphatase) (Ap4A hydrolase) (Diadenosine 5',5'-
DE p1,p4-tetraphosphate pyrophosphohydrolase).
GN APAH
OS Actinobacillus actinomycetemcomitans (Haemophilus
actinomycetemcomitans).

OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Actinobacillus.
OX NCBI_TaxID=714;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Y4;
RA Saarela M., Fives-Taylor P.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Hydrolyzes diadenosine 5',5'-p1,p4-tetraphosphate to
CC Yield ADP (By similarity).
CC -!- CATALYTIC ACTIVITY: P(1),P(4)-bis(5'-adenosyl)tetraphosphate +
CC H(2)O = 2 ADP.
CC -!- SIMILARITY: Belongs to the Ap4A hydrolase family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF043998; AAC00202.1; -.
CC HAMAP; MF 00199; -; 1.
DR InterPro; IPR004617; ApAH.
DR InterPro; IPR004843; M-ppestrase.
DR InterPro; IPR006186; T_phtase_apAH.
DR Pfam; PF00149; Metallophos; 1.
DR ProDom; PD000252; T_phtase_apAH; 1.
DR TIGRFAMs; TIGR00668; apAH; 1.
KW Hydrolase.
SQ SEQUENCE 275 AA; 31480 MW; 0843F4FE11FF6DAD CRC64;
Query Match 49.3%; Score 37; DB 1; Length 275;
Best Local Similarity 40.0%; Pred. No. 15;
Matches 6; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
OY 2 EKVOYLTRSAIRRAS 16
DB 259 EDKQYFTQSARKSN 273
RESULT 12
ID RFSD XANAC STANDARD; PRT; 625 AA.
AC Q8PG33;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE RNA polymerase sigma factor rpoD (Sigma-70).
GN RPOD OR XAC3788.
OS Xanthomonas axonopodis (pv. citri).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=92829;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=306 / ATCC 13902 / XV 101;
RX MEDLINE=22022145; PubMed=12024217;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Camarotte G., Cannavan P., Cardoso J., Chamberg F., Clapina L.P.,
RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., Bl-Dorri H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,


```
Qy 2 EKVOYLTRSAIRR 14
Db 26 ENIQGITKPAIR 38

RESULT 15
RL19_COREF
ID RL19_COREF STANDARD; PRT; 113 AA.
AC Q9P56;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE 50S ribosomal protein L19.
GN RPL5 OR CE1932.
OS Corynebacterium efficiens.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OC NCBI_TaxID=152794;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
RX MEDLINE=22723752; PubMed=12840036;
RA Nishio Y., Nakamura Y., Kawarabayashi Y., Usuda Y., Kimura E.,
RA Sugimoto S., Matsui K., Yamagishi A., Kikuchi H., Ikeo K.,
RA "Cajobari T.;
RT "Comparative complete genome sequence analysis of the amino acid
RT replacements responsible for the thermostability of Corynebacterium
RT efficiens."
RL Genome Res. 13:1572-1579(2003).
CC -!- FUNCTION: This protein is located at the 30S-50S ribosomal subunit
CC interface and may play a role in the structure and function of the
CC aminoacyl-tRNA binding site (By similarity).
CC -!- SIMILARITY: Belongs to the L19p family of ribosomal proteins.
CC
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CC
CC EMBL; AP005220; BAC18742.1; ALT_INIT.
CC HAMAP; MF 00402; -; 1.
CC InterPro; IPR001857; Ribosomal L19.
CC Pfam; PF01245; Ribosomal L19; 1.
CC PRINTS; PR00061; RIBOSOMAL_L19.
CC ProDom; PD002979; Ribosomal L19; 1.
CC TIGRFAMs; TIGR01024; rplS_bact; 1.
CC PROSITE; PS01015; RIBOSOMAL_L19; 1.
CC RIBOSOMAL protein; Complete proteome.
CC SEQUENCE 113 AA; 13008 MW; 9BDIC9D25ADA453A CRC64;

Query Match 48.0%; Score 36; DB 1; Length 113;
Best Local Similarity 40.0%; Pred. No. 9.1;
Matches 6; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MEKVOYLTRSAIRR 15
Db 80 LEKIEVRRGDVRR 94

RESULT 16
RL19_COREF
ID RL19_COREF STANDARD; PRT; 113 AA.
AC Q8NNZ0;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 50S ribosomal protein L19.
GN RPL5 OR CGL2037.
OS Corynebacterium glutamicum (Brevibacterium flavum).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OC NCBI_TaxID=152794;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
RX MEDLINE=22723752; PubMed=12840036;
RA Nishio Y., Nakamura Y., Kawarabayashi Y., Usuda Y., Kimura E.,
RA Sugimoto S., Matsui K., Yamagishi A., Kikuchi H., Ikeo K.,
RA "Cajobari T.;
RT "Comparative complete genome sequence analysis of the amino acid
RT replacements responsible for the thermostability of Corynebacterium
RT efficiens."
RL Genome Res. 13:1572-1579(2003).
CC -!- FUNCTION: This protein is located at the 30S-50S ribosomal subunit
CC interface and may play a role in the structure and function of the
CC aminoacyl-tRNA binding site (By similarity).
CC -!- SIMILARITY: Belongs to the L19p family of ribosomal proteins.
CC
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CC
CC EMBL; AP005220; BAC18742.1; ALT_INIT.
CC HAMAP; MF 00402; -; 1.
CC InterPro; IPR001857; Ribosomal L19.
CC Pfam; PF01245; Ribosomal L19; 1.
CC PRINTS; PR00061; RIBOSOMAL_L19.
CC ProDom; PD002979; Ribosomal L19; 1.
CC TIGRFAMs; TIGR01024; rplS_bact; 1.
CC PROSITE; PS01015; RIBOSOMAL_L19; 1.
CC RIBOSOMAL protein; Complete proteome.
CC SEQUENCE 113 AA; 13008 MW; 9BDIC9D25ADA453A CRC64;

Query Match 48.0%; Score 36; DB 1; Length 113;
Best Local Similarity 40.0%; Pred. No. 9.1;
Matches 6; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MEKVOYLTRSAIRR 15
Db 80 LEKIEVRRGDVRR 94

RESULT 17
P2C1_ARATH
ID P2C1_ARATH STANDARD; PRT; 434 AA.
AC P49597; Q43717; Q94C87;
DT 01-FEB-1996 (Rel. 33, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Protein phosphatase 2C AB11 (EC 3.1.3.16) (PP2C) (Abscisic acid-
DE insensitive 1).
GN AB11 OR AT4G26080 OR F20B18.190.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OC NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A. AND VARIANT ASP-180.
RC STRAIN=cv. Landsberg erecta;
RX MEDLINE=94255767; PubMed=8197457;
RA Meyer K., Leube M.P., Grill E.;
RT "A protein phosphatase 2C involved in ABA signal transduction in
RT Arabidopsis thaliana."
RL Science 264:1452-1455(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia; TISSUE=Leaf;
RX MEDLINE=95007758; PubMed=7923358;
RA Mindrinos M., Katagiri F., Yu G.L., Ausubel F.M.;
RT "The A. thaliana disease resistance gene RPS2 encodes a protein
RT containing a nucleotide-binding site and leucine-rich repeats."
RL Cell 78:1089-1099(1994).
RN [3]
```


RP SEQUENCE FROM N.A.
 RC STRAIN=cv, Columbia; TISSUE=Leaf;
 RX MEDLINE=94235786; PubMed=7910981;
 RA Leung J., Bouvier-Durand M., Morris P.C., Guerrier D., Chefdor F.,
 RA Graudat J.,
 RT "Arabidopsis ABA response gene AB11: features of a calcium-modulated
 protein phosphatase.",
 RN Science 264:1448-1452 (1994).
 [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv, Columbia;
 RX MEDLINE=20083488; PubMed=10617198;
 RA Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G.,
 RA Pohl T., Duesterhoef A., Stiekema W., Entian K.-D., Terryn N.,
 RA Harris B., Anstorge W., Brandt P., Grivell L.A., Rieger M.,
 RA Weichselgartner M., de Simone V., Obermaier B., Maché R., Mueller M.,
 RA Kreis M., Dalseny M., Puidomenech P., Watson M., Schmidheini T.,
 RA Reichert B., Portetle D., Perez-Alonso M., Boutry M., Bancroft I.,
 RA Vos P., Hohnselt J., Zimmermann W., Wedler H., Ridley P.,
 RA Langham S.-A., McCullagh B., Bilham L., Robben J.,
 RA Van der Schueren J., Grymonprez B., Chuang Y.-J., Vandenbussche F.,
 RA Braeken M., Weltjens I., Voet M., Bastiaens I., Aert R., Defoor E.,
 RA Weitzenecker T., Bothe G., Rampsperger U., Hilbert H., Braun M.,
 RA Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W.,
 RA Mooijman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,
 RA Berniser S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,
 RA De Keyser A., Buyschaert C., Giesen J., Villarroel R., De Clercq R.,
 RA Van Montagu M., Rogers J., Cronin A., Quail M.A., Bray-Allen S.,
 RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McIay K., Mayes R.,
 RA Pettitt A., Rajandream M.A., Lyne M., Benes V., Reckmann S.,
 RA Borkova D., Bloeker H., Scharfe M., Grimm M., Moehner T.-H.,
 RA Dose S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fartmann B., Granderath K., Dauner D., Herzl A.,
 RA Neumann S., Argitoni A., Vitale D., Lignori R., Piravandi E.,
 RA Massenot O., Quigley F., Clabaud G., Muendlein A., Felber R.,
 RA Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,
 RA Cheford F., Cooke R., Berger C., Monfort A., Casacuberta E.,
 RA Gibbons T., Weber N., Vandenbol M., Barges M., Terol J., Torres A.,
 RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,
 RA Heijnen L., Schwarz S., Scholler P., Heber S., Francis P., Bielke C.,
 RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
 RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,
 RA Farnell L., Dedina N., Gnoj L., Schutz K., Huang E., Spiegler L.,
 RA Sekhon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,
 RA Stoneking T., Kalicki J., Graves T., Harmon G., Edwards J.,
 RA Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
 RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
 RA Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.W.,
 RA Nelson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D.,
 RA Du H., Ali J., Bernhoff A., Jones K., Drone K., Cotton N., Joshua C.,
 RA Antonoli B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
 RA Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah R.,
 RA Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S.,
 RA Granat S., Shohdy N., Hasegawa A., Hameed A., Lodhi M., Johnson A.,
 RA Chen E., Marra M.A., Martensen R., McCombie W.R.;
 RT "Sequence and analysis of chromosome 4 of the plant Arabidopsis
 thaliana".
 RL Nature 402:769-777 (1999).
 [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv, Columbia;
 RX MEDLINE=22954850; PubMed=14593172;
 RA Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J.,
 RA Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,
 RA Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,
 RA Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.N., Toriumi M.J.,
 RA Chan M.M., Tang C.C., Chodera C.S., Deng J.M., Akiyama K., Ansari Y.,
 RA Arakawa T., Bann J., Banno F., Bowser L., Brooks S.Y., Carninci P.,
 RA Chao Q., Choy N., Enju A., Goldsmith A.D., Gurjal M., Hansen N.F.,
 RA Hayashizaki Y., Johnson-Hopson C., Heuan V.W., Iida K., Karnes M.,
 RA Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai I.,
 RA Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,
 RA Satou M., Tamse R., Vaysberg M., Wallender E.K., Wong C., Yamamura Y.,

RA Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
 RT "Empirical analysis of transcriptional activity in the Arabidopsis
 Genome".
 RL Science 302:842-846 (2003).
 CC -!- FUNCTION: Involved in abscisic acid (ABA) signaling pathway.
 CC -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
 phosphate.
 CC -!- COFACTOR: Binds 2 magnesium or manganese ions (By similarity).
 CC -!- SIMILARITY: Belongs to the PP2C family.
 CC
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 CC
 DR EMBL; X78886; CRA55484.1; -
 DR EMBL; U12856; AAA50237.1; -
 DR EMBL; X77116; CRA54383.1; -
 DR EMBL; AL049483; CAB39673.1; -
 DR EMBL; AL161564; CAB79463.1; -
 DR EMBL; AV035073; AAK59578.1; -
 DR PIR; T04263; T04263.
 DR HSP; F35813; IAGQ.
 DR InterPro; IPR002046; EF-hand.
 DR InterPro; IPR001932; PP2C-like.
 DR InterPro; IPR002022; PP2C.
 DR Pfam; PF00481; PP2C; 1.
 DR SMART; SM00331; PP2C_SIG; 1.
 DR SMART; SM00332; PP2C; 1.
 DR PROSITE; PS00018; EF_HAND; 1.
 DR PROSITE; PS01032; PP2C; 1.
 KW Hydrolyase; Magnesium; Manganese; Multigene family; Calcium-binding.
 CA BIND 93 104
 FT DOMAIN 417 420
 FT VARIANT 180 180
 FT CONFLICT 24 24 G -> D (WILTY PHENOTYPE AND ABA-
 FT CONFLICT 105 105 I -> V (IN REF. 5).
 FT CONFLICT 434 AA; 47505 MW; 44454P04195FS72 CRC64;
 SQ
 Query Match 48.0%; Score 36; DB 1; Length 434;
 Best Local Similarity 43.8%; Pred. No. 39;
 Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
 QY 1 MEKQVLTGSAIRAS 16
 Db 396 MSAAEYLSKLAIOKGS 411
 RESULT 18
 2ASA HUMAN STANDARD; PRT; 486 AA.
 ID 2ASA HUMAN STANDARD; PRT;
 AC Q15172;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Serine/threonine protein phosphatase 2A, 56 kDa regulatory subunit,
 DE alpha isoform (PP2A, B subunit, B' alpha isoform) (PP2A, B subunit,
 DE B56 alpha isoform) (PP2A, B subunit, PR61 alpha isoform) (PP2A, B
 DE subunit, R5 alpha isoform).
 GN PP2R5A.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Breast cancer;
 RX MEDLINE=96064678; PubMed=7592815;
 RA McCright B., Virshup D.M.;

RPSD	XANCP	STANDARD;	PRT;	624 AA.
ID	RP5D XANCP		PRT;	624 AA.
AC	Q8P4H2;			
DT	10-OCT-2003 (Rel. 42, Created)			
DT	10-OCT-2003 (Rel. 42, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	RNA polymerase sigma factor rpoD (Sigma-70).			
GN	RP0D OR XCC3736.			
OS	Xanthomonas campestris (pv. campestris).			
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;			
OC	Xanthomonadaceae; Xanthomonas.			
OX	NCBI_TaxID=340;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=ATCC 33913 / NCPPB 528;			
RC	MEDLINE=22022145; PubMed=12024217;			
RA	da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furian L.R.,			
RA	Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,			
RA	Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,			
RA	Camarote G., Cannavan F., Cardozo J., Chambergo F., Chapina L.P.,			
RA	Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,			
RA	Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,			
RA	Fornighieri E.F., Franco M.C., Greggio C.C., Gruber A.			
RA	Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,			
RA	Locai E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,			
RA	Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,			
RA	Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,			
RA	Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,			
RA	Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,			
RA	Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,			
RA	Setubal J.C., Kitajima J.P.			
RT	"Comparison of the genomes of two Xanthomonas pathogens with differing			
RT	host specificities."			
RL	Nature 417:459-463(2002).			
CC	!- FUNCTION: The sigma factor is an initiation factor that promotes			
CC	attachment of the RNA polymerase to specific initiation sites and			
CC	then is released. This is the primary sigma-factor of this			
CC	bacteria [By similarity].			
CC	!- SIMILARITY: Belongs to the sigma-70 factor family.			
CC				
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CC	or send an email to license@isb-sib.ch).			
CC				
CC	EMBL; AE012494; AA042993.1; -			
DR	InterPro; IPR009043; RNA_pol_sigma.			
DR	InterPro; IPR007631; Sigma70_ner.			
DR	InterPro; IPR007127; Sigma70_r1.			
DR	InterPro; IPR009042; Sigma70_r1_2.			
DR	InterPro; IPR007627; Sigma70_r2.			
DR	InterPro; IPR007624; Sigma70_r3.			
DR	InterPro; IPR007630; Sigma70_r4.			
DR	InterPro; IPR000943; Sigma_70.			
DR	Pfam; PF04546; sigma70_ner_1.			
DR	Pfam; PF03979; sigma70_r1_1.			
DR	Pfam; PF00140; sigma70_r1_2.			
DR	Pfam; PF04542; sigma70_r2.			
DR	Pfam; PF04539; sigma70_r3.			
DR	Pfam; PF04545; sigma70_r4.			
DR	PRINTS; PR00046; SIGMA70FACT.			
DR	PROSITE; PSC0715; SIGMA70_1.			
DR	PROSITE; PSC0716; SIGMA70_2.			
KW	Transcription regulation; Sigma factor; DNA-directed RNA polymerase;			
KW	DNA-binding; Complete proteome.			
FT	DOMAIN 413 426			
FT	DNA_BIND 583 602			
FT	SEQUENCE 624 AA; 69947 MW; 1F5C8CA093F7F1AF CRC64;			

```
Best Local Similarity 50.0%; Pred. No. 57;
Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRAS 16
Db 357 MEKANYLTAEIKDIS 372

RESULT 20
CHLD_SINYP7 STANDARD; PRT; 677 AA.
AC 007345;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Magnesium-chelatase subunit chld (Mg-protoporphyryn IX chelatase) (Mg-
GN chelatase subunit D).
OS Synechococcus sp. (strain PCC 7942) (Anacystis nidulans R2).
CC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
OX NCBI_TaxID=1140;
RN [1]
RP SEQUENCE FROM N.A.
RA Masuda T., Nakayama M., Ohta H., Takayama K.-I.;
RT "Cloning and sequencing of a chld gene encoding a subunit of
RT magnesium-chelatase from the cyanobacterium Synechococcus sp. PCC
RT 7942."
RL (In) Plant Gene Register PGR97-091.
CC -!- FUNCTION: Involved in chlorophyll biosynthesis; introduces a
CC magnesium ion into protoporphyryn IX to yield Mg-protoporphyryn
CC IX.
CC -!- PATHWAY: Chlorophyll biosynthesis.
CC -!- SIMILARITY: BELONGS TO THE MG-CHELATASE SUBUNITS D/I FAMILY.
CC -!- SIMILARITY: Contains 1 VWFA domain.
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CC or send an email to license@isb-sib.ch).
CC EMBL; AB003135; BAA20346.1; -
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR000523; Mg_Chelatase_chit.
DR InterPro; IPR002035; VWF A.
DR Pfam; PF01078; Mg_chelatase; 1.
DR Pfam; PF03092; VwfA; 1.
DR SMART; SM00382; AAA; 1.
DR SMART; SM00327; VWFA; 1.
DR PROSITE; PS50234; VWFA; 1.
KW Photosynthesis; Chlorophyll biosynthesis; ATP-binding.
FT DOMAIN 481 676
FT DOMAIN 329 383
FT DOMAIN 677 AA; 73367 MW; 7E2988E096DF5506 CRC64;
SQ SEQUENCE 677 AA; 73367 MW; 7E2988E096DF5506 CRC64;

Query Match 48.0%; Score 36; DB 1; Length 677;
Best Local Similarity 58.3%; Pred. No. 63;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 MEKVQYLTRSAIR 13
Db 267 EQIGYLVREAIR 278

RESULT 21
DVL2_XENLA STANDARD; PRT; 736 AA.
ID DVL2_XENLA
AC P51142.
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
```

```
DE segment polarity protein dishevelled homolog DVL-2 (Dishevelled-2)
DE (DSH homolog 2) (Xsh).
OS Xenopus laevis (African clawed frog).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipelidae;
CC Xenopodinae; Xenopus.
OX NCBI_TaxID=83355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Oocyte;
RX MEDLINE=95324391; PubMed=7600981;
RA Sokol S.Y., Klingensmith J., Perrimon N., Itoh K.;
RT "Dorsalizing and neuralizing properties of Xsh, a maternally
RT expressed Xenopus homolog of dishevelled."
RL Development 121:1637-1647(1995).
RN [2]
RP ERRATUM.
RX MEDLINE=96017659; PubMed=7589081;
RA Sokol S.Y., Klingensmith J., Perrimon N., Itoh K.;
RL Development 121:3487-3487(1995).
CC -!- FUNCTION: May play a role in the signal transduction pathway
CC mediated by multiple Wnt genes. Plays a role in dorsal axis
CC formation and in neural induction.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -!- TISSUE SPECIFICITY: Ubiquitous protein found equally distributed
CC in both animal-vegetal and dorsal-ventral directions.
CC -!- DEVELOPMENTAL STAGE: Maternal gene detected in different
CC developmental stages being most abundant in eggs.
CC -!- SIMILARITY: Belongs to the DSH family.
CC -!- SIMILARITY: Contains 1 DEP domain.
CC -!- SIMILARITY: Contains 1 PDZ/DHR domain.
CC -!- SIMILARITY: Contains 1 DIX domain.
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CC EMBL; U31552; AAB00688.1; -
DR PIR; I51691; I51691.
DR HSSP; Q12923; 3PDZ.
DR InterPro; IPR000391; DEP.
DR InterPro; IPR008339; Dishevel1.
DR InterPro; IPR003351; Dishevelled.
DR InterPro; IPR008341; Dishevelled_2.
DR InterPro; IPR001158; DIX.
DR InterPro; IPR001478; PDZ.
DR Pfam; PF00610; DEP; 1.
DR Pfam; PF02377; Dishevelled; 1.
DR Pfam; PF00778; DIX; 1.
DR Pfam; PF00595; PDZ; 1.
DR PRINTS; PR01760; DISHEVELLED.
DR PRINTS; PR01762; DISHEVELLED2.
DR ProDom; PD003639; DIX; 1.
DR SMART; SM00021; DAX; 1.
DR SMART; SM00049; DEP; 1.
DR SMART; SM00228; PDZ; 1.
DR PROSITE; PS50186; DEP; 1.
DR PROSITE; PS50841; DIX; 1.
DR PROSITE; PS50106; PDZ; 1.
KW Wnt signalling pathway; Developmental protein.
FT DOMAIN 1 82
FT DOMAIN 99 113
FT DOMAIN 222 227
FT DOMAIN 254 326
FT DOMAIN 428 502
FT DOMAIN 680 687
FT DOMAIN 736 AA; 79787 MW; AF6C9A1662DD7CEB CRC64;
SQ SEQUENCE 736 AA; 79787 MW; AF6C9A1662DD7CEB CRC64;

Query Match 48.0%; Score 36; DB 1; Length 736;
```


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CC
DR EMBL; AB003477; AAP47742.1; -;
DR EMBL; AY071444; AAL49066.1; -;
CC FlyBase; FBGN0035422; CG12740.
DR GO; GO:005842; C:cytosolic large ribosomal subunit (sensu Eu. .); ISS.
DR GO; GO:0003735; F:structural constituent of ribosome; ISS.
DR GO; GO:0056412; P:protein biosynthesis; ISS.
DR GO; GO:0002672; Ribosomal_L28e.
DR InterPro; IPR002672; Ribosomal_L28e.
DR Pfam; PF01778; Ribosomal_L28e; 1.
DR ProDom; PD010767; Ribosomal_L28e; 1.
DR Ribosomal protein.
SQ SEQUENCE 144 AA; 16029 MW; 14D5C7866F585113 CRC64;

Query Match 46.7%; Score 35; DB 1; Length 144;
Best Local Similarity 70.0%; Pred. No. 18;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 7 LTRS AIRRAS 16
DB 110 LTQAALRRAS 119

RESULT 25
AMIR_PSEAE STANDARD; PRT; 196 AA.
ID AMIR_PSEAE
AC P10932;
DT 01-JUL-1989 (Rel. 11, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Aliphatic amidase regulator.
GN AMIR OR PA3363.
GC Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OX Pseudomonadaceae; Pseudomonas.
NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PAC433;
RX MEDLINE=89211409; PubMed=2495988;
RA Lowe N., Rice P.M., Drew R.E.;
RT "Nucleotide sequence of the aliphatic amidase regulator gene (amir)
of Pseudomonas aeruginosa.";
RL FEBS Lett. 246:39-43(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Huftagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
opportunistic pathogen.";
RL Nature 406:959-964(2000).
RN [3]
RP CHARACTERIZATION.
RX MEDLINE=95286483; PubMed=7539417;
RA Wilson S.A., Drew R.E.;
RT "Transcriptional analysis of the amidase operon from Pseudomonas
aeruginosa.";
RL J. Bacteriol. 177:3052-3057(1995).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF COMPLEX WITH AMIC.
RC STRAIN=PAC1;
RX MEDLINE=99437995; PubMed=10508151;
RA O'Hara B.P., Norman R.A., Wan P.T., Roe S.M., Barrett T.E., Drew R.E.,

```
RA Pearl L.H.;
RT "Crystal structure and induction mechanism of AmiC-AmiR: a
RL ligand-regulated transcription antitermination complex.";
RL EMBO J. 18:5175-5186(1999).
CC -!- FUNCTION: Positive controlling element of amiE, the gene for
CC aliphatic amidase. Acts as a transcriptional antitermination
CC factor. It is thought to allow RNA polymerase read through a rho-
CC independent transcription terminator between the amiE promoter and
CC gene.
CC -!- SUBUNIT: Forms a complex with amiC.
CC -----
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CC -----
DR EMBL; X13776; CA32023.1; -.
DR EMBL; AB004759; BAG06751.1; -.
DR PIR; B83226; B83226.
DR PIR; S03884; S03884.
DR PDB; 1Q00; 23-DEC-99.
DR InterPro; IPR005561; ANTAR.
DR Pfam; PF03861; ANTAR; 1_reg_antiterm.
DR PIRSF; PIRSF036382; Res_reg_antiterm; 1.
KW Transcription regulation; Transcription antitermination; 3D-structure;
KW Complete proteome.
FT CONFLICT 48 48 S -> A (IN REF. 1).
FT CONFLICT 64 64 R -> G (IN REF. 1).
FT CONFLICT 141 141 E -> D (IN REF. 1).
FT CONFLICT 154 154 A -> V (IN REF. 1).
FT CONFLICT 170 170 Y -> H (IN REF. 1).
FT HELIX 3 9
FT HELIX 10 12
FT STRAND 14 18
FT HELIX 23 35
FT TURN 36 36
FT STRAND 38 42
FT STRAND 55 59
FT TURN 64 64
FT HELIX 65 75
FT TURN 78 79
FT STRAND 81 86
FT HELIX 91 100
FT TURN 101 101
FT STRAND 104 107
FT HELIX 112 114
FT HELIX 115 160
FT TURN 161 161
FT HELIX 164 176
FT TURN 177 179
FT HELIX 182 189
SQ SEQUENCE 196 AA; 21903 MW; 306A4F30E8E4C6C0 CRC64;

Query Match 46.7%; Score 35; DB 1; Length 196;
Best Local Similarity 53.8%; Pred. No. 26;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 EKQVLTSAIR 14
Db 166 EAHQVLSREAWKR 178
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Search completed: October 1, 2004, 12:18:18
Job time : 9.8 secs

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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: October 1, 2004, 11:56:56 ; Search time 50.8 Seconds
(without alignments)
99.376 Million cell updates/sec

Title: US-09-830-779-19_COPY_1_16

Perfect score: 75

Sequence: 1 MEKVQLTRSAIRAS 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :

SPTREMBL_25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rhodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	54.7	116	16	Q82JW4 streptomyc
2	41	54.7	17	Q9UZF5	Q9UZF5 pyrococcus
3	40	53.3	527	12	Q9Q5Q3 grapevine 1
4	40	53.3	998	11	Q8CFM4
5	40	53.3	1104	16	Q87QO3
6	40	53.3	1108	17	Q58310
7	39	52.0	364	16	Q9A0Y9
8	39	52.0	406	16	Q88L71
9	39	52.0	421	2	Q9AM36
10	39	52.0	481	17	Q9VLD2
11	39	52.0	644	5	Q868U8
12	38	50.7	119	17	Q28525
13	38	50.7	122	17	Q974N9
14	38	50.7	208	16	Q89J03
15	38	50.7	211	16	Q7UFR1
16	38	50.7	252	3	Q9HF62

Q99ZW6 streptococ
Q8P177 streptococ
Q87811 streptococ
Q8K7R5 streptococ
Q9F8B7 streptococ
Q84S07 oryza sativ
Q8MMG5 dictyosteli
Q8DJ60 synecococ
Q8UWM3 rhodopirell
Q8G4I3 bifidobacte
Q26701 methanobact
Q33293 mycobacteri
Q7TX98 mycobacteri
Q92RE5 rhizobium m
Q8YZH6 anabaena sp
Q8E5S3 streptococ
Q8A046 streptococ
Q8DBN7 vibrio vuln
Q7VDP9 prochloroco
Q9HDW2 schizosacch
Q9V815 drosophila
Q9V816 drosophila
Q8MLH7 drosophila
Q9SB74 arabidopsis
Q61185 blepharisma
Q61184 blepharisma
Q61183 blepharisma
Q61182 blepharisma
Q62614 proteozua
Q62586 blepharisma
Q8MM34 ursus marit
Q82VU6 nitrosomona
Q27875 trichomonas
Q07154 mycobacteri
Q8FP56 corynebacte
Q97BD7 thermoplasm
Q8CF99 rattus norv
Q27417 methanobact
Q87Q99 vibrio para
Q8IRB4 drosophila
Q89VDS bradyrhizob
Q66251 actinobacil
Q96847 dictyosteli
Q23896 dictyosteli
Q92P72 rhizobium m
Q9VZC7 drosophila
Q82RMI streptomyc
Q914C6 pseudomonas
Q64082 bacterioph
Q31939 bacillus su
Q9REV7 pseudomonas
Q8F7A1 leptospira
Q7XZV4 oryza sativ
Q82158 salmonella
Q8TB19 homo sapien
Q972B3 sulfobolus
Q08348 xanthomonas
Q93Z21 sodalis glo
Q8NF21 homo sapien
Q9UVJ6 botrytis ci
Q7XNF3 oryza sativ
Q82HP5 streptomyc
Q861F1 dictyosteli
Q9T168 myotis daub
Q9WSX6 marek's dis
Q8X8E7 escherichia
Q83859 nilaparvata
Q8XR14 raietonia s
Q8S6W4 oryza sativ
Q8LM84 oryza sativ
Q9EL60 wheat strea
Q9VGW4 drosophila
Q8PB15 xanthomonas

Q8pn39 xanthomonas
Q30735 macaca neme
Q81y90 homo sapien
Q8yw51 anabaena sp
Q92ry5 rhizobium m
Q9nwf6 homo sapien
Q8cs49 staphylococ
Q8ar53 volvox cart
Q91vul arabidopsis
Q82c01 streptomyce
Q832p8 enterococcus

ALIGNMENTS

RESULT 1
Q82JW4 PRELIMINARY; PRT; 116 AA.
AC Q82JW4
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative ribosomal protein L19.
GN RPLS OR S4V2640.
OS Streptomyces avermitilis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=33903;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RA MEDLINE=21477403; PubMed=12692562;
RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
RA "Genome sequence of an industrial microorganism Streptomyces
RT avermitilis: deducing the ability of producing secondary
RT metabolites";
RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RA MEDLINE=22608306; PubMed=12692562;
RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
RA Sakaki Y., Hattori M., Omura S.;
RA "Complete genome sequence and comparative analysis of the industrial
RT microorganism Streptomyces avermitilis";
RL Nat. Biotechnol. 21:526-531(2003).
DR EMBL; AP005031; BAC70351.1; -
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0005840; C:ribosome; IEA.
DR GO; GO:0003735; P:structural constituent of ribosome; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR InterPro; IPR001857; Ribosomal_L19.
DR Pfam; PF01245; Ribosomal_L19; 1.
DR PRINTS; PR00061; RIBOSOMAL_L19.
DR ProDom; PD02979; Ribosomal_L19; 1.
DR TIGRfam; TIGR01024; rplS bact; 1.
DR PROSITE; PS01015; RIBOSOMAL_L19; 1.
DR Ribosomal protein; Complete_protome.
KW RIBOSOMAL PROTEIN; Complete_protome.
SQ SEQUENCE 116 AA; 13186 MW; 47081773B07F6EB6 CRC64;

Query Match 54.7%; Score 41; DB 16; Length 116;
Best Local Similarity 46.7%; Pred. No. 7.5;
Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
QY 1 MEKVQLTRSAIRA 15
DB 81 VEKIELVTRGDVRR 95
RESULT 2

Q9UZT5 PRELIMINARY; PRT; 451 AA.
ID Q9UZT5
AC Q9UZT5
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Phospho-sugar mutase.
GN PYRAB10610 OR PAB1666.
OS Pyrococcus abyssi.
OC Archaea; Euryarchaeota; Thermococci; Thermococcaceae; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=29292;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GES / Orsay;
RA Heilig R.;
RT "Pyrococcus abyssi genome sequence: insights into archaeal chromosome
RL structure and evolution.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ248286; CAB49971.1; -
DR PIR; P75083; F75083.
DR GO; GO:0016868; F:intramolecular transferase activity, phosph. . .; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR005841; PG_PMM_mutase.
DR InterPro; IPR005844; PG_PMM_ABAI.
DR InterPro; IPR005845; PG_PMM_ABAII.
DR InterPro; IPR005846; PG_PMM_ABAIII.
DR InterPro; IPR005843; PG_PMM_C.
DR Pfam; PF00408; PGM_PMM_1.
DR Pfam; PF02878; PGM_PMM_1; 1.
DR Pfam; PF02879; PGM_PMM_II; 1.
DR Pfam; PF02880; PGM_PMM_III; 1.
DR PRINTS; PR00509; PGM_PMM.
DR PROSITE; PS00710; PGM_PMM; 1.
KW Complete_protome.
SQ SEQUENCE 451 AA; 49786 MW; F337BA57646E7269 CRC64;
Query Match 54.7%; Score 41; DB 17; Length 451;
Best Local Similarity 50.0%; Pred. No. 32;
Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
QY 1 MEKVQLTRSAIRAS 16
DB 435 MEKAEKLVDAIKRAS 450
RESULT 3
Q906Q3 PRELIMINARY; PRT; 527 AA.
ID Q906Q3
AC Q906Q3
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RNA-dependent RNA polymerase (fragment).
GN POL.
OS Grapevine leafroll-associated virus 1.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Closteroviridae;
OC Ampelovirus.
OX NCBI_TaxID=47985;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=20141373; PubMed=10675398;
RA Fazali C.F., Rezaian M.A.;
RT "Nucleotide sequence and organization of ten open reading frames in
RT the genome of Grapevine leafroll-associated virus 1 and identification
RL of three subgenomic RNAs.";
RL J. Gen. Virol. 81:605-615(2000).
DR EMBL; AF195822; AAF22738.1; -
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR GO; GO:0019079; P:viral genome replication; IEA.
DR InterPro; IPR001788; RNA_dep_RNAPol2.

DR InterPro; IPR007095; RNA_pol_DS_PS.
 DR InterPro; IPR007094; RNA_pol_PSVir.
 DR Pfam; PF00978; RNA_dep_RNAPol2; 1.
 KW RNA-directed RNA polymerase.
 FT NON_TER
 SQ SEQUENCE 527 AA; 59276 MW; C445CE1169B46132 CRC64;
 Query Match 53.3%; Score 40; DB 12; Length 527;
 Best Local Similarity 80.0%; Pred. No. 59;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 5 QYVLSAIRR 14
 DB 95 QVWRSAIRR 104
 ||:|||||
 ||:|||||

RESULT 4
 ID Q8CFM4 PRELIMINARY; PRT; 998 AA.
 AC Q8CFM4;
 DT 01-NAR-2003 (TrEMBLrel. 23, Created)
 DT 01-VAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]_
 RP SEQUENCE FROM N.A.
 RC STRAIN=CSYBL/6J; TISSUE=Breast tumor;
 RA Strausberg R.;
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBSJ databases.
 DR EMBL; BC013626; AAH13626.1; -
 DR InterPro; IPR008160; Collagen.
 DR Pfam; PF01391; Collagen; 12.
 KW Hypothetical protein.
 FT NON_TER
 SQ SEQUENCE 998 AA; 95451 MW; 2AB4BA953E7084A6 CRC64;
 Query Match 53.3%; Score 40; DB 11; Length 998;
 Best Local Similarity 42.9%; Pred. No. 1.2e+02;
 Matches 6; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

OY 1 MEKVQLTRSAIRR 14
 DB 974 METIQWISRSTLKR 987
 ||:|||||
 ||:|||||

RESULT 5
 ID Q87GQ3 PRELIMINARY; PRT; 1104 AA.
 AC Q87GQ3;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hypothetical protein.
 GN VPA122.
 OS Vibrio parahaemolyticus.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; Vibrrio.
 OX NCBI_TaxID=670;
 RN [1]_
 RP SEQUENCE FROM N.A.
 RC STRAIN=RIMD 2210633 / Serotype O3:K6;
 RX MEDLINE=22508454; PubMed=12620739;
 RA Maximo K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
 RA Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
 RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
 RT "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
 distinct from that of V. cholerae."
 RL Lancet 361:743-749(2003).
 DR EMBL; AP005088; BAC62605.1; -.

KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 1104 AA; 125574 MW; 61C89EE3AB30C5DD CRC64;
 Query Match 53.3%; Score 40; DB 16; Length 1104;
 Best Local Similarity 42.9%; Pred. No. 1.3e+02;
 Matches 6; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

OY 1 MEKVQLTRSAIRR 14
 DB 853 LSKIEHTPSAVRR 866
 ||:|||||
 ||:|||||

RESULT 6
 ID O58310 PRELIMINARY; PRT; 1108 AA.
 AC O58310;
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)
 DT 01-JAN-1999 (TrEMBLrel. 09, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE 1108AA long hypothetical cell division control protein.
 GN PH0606.
 OS Pyrococcus horikoshii.
 OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
 OC Pyrococcus.
 OX NCBI_TaxID=53953;
 RN [1]_
 RP SEQUENCE FROM N.A.
 RC STRAIN=OT3;
 RX MEDLINE=98344137; PubMed=9679194;
 RA Kawarabayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
 RA Yamamoto S., Sekine M., Baba S.-I., Koeugi H., Hosoyama A., Nagai Y.,
 RA Sakai M., Ogura K., Osuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
 RA Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
 RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
 RA Masuchi Y., Shizuya H., Kikuchi H.;
 RT "Complete sequence and gene organization of the genome of a hyper-
 thermophilic archaeobacterium, Pyrococcus horikoshii OT3";
 RL DNA Res. 5:55-76(1998).
 DR EMBL; AP000003; BAA29695.1; -
 DR PIR; E71104; E71104.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0008094; F:DNA dependent ATPase activity; IEA.
 DR GO; GO:0000910; P:cytokinesis; IEA.
 DR GO; GO:0006270; P:DNA replication initiation; IEA.
 DR GO; GO:0016539; P:protein splicing; IEA.
 DR InterPro; IPR003586; Hedgehog_hintC.
 DR InterPro; IPR003587; Hedgehog_hintN.
 DR InterPro; IPR006142; Intein.
 DR InterPro; IPR001208; Intein_S.
 DR InterPro; IPR001208; MCM_2.
 DR InterPro; IPR008045; MCM_2.
 DR Pfam; PF00493; MCM; 1.
 DR PRINTS; PR00379; INTEIN.
 DR PRINTS; PR01657; MCMFAMILY.
 DR PRINTS; PR01658; MCMFAMILY.
 DR PRINTS; PR01658; MCMFAMILY.
 DR PRODOR; PD001041; MCM; 2.
 DR SMART; SM00305; HintC; 2.
 DR SMART; SM00306; HintN; 2.
 DR SMART; SM00350; MCM; 1.
 DR TIGRFAMs; TIGR01443; Intein_Cterm; 2.
 DR TIGRFAMs; TIGR01445; Intein_Nterm; 2.
 DR PROSITE; PS50818; INTEIN_CTER; 2.
 DR PROSITE; PS50817; INTEIN_NTER; 2.
 DR PROSITE; PS50051; MCM_2_3.
 KW Cell division, Complete proteome.
 SQ SEQUENCE 1108 AA; 125967 MW; 92D2578B31351F75 CRC64;
 Query Match 53.3%; Score 40; DB 17; Length 1108;
 Best Local Similarity 53.3%; Pred. No. 1.3e+02;
 Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

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Query Match 52.0%; Score 39; DB 16; Length 406;
Best Local Similarity 75.0%; Pred. No. 70;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRA 15
||| ||| ||| ||| |||
Db 668 MEKVQYLTRSAIRRA 682

RESULT 7
Q9A0Y9 PRELIMINARY; PRT; 364 AA.
AC Q9A0Y9;
DT 01-JUN-2001 (TREMELrel. 17, Created)
DT 01-JUN-2001 (TREMELrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMELrel. 19, Last annotation update)
DE Hypothetical protein SPY0549.
GN SPY0549.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SF370 / ATCC 700294 / Serotype M1;
RC MEDLINE=21192684; PubMed=11296236;
RA Ferrer J.J., McShan W.M., Ajdic D.J., Savic G., Lyon K.,
RA Primeaux C., Szatse S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,
RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
RA "Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663 (2001).
RL EMBL; AE006512; AAK33542.1; -.
DR Hypothetical protein; Complete proteome.
SQ SEQUENCE 364 AA; 41754 MW; 038B8D36F4234020 CRC64;

Query Match 52.0%; Score 39; DB 16; Length 364;
Best Local Similarity 53.8%; Pred. No. 62;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 EKQVYLRSAIRRR 14
||| ||| ||| |||
Db 307 EKQVYLRSAIRRR 319

RESULT 8
Q88LL1 PRELIMINARY; PRT; 406 AA.
AC Q88LL1;
DT 01-JUN-2003 (TREMELrel. 24, Created)
DT 01-JUN-2003 (TREMELrel. 24, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE Hypothetical protein.
GN PP1920.
OS Pseudomonas putida (strain KT2440).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=160486;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=22423060; PubMed=12534463;
RA Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
RA Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
RA Brinkac L., Beanan M., DeBoy R.T., Daugherty S., Kolonay J.,
RA Madupu R., Nelson W., White O., Peterson J., Khouri H., Hance I.,
RA Chris Lee P., Holtzapple E., Scanlan D., Tran K., Moazzaz A.,
RA Utterback T., Rizzo M., Lee K., Kosack D., Mostl D., Wedler H.,
RA Lauber J., Stjepandic D., Hohnselt J., Straetz M., Heim S.,
RA Kievtz C., Eisen J., Timmis K.N., Duesterhoeft A., Tuemmler B.,
RA Fraser C.M.;
RA "Complete genome sequence and comparative analysis of the
RT metabolically versatile Pseudomonas putida KT2440.";
Environ. Microbiol. 4:799-808 (2002).
RL EMBL; AE016781; AAN67537.1; -.
DR TIGR; PP1920; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 406 AA; 47318 MW; 7CDBC30DFD0D3C6E2 CRC64;

Query Match 52.0%; Score 39; DB 2; Length 421;
Best Local Similarity 50.0%; Pred. No. 73;
Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRA 16
||| ||| ||| |||
Db 6 MEKVQYLTRSAIRRA 21

RESULT 10
Q9VID2 PRELIMINARY; PRT; 481 AA.
AC Q9VID2;
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE Hypothetical protein PYAB04950.
GN PYAB04950 OR PA50334.
OS Pyrococcus abyssi.
OC Archaea; Euryarchaeota; Thermococci; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=29292;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GES / Orsay;
RA Heilig R.;
RA "Pyrococcus abyssi genome sequence: insights into archaeal chromosome
RT structure and evolution.";
Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RL EMBL; A0248284; CAB49417.1; -.
DR PIR; B75167; B75167.

Query Match 52.0%; Score 39; DB 16; Length 406;
Best Local Similarity 75.0%; Pred. No. 70;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 KQVYLRSAIRR 14
||| ||| ||| |||
Db 273 KQVYLRSAIRR 284

RESULT 9
Q9AM36 PRELIMINARY; PRT; 421 AA.
AC Q9AM36;
DT 01-JUN-2001 (TREMELrel. 17, Created)
DT 01-JUN-2001 (TREMELrel. 17, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE [Fe] hydrogenase large subunit.
GN HYDA.
OS Desulfovibrio desulfuricans.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales;
OC Desulfovibrionaceae; Desulfovibrio.
OX NCBI_TaxID=876;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=G20;
RA Ringbauer J.A. Jr., Wall J.D.;
RA "[Fe] hydrogenase of Desulfovibrio desulfuricans G20.";
Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF331719; AAK11625.1; -.
DR HSSP; P00193; 1DUR.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR001450; 4Fe4S ferredoxin.
DR InterPro; IPR009016; Fe_hydrog.
DR InterPro; IPR004108; Fe_hyd_1g_C.
DR Pfam; PF000037; Ier4; 2.
DR Pfam; PF02906; Fe_hyd_1g_C; 1.
DR PROSITE; PS00198; 4Fe4S_FERREDOXIN; 2.
KW 4Fe-4S; Iron; Iron-sulfur.
SQ SEQUENCE 421 AA; 46120 MW; 1116557AB0C94219 CRC64;

Query Match 52.0%; Score 39; DB 2; Length 421;
Best Local Similarity 50.0%; Pred. No. 73;
Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 MEKVQYLTRSAIRRA 16
||| ||| ||| |||
Db 6 MEKVQYLTRSAIRRA 21

RESULT 10
Q9VID2 PRELIMINARY; PRT; 481 AA.
AC Q9VID2;
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE Hypothetical protein PYAB04950.
GN PYAB04950 OR PA50334.
OS Pyrococcus abyssi.
OC Archaea; Euryarchaeota; Thermococci; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=29292;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GES / Orsay;
RA Heilig R.;
RA "Pyrococcus abyssi genome sequence: insights into archaeal chromosome
RT structure and evolution.";
Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RL EMBL; A0248284; CAB49417.1; -.
DR PIR; B75167; B75167.

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DR GO: GO:0015020; C-membrane; IEA.
DR GO: GO:0005267; P-potassium channel activity; IEA.
DR GO: GO:0006813; P-potassium ion transport; IEA.
DR InterPro: IPR001622; K-channel pore.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 481 AA; 55655 MW; 685FE30056A45259 CRC64;

Query Match 52.0%; Score 39; DB 17; Length 481;
Best Local Similarity 50.0%; Pred. No. 84;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 EKQVQLTRSAIRRA 15
DQ 38 EKIKYKRAFERA 51

RESULT 11
Q86808 PRELIMINARY; PRT; 644 AA.
AC Q86808;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Beta-/gamma-plaetin precursor.
OS Euploties sediculatus.
OC Eukaryota; Alveolata; Ciliophora; Spirotrichea; Hypotrichia;
OC Euplotida; Euplotidae; Euploties.
OX NCBI_TaxID=5940;
RN [1] SEQUENCE FROM N.A.
RP SEQUENCE FROM N.A.
RX PubMed12615971;
RA Klotzel J.A., Baroin-Tourancheau A., Miceli C., Barchetta S.,
RA Farmer J., Banerjee D., Fleury-Aubusson A.;
RT "Cytoskeletal proteins with N-terminal signal peptides: plateins in
RT the ciliate Euploties define a new family of articularins.";
RN [2] J. Cell Sci. 116:1291-1303(2003).
RP SEQUENCE FROM N.A.
RX MEDLINE=22559397; PubMed=12674476;
RA Klotzel J.A., Baroin-Tourancheau A., Miceli C., Barchetta S.,
RA Farmer J., Banerjee D., Fleury-Aubusson A.;
RT "Plateins: a novel family of signal peptide-containing articularins in
RT euplotid ciliates.";
RL J. Eukaryot. Microbiol. 50:19-33(2003).
DR EMBL; AY124991; AAM94464.1; -.
KW SIGNAL.
FT SIGNAL.
SQ SEQUENCE 644 AA; 74972 MW; 7298E314BFB7417A CRC64;

Query Match 52.0%; Score 39; DB 5; Length 644;
Best Local Similarity 54.5%; Pred. No. 1.le-02;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 3 KQVQLTRSAIR 13
DQ 395 EIQVYTVRAVR 405

RESULT 12
Q26525 PRELIMINARY; PRT; 119 AA.
AC Q26525;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein MTH425.
GN MTH425.
OS Methanobacterium thermoautotrophicum.
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
OC Methanobacteriaceae; Methanothermobacter.
OX NCBI_TaxID=187420;
RN [1] SEQUENCE FROM N.A.
RP SEQUENCE FROM N.A.

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RC STRAIN=Delta H;
RA MEDLINE=98037514; PubMed=9371463;
RA Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,
RA Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
RA Harrison D., Hoang L., Keagle P., Lumm W., Pochier B., Qiu D.,
RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
RA Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabakar S.,
RA McQuigall S., Shimer G., Goyal A., Pietrowski S., Church G.M.,
RA Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
RT "Complete genome sequence of Methanobacterium thermoautotrophicum
RT deltaH: functional analysis and comparative genomics.";
RL J. Bacteriol. 179:7135-7155(1997).
DR EMBL; AE000827; AAB84931.1; -.
DR PIR; D69155; D69155.
DR GO: GO:0005874; C-microtubule; IEA.
DR GO: GO:0005525; F:GTP binding; IEA.
DR GO: GO:0005198; F:structural molecule activity; IEA.
DR GO: GO:0007018; P:microtubule-based movement; IEA.
DR InterPro: IPR002453; Beta tubulin.
KW PROSITE; PS00228; TUBULIN_B_AUTOREG; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 119 AA; 13045 MW; DE5119ED7630F098 CRC64;

Query Match 50.7%; Score 38; DB 17; Length 119;
Best Local Similarity 37.5%; Pred. No. 29;
Matches 6; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 MEKVQVLTSAIRAS 16
DQ 35 MDNIMYLTQSTVYQSS 50

RESULT 13
Q974N9 PRELIMINARY; PRT; 122 AA.
AC Q974N9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein ST0620.
GN ST0620.
OS Sulfolobus tokodaii.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OX NCBI_TaxID=111955;
RN [1] SEQUENCE FROM N.A.
RP SEQUENCE FROM N.A.
RX STRAIN=JCM 10545 / 7;
RX MEDLINE=21456156; PubMed=11572479;
RA Kawarabayashi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
RA Sekine M., Baba S.-I., Aikai A., Kosugi H., Hosoyama A., Fukui S.,
RA Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
RA Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
RA Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
RA Oshima T., Kikuchi H.;
RT "Complete genome sequence of an aerobic thermoacidophilic
RT Crenarchaeon, Sulfolobus tokodaii strain7.";
RL DNA Res. 8:123-140(2001).
DR EMBL; AP000983; BAB65618.1; -.
DR InterPro: IPR008301; UCP016498.
DR PIRSF; PIRSF016498; UCP016498; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 122 AA; 14467 MW; 988A31A274842EB3 CRC64;

Query Match 50.7%; Score 38; DB 17; Length 122;
Best Local Similarity 42.9%; Pred. No. 30;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 MEKVQVLTSAIR 14
DQ 26 MKKIKYLTBEALMK 39

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RESULT 14

Q89J03 PRELIMINARY; PRT; 208 AA.
 ID Q89J03
 AC Q89J03
 DT 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Bll5481 protein.
 GN Bll5481
 OS Bradyrhizobium japonicum.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Bradyrhizobiaceae; Bradyrhizobium.
 CX NCBI_TaxID=375;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=USDA 110;
 RX MEDLINE=22484998; PubMed=12597275;
 RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiyama T.,
 RA Sasamoto S., Watanabe A., Idesawa K., Iriiguchi M., Kawashima K.,
 RA Kohara M., Matsumoto M., Shimpou S., Tsuruoka H., Wada T., Yamada M.,
 RA Tabata S.;
 RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
 Bradyrhizobium japonicum USDA110.";
 RL DNA Res. 9:189-197(2002).
 DR EMBL; AP005955; BAC50746.1; -.
 KW Complete proteome.
 SQ SEQUENCE 208 AA; 22494 MW; E461C88B14783C7A CRC64;

Query Match 50.7%; Score 38; DB 16; Length 208;
 Best Local Similarity 72.7%; Pred. No. 53;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 QYLTRSAIRRA 15
 DB 74 CELTRALERA 84

RESULT 15

Q7UFR1 PRELIMINARY; PRT; 211 AA.
 ID Q7UFR1
 AC Q7UFR1
 DT 01-OCT-2003 (TREMBlrel. 25, Created)
 DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Thymidine kinase Tdk (EC 2.7.1.21).
 GN TDK OR RB8399.
 OS Rhodospirillum rubrum.
 OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
 OC Planctomycetaceae; Pirellula.
 CX NCBI_TaxID=117;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1;
 RX MEDLINE=22735913; PubMed=2835416;
 RA Glickner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
 RA Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,
 RA Schlesner H., Aumann R., Reinhardt R.;
 RT "Complete genome sequence of the marine planctomycete Pirellula sp.
 strain 1.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
 DR EMBL; BX294147; CAD78621.1; -.
 KW Kinase; Transferase; Complete proteome.
 SQ SEQUENCE 211 AA; 23976 MW; 2FF54BF18F094376 CRC64;

Query Match 50.7%; Score 38; DB 16; Length 211;
 Best Local Similarity 37.5%; Pred. No. 54;
 Matches 6; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 1 MEKQYLTRSAIRRAS 16
 DB 86 VDEAQFLTRTQVRQLS 101

RESULT 16

Q9HF62 PRELIMINARY; PRT; 252 AA.
 ID Q9HF62
 AC Q9HF62
 DT 01-WAR-2001 (TREMBlrel. 16, Created)
 DT 01-WAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE YCLO16C (Fragment).
 GN YCLO16C.
 OS Ashbya gossypii (Yeast) (Eremothecium gossypii).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Ashbya.
 CX NCBI_TaxID=33169;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wendland J., Philippsen P.;
 RT "Isolation and characterization of the Ashbya gossypii BUD3 gene.";
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF210625; AAG41241.1; -.
 FT NON_TER 252
 SQ SEQUENCE 252 AA; 27793 MW; 20B2C7F284042B76 CRC64;

Query Match 50.7%; Score 38; DB 3; Length 252;
 Best Local Similarity 54.5%; Pred. No. 66;
 Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 EKQYLTRSAI 12
 DB 228 ERIQYLSRSTL 238

RESULT 17

Q99ZW6 PRELIMINARY; PRT; 376 AA.
 ID Q99ZW6
 AC Q99ZW6
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Putative coproporphyrinogen III oxidase (EC 1.3.3.3).
 GN HEMN OR SPV1040.
 OS Streptococcus pyogenes.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 CX NCBI_TaxID=1314;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SF370 / ATCC 700294 / Serotype M1;
 RX MEDLINE=21192864; PubMed=11298296;
 RA Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
 RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
 RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,
 RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
 RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
 DR EMBL; AB006549; AAK3932.1; -.
 DR GO; GO:0005737; Cytoplasm; IEA.
 DR GO; GO:0004103; F:coproporphyrinogen oxidase activity; IEA.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR GO; GO:0006779; P:porphyrin biosynthesis; IEA.
 DR InterPro; IPR006638; Elp3.
 DR InterPro; IPR004559; HmnN rel.
 DR InterPro; IPR007197; Radical SAM.
 DR Pfam; PF04055; Radical SAM; 1.
 DR SMART; SM00729; Elp3; 1.
 DR TIGRPFAM; TIGR00539; hmnN rel; 1.
 KW Oxidoreductase; Complete proteome.
 SQ SEQUENCE 376 AA; 43111 MW; 737548C68DB358E3 CRC64;

Query Match 50.7%; Score 38; DB 16; Length 376;
 Best Local Similarity 53.3%; Pred. No. 1e+02; 5; Indels 0; Gaps 0;
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 EKQYLTRSAIRRAS 16

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Db 102 EKIAVLQSAVNRI 116
||: ||||: ||
Query Match 50.7%; Score 38; DB 16; Length 398;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

RESULT 18
Q8P177 PRELIMINARY; PRT; 376 AA.
ID Q8P177
AC Q8P177;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Putative coproporphyrinogen III oxidase.
GN HEMN OR SPYM18_1022.
OS Streptococcus pyogenes (serotype M18).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=186103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS8232 / Serotype M18;
RX MEDLINE=21927593; PubMed=11917108;
RA Smoot J.C., Barbican K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S.,
RA Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F.,
RA Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,
RA Kapur V., Daly J.A., Veasy L.G., Musser J.M.;
RT "Genome sequence and comparative microarray analysis of serotype M18
RT group A Streptococcus strains associated with acute rheumatic fever
RT outbreaks";
RT Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673 (2002).
DR EMBL; AE010030; AAL97657.1; -.
DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:0004109; F:coproporphyrinogen oxidase activity; IEA.
DR GO; GO:0006779; P:porphyrin biosynthesis; IEA.
DR InterPro; IPR004559; HemN_rel.
DR InterPro; IPR007197; Radical_SAM.
DR Pfam; PF04055; Radical_SAM; I.
DR TIGRFAMs; TIGR00539; hemN_rel; 1.
DR Complete proteome; Hypothetical protein.
KW SEQUENCE 376 AA; 43093 MW; 7236F821EB82BEE5 CRC64;

Query Match 50.7%; Score 38; DB 16; Length 376;
Best Local Similarity 53.3%; Pred. No. 1e+02;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 EKVOYLTRSAIRAS 16
||: ||||: ||
Db 102 EKIAVLQSAVNRI 116

RESULT 19
Q878L1 PRELIMINARY; PRT; 398 AA.
ID Q878L1
AC Q878L1;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative coproporphyrinogen III oxidase.
GN SP51180.
OS Streptococcus pyogenes (serotype M3).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=198466;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SSI-1 / Serotype M3;
RA Nakagawa I., Kurokawa K., Nakata M., Tomiyasu Y., Yamashita A.,
RA Yamazaki K., Okahashi N., Kawabata S., Yasunaga T., Hattori M.,
RA Hayashi H., Hamada S.;
RT "The genome of invasive Streptococcus pyogenes; a comparative analysis
RT of S. pyogenes SSI-1, SP370 and MGAS8232.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP005144; BAC64275.1; -.
DR InterPro; IPR007197; Radical_SAM.

DR Pfam; PF04055; Radical_SAM; 1.
SQ SEQUENCE 398 AA; 45841 MW; 669A0563D1206261 CRC64;

Query Match 50.7%; Score 38; DB 16; Length 398;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 EKVOYLTRSAIRAS 16
||: ||||: ||
Db 134 EKIAVLQSAVNRI 148

RESULT 20
Q8K7R5 PRELIMINARY; PRT; 408 AA.
ID Q8K7R5
AC Q8K7R5;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Putative coproporphyrinogen III oxidase.
GN HEMN OR SPYM3_0673.
OS Streptococcus pyogenes (serotype M3).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=198466;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS315 / Serotype M3;
RX MEDLINE=22133808; PubMed=12122206;
RA Beres S.B., Sylva G.L., Barbican K.D., Lei B., Hoff J.S.,
RA Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D.,
RA Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
RA Schlievert P.M., Musser J.M.;
RT "Genome sequence of a serotype M3 strain of group A Streptococcus:
RT phage-encoded toxins, the high-virulence phenotype, and clone
RT emergence.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083 (2002).
DR EMBL; AE014150; AAM79280.1; -.
DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:0004109; F:coproporphyrinogen oxidase activity; IEA.
DR GO; GO:0006779; P:porphyrin biosynthesis; IEA.
DR InterPro; IPR006638; Elp3.
DR InterPro; IPR004559; HemN_rel.
DR InterPro; IPR007197; Radical_SAM.
DR Pfam; PF04055; Radical_SAM; I.
DR SMART; SM00729; Elp3; I.
DR TIGRFAMs; TIGR00539; hemN_rel; 1.
DR Complete proteome; Hypothetical protein.
KW SEQUENCE 408 AA; 46987 MW; C3113FBA0B1A5AD CRC64;

Query Match 50.7%; Score 38; DB 16; Length 408;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 EKVOYLTRSAIRAS 16
||: ||||: ||
Db 134 EKIAVLQSAVNRI 148

RESULT 21
Q9F8B7 PRELIMINARY; PRT; 578 AA.
ID Q9F8B7
AC Q9F8B7;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE DeoR regulator.
OS Streptococcus agalactiae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1311;
RN [1]
RP SEQUENCE FROM N.A.
```

EX MEDLINE=20402586; PubMed=10944228;
RA Lachenauer C.S., Creti R., Michel J.L., Madoff L.C.;
RT "Mosaicism in the alpha-like protein genes of group B streptococci.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:9630-9635(2000).
CC -1- SIMILARITY: BELONGS TO THE DEOR FAMILY OF TRANSCRIPTIONAL
CC REGULATORS.
DR EMBL; AF248038; AAG09976.1; -;
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR InterPro; IPR001034; HTH_Deor.
DR Pfam; PF00455; deor_1.
DR SMART; SM00420; HTH_Deor; 1.
DR PROSITE; PS00894; HTH_Deor_FAMILY; 1.
KW DNA-binding; Transcription; Transcription regulation.
SQ SEQUENCE 578 AA; 66770 MW; CIDE74FB5943B8E3 CRC64;

Query Match 50.7%; Score 38; DB 2; Length 578;
Best Local Similarity 50.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 3 KVVYLTRSAIRRAS 16
Db 306 KIQLTRQFIQIS 319

RESULT 22
Q84SQ7 PRELIMINARY; PRT; 882 AA.
AC Q84SQ7;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein OSUNB0047D08.27.
GN OSUNB0047D08.27.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Euphorbiaceae; Oryzaeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Buell C.R., Yuan Q., Qiyang S., Liu J., Gansberger K., Jones K.M.,
RA Overton II L.L., Tsitrin T., Kim M.M., Bera J.J., Jin S.S.,
RA Fadrosch D.W., Tallon L.J., Koo H., Zismann V., Heiao J., Blunt S.,
RA Vanaken S.S., Riedmuller S.B., Uterback T.T., Feldblyum T.V.,
RA Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J.,
RA White O., Salzberg S.L., Fraser C.M.;
RT "Oryza sativa chromosome 3 BAC OSUNB0047D08 genomic sequence.";
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Buell R.;
RL EMBL; AC137925; AAO73264.1; -;
KW Hypothetical protein.
SQ SEQUENCE 882 AA; 96573 MW; 5CDCB01A2569CEC0 CRC64;

Query Match 50.7%; Score 38; DB 10; Length 882;
Best Local Similarity 56.2%; Pred. No. 2.5e+02;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 MEKVYLTRSAIRRAS 16
Db 300 VEYSQLTRQAARRAN 315

RESULT 23
Q8MMG5 PRELIMINARY; PRT; 1223 AA.
ID Q8MMG5

AC Q8MMG5;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to Homo sapiens (Human). similar to SWI/SNF related, matrix
DE associated, actin dependent regulator of chromatin, subfamily C,
DE member 1.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AX4;
RX MEDLINE=22092622; PubMed=12097910;
RA Glockner G., Eichinger L., Szafranski K., Pachebat J., Dear P.,
RA Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K.,
RA Tunngal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.;
RT "Sequence and analysis of chromosome 2 of Dictyostelium discoideum.";
RL Nature 418:79-85(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AX4;
RA Baumgart C.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC116989; AAM43749.2; -;
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001005; Myb_DNA_binding.
DR InterPro; IPR001673; S_mold_repeat.
DR Pfam; PF00526; S_mold_repeat; 13.
DR SMART; SM00717; SANT; 1.
DR PROSITE; PS00090; MYB_3; 1.
SQ SEQUENCE 1223 AA; 136240 MW; B7D92B2925F39C72 CRC64;

Query Match 50.7%; Score 38; DB 5; Length 1223;
Best Local Similarity 80.0%; Pred. No. 3.6e+02;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 QYLTRSAIRR 14
Db 696 QYLTLTAIRR 705

RESULT 24
Q8DJ60 PRELIMINARY; PRT; 1541 AA.
ID Q8DJ60;
AC Q8DJ60;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Ferredoxin-dependent glutamate synthase.
DE GLSF OR TLL1368.
GN Synechococcus elongatus (Thermosynechococcus elongatus).
OS Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
OX NCBI_TaxID=32046;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BF-1;
RX MEDLINE=22225144; PubMed=12240834;
RA Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S.,
RA Watanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y.,
RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Nakazaki N.,
RA Shimo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the thermophilic cyanobacterium
Thermosynechococcus elongatus BP-1.";
RL Nature Res. 9:123-130(2002).
RL EMBL; AF005373; BAC08920.1; -;
DR GO; GO:0015930; F:glutamate synthase activity; IEA.
DR GO; GO:0006537; P:glutamate biosynthesis; IEA.
DR GO; GO:0006807; P:nitrogen metabolism; IEA.
DR InterPro; IPR002489; DUFL4.
DR InterPro; IPR002932; Glu_synthase.
DR InterPro; IPR006982; Glu_synth_cent.

DR InterPro: IPR006981; Glu synth_NTN.
DR Pfam: PF01645; Glu synthase; 1.
DR Pfam: PF04897; Glu synth_NTN; 1.
DR Pfam: PF04898; Glu synth_central; 1.
DR Pfam: PF01493; GXGXG; 1.
KW Complete proteome.
SQ SEQUENCE 1541 AA; 168017 MW; 9CB26077859306A6 CRC64;

Query Match 50.7%; Score 38; DB 16; Length 1541;
Best Local Similarity 53.3%; Pred. No. 4.6e+02;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 MEKQVLTRESAIRRA 15
: : : : :
Db 162 LERQLYLRKRRIERA 176

RESULT 25

O7UWM3 PRELIMINARY; PRT; 68 AA.
ID Q7UWM3
AC Q7UWM3; 01-OCT-2003 (Tremblrel. 25, Created)
DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Hypothetical protein.
GN R51931
OS Rhodospirillum rubrum.
OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
OC Planctomycetaceae; Pirellula.
OX NCBI_TaxID=117;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1;
RX MEDLINE=22735913; PubMed=12835416;
RA Gloeckner F.C.; Kube M.; Bauer M.; Teeling H.; Lombardot T.;
RA Ludwig W.; Gade D.; Beck A.; Borzym K.; Heitmann K.; Rabus R.;
RA Schlesner H.; Amann R.; Reinhardt R.;
RT "Complete genome sequence of the marine planctomycete Pirellula sp.
RT strain 1."
RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
DR EMEL; BX294136; CAD72339.1; -
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 68 AA; 7494 MW; 7EC1DF98DB5F67C CRC64;

Query Match 50.0%; Score 37.5; DB 16; Length 68;
Best Local Similarity 56.7%; Pred. No. 20;
Matches 10; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

QY 3 KVQVLTRESAI-REAS 16
: : : : :
Db 44 KLTFLSRSAISRAS 58

Search completed: October 1, 2004, 12:17:35
Job time : 50.8 secs

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